

24074

## SEARCH REQUEST FORM

Examiner # (Mandatory): 77334 Requester's Full Name: Karen LacoursiereArt Unit 1635 Location (Bldg/Room#): CM 11009 Phone (circle 305 306 308) 7523  
(mail box HICKEY)Serial Number: 09/383,894 Results Format Preferred (circle): PAPER DISK E-MAILTitle of Invention I Type Calcium ChannelInventors (please provide full names): Ming LiEarliest Priority Date: 8-26-98

Keywords (include any known synonyms registry numbers, explanation of initialisms):

Please search SQID No's 1-2

PCTUS99

RECEIVED  
JAN 12 2000  
(STIC)

## Search Topic:

Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s).

PLEASE RUSH.  
(SHORT DOCKET)May Elliott

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## STAFF USE ONLY

Searcher: HARTSearcher Phone #: 305-9203Searcher Location: 12C14Date Picked Up: 1/13/00Date Completed: 1/19/00Clerical Prep Time: 5Terminal Time: 10Number of Databases: 11

## Type of Search

1 N.A. Sequence1 A.A. Sequence

Structure (#)

Bibliographic

Litigation<sup>1</sup>

Fulltext

Procurement

Other

## Vendors (include cost where applicable)

STN

Questel/Orbit

Lexis/Nexis

WWW/Internet

X In-house sequence systems (list)

Dialog

Dr. Link

Westlaw

Other (specify)

A0502



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2000, 23:06:38 ; Search time 2469.38 Seconds

(without alignments) 12344.368 Million cell updates/sec

Title: PCT-US99-19675-1

Sequence: 1 atgacgagagagagagatgctg.....gtcccgacacagagctg 7129

Scoring table: IDENTITY\_NUC

Searched: 780561 seqs, 2137953050 residues

Database: GenEmbl.\*

Word size: 0

Number of hits that pass the threshold: 1561122

1: gb\_dal.\*  
2: gb\_dal.\*  
3: gb\_dal.\*  
4: gb\_dal.\*  
5: gb\_dal.\*  
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40: gb\_dal.\*  
41: gb\_dal.\*  
42: gb\_dal.\*  
43: gb\_dal.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	7129	100.0	7286	12	AF125161	AF125161 Rattus no
2	6848.2	96.1	7542	12	RNCA1G	AF0272984 Rattus no
3	6556.8	92.0	7625	12	MW012569	AF012569 Mus muscu
4	5453.8	76.6	7274	41	AF126966	AF126966 Homo sapi
5	5444.2	75.4	7253	41	AF126965	AF126965 Homo sapi
6	3665.6	51.4	4903	9	AB012043	AB012043 Homo sapi
7	2309.6	32.1	7898	41	AF124351	AF124351 Homo sapi
8	2289.6	31.3	7761	11	AF073931	AF073931 Homo sapi
9	2231.2	26.2	5740	41	AF129133	AF129133 Homo sapi
10	1865.4	24.2	6503	12	AF086827	AF086827 Rattus no
11	1725.4	24.1	1344	41	HOMOCALC2	AF0292229 Homo sapi
12	1001.5	14.1	1479	41	HOMOCALC1	AF0292228 Homo sapi
13	792.2	11.1	1479	41	HOMOCALC1	AF0292228 Homo sapi
14	638	8.9	135259	1	AC004590	AC004590 Homo sapi
15	195.2	2.7	37297	33	HS30266	AL031703 Homo sapi
16	174.4	2.6	43589	35	CEIC54D2	U037548 Caenorhadi
17	168.4	2.4	7823	10	HDMKMA	M81758 Homo sapien
18	168.4	2.4	6957	12	RATNCVMS	M26643 Rat skeleta
19	163.3	2.4	5523	12	RNY17153	Y17153 Rattus norv
20	159.8	2.2	213721	10	HS172820	AL022319 Human DNA
21	159.8	2.2	6539	10	HSCACHA5	Z34813 H. sapiens (
22	159.8	2.2	6482	10	HSCACHA6	Z34814 H. sapiens (
23	153.4	2.2	6386	36	AC066915	U66915 Aplysia cal
24	153.4	2.2	7499	10	HDMCACH	L295229 Homo sapien
25	152.4	2.1	54589	33	HS357D8	AL031715 Homo sapi
26	150.2	2.1	6539	10	HSCACHA4	Z34812 H. sapiens (
27	148.8	2.1	6344	12	RNY53833	U53833 Rattus norv
28	145.6	2.0	6524	5	A58853	A58853 Sequence 1
29	145.6	2.0	6524	5	PNSNS	X92184 R. norvegicu
30	145.6	2.0	6096	36	BG073583	U73583 Blatella g
31	145.6	2.0	6096	36	BG073584	U73584 Blatella g
32	144.2	2.0	7545	12	RATSCAL	M27902 Rat cardiac
33	144	2.0	5505	3	ECU25990	U25990 Equus cabal
34	144	2.0	7052	5	A58857	A58857 Sequence 5
35	144	2.0	6527	5	A58859	A58859 Sequence 7
36	142.8	2.0	5068	35	BG071083	U71083 Blatella g
37	142.8	2.0	8608	3	OCBCB11	X67856 O. cuniculus
38	142.8	2.0	7792	3	OCBCB11	X67856 O. cuniculus
39	142.8	2.0	6566	10	HSCACHA13	Z34820 H. sapiens (
40	141.6	2.0	6515	10	HSCACHA1	Z34809 H. sapiens (
41	141	2.0	6160	10	HUMCACHA	L33796 Human dilyd
42	140.8	2.0	6036	9	HSAD4874	AJ224874 Homo sapi
43	140.8	2.0	5813	41	AF067227	AF067227 Homo sapi
44	138.8	1.9	6556	12	AF049239	AF049239 Rattus no
45	138.8	1.9	6586	12	AF049240	AF049240 Rattus no

# ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
1	AF125161	Rattus norvegicus T-type calcium channel mRNA, complete cds.	AF125161	94633669	AF125161.1	GI:4633669	Norway rat	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	Zhang, H., Hu, F., Bhattacharjee, A., Zhang, M., Wu, S., Berggren, P. and Li, M.	Cloning of a T-type Ca2+ channel isoform from a rat pancreatic b-cell line	Unpublished

*amino acid seq (see) for identity*





Db	1298	GTGGGCTCTTCTTCAATATCAACTGTGCTGGTGGTGGTGGCAAGTTCTCCGAG	1357
Qy	1201	accaaacagccgggagagatcagctgaatgcyggagacggtgtaagatthcgttccaatgct	1260
Db	1358	ACCAAAACACGGGAGAGTACAGCTGATGCGGGAGCAGCGTGAAGATTCCGTGCATATGT	1411
Qy	1261	agcaacccgtgaaagttctctctgagccaggaacgtgcataaagaagctactcaagtactg	1320
Db	1418	AGCAACCTTGCAAGCTTCTCTGAAGCAGGACGCTGTATAGGAGGATTAAGTCAAGTACGTg	1477
Qy	1321	gtgtacatctcccgaaagacagcccgaaagctgtggcccaagttccctaaggctataagcgtg	1380
Db	1478	GTTATCATCTCTCCGAAAAAGCAGGCCGGAAGGCTGGCCAGGTTCTTAAGGCTTAAGGCTGg	1537
Qy	1381	cggggctgggctctctgaagagcccaatggtcccgtaagtgtggcagaagcccaagccagtggtc	1440
Db	1538	CGGGCTGGGCTCTCAGACGCCACAGTGGCCCGTATGTGGGAGAGGCCACAGCCAGTGGC	1597
Qy	1441	agctggaactgcgtcacaccgctgcgtctgtctgtcccaaccctgtgtcaacacataaacac	1500
Db	1598	AGGTGACATCGGTCAACACGTCGTCTGTCTGTCCACACACTGGTCCACACATCAACAC	1657
Qy	1501	caacataccactacacaccctgtggttaatgtggagcgtcaagttcccccgggcccagccagag	1560
Db	1658	CACCATATCACCACTATCACCTGGGTAAATGGAGACGCTAGATTTCCCGGGCCAGCCAGAG	1717
Qy	1561	atccagagacaggaatgaccaatggtgtctccggcgctatgctaccacacccctacacc	1620
Db	1718	ATCCAGAGACAGGGAATGCCAATGGGTTCTGCGGCTATGTCTATGCACACACCTCTACACC	1777
Qy	1621	actccctctggggccctccgaggggtgtcgaggtctgtacacagacttctacatgtctac	1680
Db	1778	ACTCCCTCTGGGGGCCCTCCACGAGGGGTGCGAGATCTGTACACAGCTTACCATCTGTAC	1837
Qy	1681	tgcacactggagagccagtcacgtgtgtccaggaacccccctcccaagtcccatgcygaagcactc	1740
Db	1838	TGCCACTTGGAGCCAGTCCGTTGTCGAAGCACCCCTCTCCAGATGCCATTCGGAAGCACT	1897
Qy	1741	ggtaggactgtgggttaagtgtggaaggtgtuacccacactgtcatacagccctccacagag	1800
Db	1898	GGTAGACTGTGGGTAGTGGGAAGGTGTACCCACTGTGCATATCCAGGCCCTCCACAGAG	1957
Qy	1801	atactgaagagataaagaactagatgtggaggtgtgccccccagccctgtggcccccaacctaac	1860
Db	1958	ATACTGAAGATTAAGCACTAGTGAAGTGTGCCCCAGGCCCTGGGCCCCCCACCTCAACC	2017
Qy	1861	agcttcaacatcccaactgtggcccttaagctcatgtacaaagctctgtgagaacagagt	1920
Db	2018	AGCTTCACACATCCCAACCGTGGGCCCTTCACTCATTCACAAACTCTTGGAAACACAGAT	2077
Qy	1921	acggagagccctgcatatgctctctcgaaaatctccagccctgtgtccaaaggcagacagtgtga	1980
Db	2078	ACGGAGAGCTGCTCCATTAACCTCTCCAAATCTCTCAGGCCCTTGTCTCCAAAGCAGACAGTGA	2137
Qy	1981	gctgtcgggccggagacgttgttccctaactgtgcccgaagagggagggagagccgaagcttc	2040
Db	2138	GCTTGCGGGCGGAGCACTTCTCTACTGTGTGCCCGAGACAGGAGCAGGAGACCCAGATGCC	2197
Qy	2041	gtctgacatgtcatgctctgactcaagacagccgagatctgtgtatgaattcaacaagaagctc	2100
Db	2198	GCTGCACATGTCAATGCTGTGATCAGACACAGGAGGCTGTATGAATTCAACAGAGAGCT	2257
Qy	2101	cagcaacagttaacccctcggtgttcccaacagccggggcgagacagccgagacgtgtggcccaat	2160
Db	2258	CAGCAACAGTAACTCCCGGATCCCCACACACCGCGGCAACGGGAGGCTTGGGCCAGAT	2317
Qy	2161	gcagagacctagttctgtctgtgcttctctggaagctgtgactgtgtgaacatctcggaaagtc	2220
Db	2318	GCAAGAGCTATGTTCTGTGCTGCTGCTTCTGTGAGGCTGAATCTGTGAACATTCGGAATATC	2277
Qy	2221	gtagaagacaaatacttttggccggggaatcatgatacgccatcctgtgtcaataaacctagc	2280

Dh	2378	GTGATAGCAAACTACTTTGGCCGGGGAATCATGATCCGCAATCCTGGTCAATACACTAGC	2437
Qy	2281	atggagatcgagttacaaagagagaccgagagagttacaaagcccttggaaatcagcaac	2340
Dh	2438	ATGGCATGAGATTACCAGAGACAGCCGAGAGGTCTCAACACCCTCGAAATACAGAAC	2497
Qy	2241	atcgcttcacagacctctcgcccttggagatgtgtgtgaacctgtcttcaagtcgc	2400
Dh	2498	ATGCTTTCACAGAGCTCTGGCCCTTGAGAGTGTGTGAACGTGTGTCTACAGCTCC	2557
Qy	2401	tttggtgtaattaaataatccctacaacatttgaatgtatctgtgtgtcaatcaagt	2460
Dh	2358	TTTGGCTTAATTAAACAACTCCACAAATCTTTGATGTGTCTCATTTGTGCTACAGTGTG	2617
Qy	2461	tggagagattctgtggcgaagagaggtgtgacctgtcggtgtgtgtggagaccttcgacctgtg	2520
Lh	2618	TGGAGATGTGGCGACAGGAGGAGTGGCTGTGCGTGTGTGGACCTTCGGCTGTATG	2677
Qy	2521	cggtgtctgaagctgtgtgccttcctgtgcggccctgaagcgaagctgtgtgtgtcatg	2580
Dh	2678	CGGGTGTGAACCTGTGTCGCTTCTCCGGCCCTGAGCGACAGCTCGTGGTCTCATG	2737
Qy	2581	aagaccatggaacagttgtggcaacctttgtatgtctctaatctgttaactatctc	2640
Dh	2738	AGACATGAGAAAGTGGCCACCTTCTGATGCTCTCTATGTGTCTCATCTTCAATCTTC	2797
Qy	2641	agcatcttgggcatgatctctcttgtgttgaagtttcgcatcttgaacggatgtggagacag	2700
Dh	2798	AGCATCTCGGGATGTCATCTCTTTGGTTGCAAATGTCATGCAATGGAAGGATGGGACAG	2857
Qy	2701	ttggcgaacggaaagaatttgcagctccctgtcttggcattgttaactgtcttcaagatt	2760
Dh	2858	TTGCCAGACCGAAGAAATTTCGACTCCCTGCTGTGGCCATGTCATGTCTTTACAGATT	2917
Qy	2761	ctgaactcaggaagactgtgaataaagtccttacaagcgatgtgcctcacatctgtcttg	2820
Dh	2918	CTGACTTCAGGAAGCTGGAAATTAAGTCTCTACAAAGCATGGCTCCACATCGCTTTGG	2977
Qy	2821	gtgtgtcttaactatcagccctcaatgaccttlttggcaactatgtgtcttctaactgtgt	2880
Dh	2978	GCTGCTCTTACTTCAATGAGCCCTCATGACTTTTGGCAATATGTCCTTTTAACCTCTG	3037
Qy	2881	gttgcacattctcttggaaagattccagcgcaagaaatgtgaaacggagaaatgtgagat	2940
Dh	3038	GTGGCATTTCTTGTGGAAGATTCCAGGACAGAGAAATGGCAACGGGAAGATGCCAGT	3097
Qy	2941	ggacagtttaagctgtatctacgtctgtcctgtcaactctcaagggggagatgtccacaagtct	3000
Dh	3098	GGACAGTTTAACCTTATTCAGCTGACCTGTCAACTCTCAAGGGGGAGATGCCACAAATCT	3157
Qy	3001	gagttcaagagcctgtattctcttcttgcaccagtgtgtgtgtgtatgtggagaaagaagaagcgc	3060
Dh	3158	GAGTCAGAGCCTGATTTCTTTTGCCCATGTGTGATGTGATGGGACAGAAACAAACGCG	3217
Qy	3061	ttggcctctgtgtgcttgggaagaaacggtggaactcgaagaagacctttgcaacccctc	3120
Dh	3218	TTGGCCCTGGGTGCTTTGGGAGAACGCGGGAATACGAAAGAGCCTTTGGCACCCCTC	3277
Qy	3121	atcatcctaagagttgtggaacaaatgtactaaccacaagagctccagcaacagtgtgtggg	3180
Dh	3278	ATCATCCATACGGCTGCGACACCAAAATGTACTACCAACGAAGCTCCACACAGGTGTGGG	3337
Qy	3151	gaagacactgtgacctgtgtcttcagcgttaccagttagcagttgtgtcgcctgtgacctgtgagct	3240
Dh	3338	GAAACACATGGGCTCTGTGCTGTGAGCTATACAGTACAGTGGTTCGCTGAGCCTCGAGCT	3397
Qy	3241	gccacacatagatgtgaaatctccgcgaagtgtccgcgagctcccgcaagcttccctgtgaat	3300
Dh	3358	GCCACCATAGATGAAGAAATCTCCGCCAAATGTGCCACACTCCCGCACATCTCCCTGGAGT	3457
Qy	3301	ggcggaagcagctgtgacccagcagcgcttccagcgaagcagcctgtgscggggcccgagc	3360
Dh	3458	GGCGGAGAGAGCTGTGACACAGAGAGGCTTCACACAGAACTACTCTGGCTGCTCTCTTATCT	3517

QY	3361	ctaagcgagagagaccgagcgagcgagaggtccctgctgctgtgtgagagggccagag	3420
Db	3518	CTAAGCGAGAGAGCCGACCGGGAGCGGAGGTCCCTGCTGTGGAGAGGGCCAGAG	3577
QY	3421	agtaagataagagagaaagttcagaagagagacggcgagccagccagcgagctgacat	3480
Db	3578	AGTACAGATAGAGAGAAATTAGAAAGAGACCGGGCCAGGCCAGGAGTGCAT	3637
QY	3481	cgcacagggggttccttggaagtgagccaaagtctcttgacctcctgacatctg	3540
Db	3638	CGCCACAGGGGTTCTCTTGGAACGTGAGGCCAAGATTCTTTGACCTGCTGACACTGTG	3697
QY	3541	caggtgcggagggcgacacgcacagccagcgagctcgacgtccctcgtgacacaaag	3600
Db	3698	CAGGTGCCGGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCTGTGAGACCAAGAC	3757
QY	3601	tgtaatggcaagtcggtctcaaggcggtttggccgacacctgaaagactgatagccca	3660
Db	3758	TGTATGGCAAGTGGGCTTCAGGGCGGCTTTGGCCGCGACCTTAGACATGATGACCCCA	3817
QY	3661	ctggaatggagatgtagcaatgtatgaaggaactctgacaaggggaagcatacaagc	3720
Db	3818	CTGATGGGAGTATGACATGATGAGGAAATCTAGCAAAAGGGAAAGCATACAAACC	3877
QY	3721	tggtgcagatcccggtctcctgcctgtttggcgagcgagatcctggtcgagctatac	3780
Db	3878	TGGTCAGATCCCGGCTTCCGCTGTGGCGGAGACGAGATTCCGTGGTCCGCTCATATC	3937
QY	3781	ttctctctgataaggttcgtctcctgtgtgcacggatatacaaccacaagtggt	3840
Db	3938	TTCTCTCTGATGAAGGTTTCGTTCTCTGTGTACCGATATCACCAACAAAGTGT	3997
QY	3841	gaccaatggtgcctcgtatcatctctccaaactgatacaaatcgatagacgccc	3900
Db	3998	GACCATGTGTGTCCTGTCATCATTTCTCACTGATACCATCCATCCATGTAGAGGCCCC	4057
QY	3901	aaaatgtgcccccaaggcgctgagcgatcttcctaaccttcacaactactcaag	3960
Db	4058	AAAATGTACCCCAAGGGCTGACGGCATTTCTGACCTCTCCAACTACATCTTCAG	4117
QY	3961	gcagctctctagctgaaatgacagtgtaggtgtgtgacactggtgtgtgtttggag	4020
Db	4118	GCAGCTTCTTAGCTGAATGACAGTGAAGGTGATGCGCTGTGGCTTTGGGGAG	4177
QY	4021	caagcctacatcgcgacgaagtgtgaatgtgtgtgacggtgtgtgtgtctatccgtc	4080
Db	4178	CAGGCTACCTGTCGACGATGTGAATGTGTGACGGCTGTGTGTGTCTCATCTTCGTC	4237
QY	4081	atcgaatccctgtctccatgtctccgaacggtgcacaaagatctcttgcatgtgag	4140
Db	4238	ATCGAATCCTGTGTCTCATGTGTGTCCGACAGCGGACCAAGATCCTTGGCATGTGAGG	4297
QY	4141	gtgtgtcgagctgtgtggaacctgtgtcactcaaggttatcaagcgggcccgaagagctg	4200
Db	4298	GTGTGTGCGGCTCTCGGACCTGTGTCACCTAGGCTATCAGCCGGGGCCAGGGACTG	4357
QY	4201	aagctgtgtgtagaacctctgaftgcatccctcaaacccattgcaaatgtgtgcat	4260
Db	4358	AAGCTGTGTGATGAACCTCTATGTCAATCCCTCAAAACCATTTGGCAATTTGGTCATT	4411
QY	4261	tgtgtgtcctctcatcaatltttggaatctcggtgtgcaagctctcaagggaaatgc	4320
Db	4418	TGTTGTGCTTCTTTCATATTTTGTGAATTTCCGGGTGTGAGCTTCCTCAAGGGAAATTC	4477
QY	4321	tttgtgtgtcagaagtgtgaagacacaggaatacactaaacaaatccgaatcggtgagcc	4380
Db	4478	TTTGTTGTGTCAAGGTGTAGGACACCGAATCTACTAACAATTCGAGTCCGCTGAGGCC	4533
QY	4381	agctacgaatgtgtccggaacagtatacaatttgacaacctgtggcaggtctgtatgtcc	4444
Db	4538	AGCTACCAATGTGGTCCGACCAAGTACAACTTTGACAACTGGGGCCAGGCTTGATGTCC	4599

QY	4441	ctgttgctgtgctccccaaggatggttgggtgacatcatgatagtatggtcgtgatgct	4500
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Db	4898	ggcagctcagccagcgtctggttaagaagccagctgcaagccctactactctgactctcg	4957
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O	5281	gtctctggcctgtggaagctctctttggaagactgtgagatgtatgtagaacaaccccttfgaaggc	5340
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O	5401	tcctacttgtgtgaacaactgtgaatgttatatgaagagacacccctccggagactgtgacagag	5460
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O	5461	tcacactgtatacaactgttcatctccctcatctactattgttgccttgcgtctgaagcc	5520
D	5841	TCCACCTGCTAACAACCTGCTATCTCCCTATCTACTTTGTGTGCTGTGCTGACGGCC	5900
O	5521	caatttgtgtcgtgtcaacgtygttcatatgctgtgtctatgaagcacttggaaagaagcaac	5580
D	5901	CAATTGTGTCTGTGCTAAGTGTCTATATAGCTGTCTATGAAGCAGACTGGAAGAAGCAAC	5960
O	5581	aaagaggtccaaagagagccgagctccagagccgagctggagctgtgagatgtgaacgctc	5640



Db	5961	AAAGAGGCCAAGGAGGAGGAGGCGCTGAGAGGCGGACGCTGAGACTGGACATGAAAGACGCTC	6029
Oy	5641	agcccgagcccccaatcccccgcctgaggagagccctctctctgcccggggttgaagtttc	5700
Db	6021	AGCCCGAGGCCCCCACTCCCGGCTGGAGAGCCCTTCTCTGGCCCGGGGTGGAGGGTGTG	6080
Oy	5701	aacgctcttgacagccctaaagcctbgyggtctcaacacacactgtcccaattggaagcagc	5760
Db	6081	AACAGTACTGTACACCCCTTAGAGCCTGGGGGCTCCACACACACTGCGCCACTTGTGACACGC	6140
Oy	5761	tcggagcttctccctctgagacccccagaatgtatccccacccccgaagaagttgcaatgcc	5820
Db	6141	TCGGGCTTCTCTCTTGAGGACCCACGATGTAACCCACCCGAGAGGTGCCAATCCCC	6200
Oy	5821	ctagagaccagacccctgctgactgtgaggaagtctgtgtgcagccgagacgactctctgcc	5880
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Oy	5881	aatacacgctcaatgctgcgcaatggagagacgtcgtgaaagttcccttaagaaacaggggc	5940
Db	6261	AATGACACACTCATGTGCTCCGCAATGGAGACACTGCTGAGAGATCCTTAGACACAGGGGC	6320
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Db	6321	TGGGGGCTCCCCAAAGCCGACGTCAAGCTCCATCTTGTCCGTTACATCCCAACACACACAC	6380
Oy	6001	acacagctgacatccctacagcttcccaaaagatgctgacatactgctccgaagctatagggcc	6060
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Oy	6061	cccaacctgaggcgcaatccctaactaaccaccaactgagcgctcccctctgtgctcagag	6120
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Oy	6121	ccctcagcgcccgagcagcaataaagacgtcaactccctgtatgtgcaagggccctgtgtacg	6180
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Oy	6181	cgggagaagccctgtgtcaaggggtgagtgtgggcctctctgcctctgaaccggtctccatcc	6240
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Oy	6241	tctcggagcggtgtcgaagcatcccaagtgtaacagcgtctccgcatccagagcaaaatgcc	6300
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Oy	6301	aagacatctcgctctgccaagccctctgccagcgccctggaacccaagctbgygccaagacct	6360
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Oy	6361	ccagagaccagaagaacacatctagaagctbgaacagagaaactgaagctbgaattctcaagaaactc	6420
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Oy	6421	cttcccagcagcccgagaagaacccctcgtctcccaacggagacctgaagaagtgtacaagtta	6480
Db	6801	CTTCCCAACACCCAGGAAGAACCCCTGTTCCTCCACGGGACCTGAAGAAAGTCAAGTGTAT	6860
Oy	6481	gagaccccgagcttgcaagcgagcgcctgtgtgtcttgctatgataaagagagaaacaccc	6540
Db	6861	GAGACCCGAGACTCTGAGGCGGAGGCTTGGGTTCTGGCTAGATGAACAGCGGAGACACTCC	6920
Oy	6541	attctctgacgctctctgagacaggggtctcccaacccccgctatgttccaagccccccaagc	6600
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Oy	6601	ctcgggggcccacactctctgggggttctctbgyagacgggcctcaagaaaaaaacctcagccaccc	6660
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Oy	6661	agtatctctataagccccccggagaagcaaggtctcgggcccccatgagttcgtctgttc	6720
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[illegible]

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BASE COUNT 1552 a 2291 c 2136 g 1646 t  
ORIGIN

Query Match 92.0%; Score 6556.8; DB 12; Length 7625;  
Best Local Similarity 95.5%; Pred. No. 0;  
Matches 6846; Conservative 0; Mismatches 277; Indels 43; Gaps 8;

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QY 61 cagctcaacgagacctctccggggcccgagcgagggcgcgagggctcgacgaaaaagac 120  
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QY 241 ccgtggttcgagcagatcagtagtctgtcattcttctcaactgltgactctggatag 300  
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REFERENCE 1 (bases 1 to 7274)  
AUTHORS Nargeot,J., Montell,A., Menessier,G., Bourinet,E. and Lory,P.  
TITLE Cloning of a full length human alpha1g cDNA (alpha1g-a isoform)  
JOURNAL Unpublished  
2 (bases 1 to 7274)  
REFERENCE Montell,A., Menessier,G., Bourinet,E., Lory,P. and Nargeot,J.  
AUTHORS Direct Submission  
TITLE Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.  
JOURNAL 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France  
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ORIGIN

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 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 3993)  
 AUTHORS Toyota,M., Ho,C., Ohe-Toyota,M., Bayliss,S.B. and Issa,J.P.  
 TITLE Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant  
 methylation of its 5' CpG island in human tumors  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3993)  
 AUTHORS Toyota,M., Bayliss,S.B. and Issa,J.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JAN-1999) The Johns Hopkins Oncology Center, 424 N  
 Bond St., Baltimore, MD 21231, USA  
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OY	3361	ctaaagcggaggaagcccggaacggggagcgagtgcttccctgctctctctggagagggccagag	3420
DB	3658	CTGAAGCGGAGAAAGCCCAAGTGAAGAGCGGGGCTCCCTTGTGTGGGAAAGGCCAGAG	3717
OY	3421	agtcagagatagagaggaagaattccaagaagagagccgggccaagcccaagcaagatgacat	3480
DB	3718	AGCCAGAGATGAAGAGGAGACTCTGAAGAGAGAGAGCGGGCCAGCGCTCGCGGCAAGTATCCAT	3777
OY	3481	cgccacaggggttctccttggagacgttgagcccaagagttcccttggacctgcttacaactctg	3540
DB	3778	CGCCACAGGGGGTCCCTTGAGCGGAGAGGCCAAGAGTTCTTTGACTCTGCCACACACACTG	3837
OY	3541	casgtgcgggggcttgcacccgacaagccagcgcgcgagctcttgctcttgagacacaagac	3600
DB	3838	CAGATGCCAGGGGCTGCATCCCACTGCAAGTGGCGGAGGGGTCTGTCTTGACAGCACAGAGAC	3897
OY	3601	tgtaaattgcaagttcggtcttlaaggcgcttggcccgcaaccccttagagactgatacccccaa	3660
DB	3898	TGCATATGGCAAGTGGCTTCAAGGGCGCCCTGGCGGCGCTCTGCGGCTGTATGATACCCCCA	3957
OY	3661	ctgagtgagatataacaaatgatatgaagaaatctg	3696
DB	3958	CTGGATGGGATACGCCGATGTGACGAGGGGAAACTTG	3993







[illegible]

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QY	2085	gttcacacagagcgtctgaacagatgtacctccggatcc-----	2124
DB	2435	attcacgagagagctccggacaggtgacggctggagaccacacgacaccccggtggac	2494
QY	2124	-----ccaagccggcgcgagacgagagccttggcccaga	2159
DB	2495	ggaacacacagagccagagccagagccagaccccaacgcccggscacagacagagcagcccc	2554
QY	2160	tgacagagcctatgtctgtcttgctcttccttggagagcctgacgttgaacatctccggaagat	2219
DB	2555	ggggagagccagagctgagatggggccgctctgggtattccttcacgggcaagctggccgcgat	2614
QY	2220	cgtagatagaacaaacttggccgggggaatcatatgacgtcactccctggtcacaacactag	2279
DB	2615	cgtagacagcagacttctacgcccgtggacatcatgattgagccatctctttacacacctgag	2674
QY	2280	catggcatctgagtcacacagacagagccgagagctcacaacagcccttgaataatgaa	2339
DB	2675	catggcccttgagatccatcatgacagcccgagagctgacatactcttgagatcagaa	2734
QY	2340	catgctcttcaacagcctctctgcctcttgagagatgctgcgtcaaacctgtcttaagctcc	2399
DB	2735	catctgtttcacacagcattgtttgcctctggagatgctctgaaagcttgcctggcgccc	2794
QY	2400	cttggctacatlaagaatccctacaacatctttagatgtgcatcttgttcatcaatgt	2459
DB	2795	tctgtgcttactatccggaacccgtaacaaactcttcgacggcattatcgtgctatcagct	2854
QY	2480	gtggagagatgttgccagacagaggaagtgcctgtgctgagcgtgcagacctccgctat	2519
DB	2855	ctggagaaatcctggggcagcggacggaacgtgctgtctgtctgctgcgcaccttccgctct	2914
QY	2520	gcggagctctgaagctgtgtgcgtctctctgcgcgcctgcagcgccagcagctcgtgtgtcat	2579
DB	2915	gcggtgtgtgaagctgtgctgcgttctctgcacgcccctgcgcgcagcctgtgctctgt	2974
QY	2580	gaaacacatgacagagctgacacctctgcacatgcgtcccatgctgcttcatctcatctt	2639
DB	2975	gaagacatgacacactggctacttcttgcacagcctgcctcatgctcttcatcttcatctt	3034
QY	2640	cagcactcctgggaatgcatctcttggttgcaagctgcacatctgaacggga---tg99ga	2696
DB	3035	cagatctctgggcattgacaccttcttcggctgcacattcacctcgaagacagacacggcgaga	3094
QY	2697	caagtttgcacaaccggagaagatcttgacatccctgcgtcttggacatctgcatcgtcttca	2756
DB	3095	cacgctgctctgacagaaagaaacttgcacatccctgcgtggtggccatctgcacgcttcca	3154
QY	2757	gattctgactcagaagaactgtgaataaagtctctctacaacagcgatggtccctcaatgctc	2816
DB	3155	gattctgacccacagagagacaggaaactgtgctctgtaacaaagccatgagcctctccactctc	3214
QY	2817	ttggagctctcttactactacgcgcctcatgacatttggcaactatgtgctcttcaact	2876
DB	3215	ctggcgccgctcttacttctgtggtgcccctcatgacacttggcacaactatgtgcttcaact	3274
QY	2877	gctggctggccattcttcttggaaagatctccagcgagaggaatctcgcgcaaacgvggaagatgc	2936
DB	3275	gctggtgacccattctctgtgagagagccttccacggcgagggccgattgcacaacagatccgacac	3334
QY	2937	gagtgacagtaagactgtatctagctgcctgcaactctcaggggggagatgacaccaa	2996
DB	3335	-----gacagagacaaagacgtc	3352
QY	2997	gtctgagtcagaagcctgattcttcttcgcgcaggtgtgtagtgtatgtaggaagaagaa	3056
DB	3353	gctccacttccagagagacatttccacaagcttcaacagaaacttccagaccacagacactgaaat	3412
QY	3057	gcgctctggcccttggcttcttggagaaacacggagaaactacagaaagagccttcttgcacc	3116

Db	3413	GTGTTCCCTGGCCGTATACCCCAACGGGCACTTGGAGGAGACAGGACGCTTGTCCCTTCC	3472
Oy	3117	ccctatcatccatacagcgtctgcagacaccaaitytcatcactaaccagaagctccagacagatgt	3176
Db	3473	CCTTATCATGTGCACAGCTTGCACCAACCCCATGCTTACCCCAAGAGCTCACATTTCTGGA	3532
Oy	3177	gggggaaagcaactggtgctcgtgcttcctgcagcgttaacaagatagacagtgtygtccgcttagac	3236
Db	3533	TGCAGCCCCAGCCTTCCCAAGACTCTTGGGTGGGACGACAGCTCCGGGGAGACCCGCCACT	3592
Oy	3237	agctgcccaccatagatataaactctccgcgaagtgtccgcagctcccgacagtccttg	3296
Db	3593	GGGAGACCA-----GAAGCTCCGGCCAGCCTCCGAAGTTCTCTCTGTCCTCCCTTG	3643
Oy	3297	gaatgcggcaagcagcttgcacccagcagcgtgtccagcagagaaacgctctggccggccccc	3356
Db	3644	GGGCGCCAGTGGGGCTTGGAGCGCCGGCGGCTCCAGCTGGAGCAAGCTTGGGCGTGCCTCC	3703
Oy	3357	cagcctaaagcagagagagcccgagcgaggagagagaggttccctgtctgtcgttagagagcca	3416
Db	3704	CAGCTTCAAGCGCGCGCGCCACAGTGTGGGAAGTAAATCCTGCTGATCGGCGAGGGCAA	3763
Oy	3417	ggagagtcagatgtagagaggaagagtlcagaagaagaccggtgcagcccgacgagcagtga	3476
Db	3764	GGGCGAGCACCGACACACCAACCTATGAGACGCGAGGGCCCGCGCCGCGCTGTGCACCC	3823
Oy	3477	ccatcgcccaagaggtgtcctctgtgaagctgtaggccaagagtlcctttgacctgcotagac	3536
Db	3824	ACTGCGGCGGGCCGAGTTCCTTGGACCCAGGGCCCTCGGGCGCGGCGGCT-----	3875
Oy	3537	ctctgcaagttgcggyggtctgcacgcgcagccagcgcgagctctgcctcttgaccca	3596
Db	3875	-----CCGCGCTTACCAATGCC	3892
Oy	3597	agactgtaatgcagagtcgggtcttcaggggtttggccgcaccccgagagcttagaccc	3656
Db	3893	CGATCGCACCGGAGGTGTGGTGGCCCTGCCACGACTTCTTCTCGCGCATCAGACCA	3952
Oy	3657	ccaactgtgtagggatgtagacaatgtagaggaactctgagcaagggaagcataca	3716
Db	3953	CCGTGAGGATCAGCCGACAGCTTGACGCGACACTGGAGGACACACTCTCCCTCCCTGCA	4012
Oy	3717	agccctgggtcagatcccggtctcctgctgtgttgcagagcgagagttcctgttcgacct	3776
Db	4013	TAAAGTGTGAGGCCCTTACAAGCCCCAGTGTGTCCGGAACCCCGAGGCTTGGCCCTCTA	4072
Oy	3777	tatcttccctccatagtcgaagtggttctgtccctgtgtcaccggtatcatcaccacaagat	3836
Db	4073	CCTCTTTCGCCACAGAACCGGTTCCGCGTCTCTCTCCGGAAGGTCAATCACACAAGAT	4132
Oy	3837	gtttgaccaatgtgtctctgtcatcatctcttcccaactgtatcacacatcogtatggagcg	3896
Db	4133	GTTTTGTACGAGGTCCCTCGTTCATCTTCCCACTCGCTACCATGCGCTGGAGAG	4192
Oy	3897	cccccaaatgtgcccccaagcgtctgtagcgcatcttccctgcagccctcccaactaatct	3956
Db	4193	GGCTGACATTTGACCCCGGACACGACGAGCGGGTCTTCAGAGTCTCCAAATTAATCTT	4252
Oy	3957	caacgcagtccttctagctgtaaatgtagcagtggaagtgtgtggaactggtgtgtcttgg	4016
Db	4253	CAGGCGCATCTTCTGTGGCGGAGATGATGTAAGGTGTGTGGCCCTGGGCTGTCTCCG	4312
Oy	4017	ggagcgaggtcactacgtgcgcagcacagctggaatgtgtgtcgtgaagcgtctgtgtcatctc	4076
Db	4313	CGGCGACGGCTTACTCTCGACAGACGACTGGAACCTCTGTGATGGGGCTCTGTCTGTGTC	4372
Oy	4077	cgtcatcgcacatcctgtgtctcatgtgtctccagacgycgaccaagaatcttgcatagtc	4136
Db	4373	CTGTGTGGACATTTGTTGTTGGCCATGGCTCGGCTGTGTGGCCCAATATCTGGGTGTCT	4432
Oy	4137	gaaggtgtcgtcggtcgtctgcggagacctgtgtccactaagggtatataagccgggcccagg	4196

[illegible]



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QY 525 cttctccgaagtcagaaacagtcgctgctgagccgctcaaggccatcaaacggtttcc 584  
Db 656 CCTCTGGGCTATACGACCGTGGGGTGTGGCGCCCTCCCGGCTATCAACCGGATGCC 715  
QY 585 cagcatgagcattctcgtacattactgctgagacacctgagctatgctggcaagctct 644  
Db 716 TAGCATGCGGATCCTGTCTACTCTGTGTGGATACGCTGCCATCTCTGGGAGTCTCT 775  
QY 645 gctgctgttcttctgctcttcttcaatcttggcaatctgagcgttccagctgtggcaag 704  
Db 776 TGTGCTGTCTCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 835  
QY 705 acgcttcgcaagcagatgcttcttctcccgagaaactcagcctccctcagtgctg---ga 761  
Db 836 CCTCTGTGGAGACCGCTGCTTCTGTGACAGTGCCTTTGTACAGAAACACACCTGACCTT 895  
QY 762 cctggagccttattaccagacagaaatgagagagagccctcatctgctcagcc 821  
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QY 882 tggccacccctgagctgagctgactatgagactataa-----cagttccagcaa 929  
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QY 930 caccacctgtgtaactgtgaacacagtaactataacactgctctgagggagagacaacc 969  
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Db 2021 GAGCTTGAACAGCCCTGATCCCTACGAGAAAGATCCGCAATGTGGCGGAGGAGCATGACT 2080  
QY 1917 gagtacgagagcctgcatagctctctgcaaa-----tctcaagccctgtctccaa 1967  
Db 2081 GGGCCAAACCCCTGACATCTGTGGGCTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2140  
QY 1968 ggcagacagtgagagcctgagcgccgagcagctgtccctactgtgcccagac---agagac 2024  
Db 2141 AGCGGGCACATGACATGTGTAGCTGAGAGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTG 2200  
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QY 2124 -----ccacagcggcgagcagcagcagcagcagcagcagcagcagcagcagcagc 2159  
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Db 2681 CTGGGAGATCGTGGGCGAGCGAGGAGGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 2740  
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Db 2741 GCGTGTGCTGAACTGTGCTGCTTCTGTCAGCCTCTGCGGCGCGCAGCTGCTGCTGCT 2800

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Db	2801	gaagacacatggaacacagctggcattcccttctgcaacgctgctcaatgcttcaattttcaattt	2860
QY	2640	caagcatctgggacatgcattctcttggttgcaagttcgcattcgaatcgaacggga--tgggga	2696
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QY	2697	caagcttcagcagccggaagaattctgcaaccctgtcctctggagcatcgtgcacatgtcttca	2756
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QY	2757	gattctgaactcaaggaaagacttgaaataaagttcctctcaacaagcgcatgctccacatcgtc	2816
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QY	3117	ccctatcatccaataagcgctgtgcgacacaaatgttccactaccacaaagctccagacagaagttgt	3176
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QY	3177	ggggaagacacctgtgcctctgcctctgcagatacgaatacgaatgagttgtctgcctgtgagctgtg	3236
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QY	3237	agctgtccacacatgagatgtgaatctctgcgcgaagtgcgcgacgtcccgacagttccctg	3296
Db	3407	gaccccgacacttggaagacacgaagaccttcgggacgacctccgaagttcttccctgctccctct	3466
QY	3297	gaatgtgcgaagaagcagctgtgacacgaacgagcgctcccaagaaacagacctgtgcgagcccc	3356
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QY	3357	caagcttaagcggagagagcccgagcggtggagagcgaggttccctgctgtctcttgagaaggcca	3416
Db	3527	gccttaagcccgccggccagctgctggagagacgtgaatgctctctgtctggcgaaggccaa	3586
QY	3417	gggaagtcaggaatgagtaggaagaattcacaagaagaagacggcgccacccacagacagcagttga	3476
Db	3587	ggggcagacacgacagacgaag-----ctgagagacggcagaaggcgctccggggcccgctgc	3640
QY	3477	ccatctgcgacacagaggttcccttgtaaggtgtagagccaagagttctcttgaacctgcgttgaaac	3556
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QY	3537	tctgcaaggtgcgggagctgtgacacgcaacagacgagcggtgcggaatctgtcctcttgacaaca	3596
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QY	3597	agactgttaatgagcaagtcggctctcaaggcgcttggcccgacacctgaagactgattgaacc	3656
Db	3751	-----tcttctcgtccgcatgacagccacacgctgtagagattga-----	3786

QY	3657	ccaactgtagtggagatgtagatcaatgatatgaggaatctgagcaaaagggaagcatca	3716
D3	3786	-----GCGAGCTTAGAGACACACTCCGAGAGACAGCTGCTGCCCGCCCTGCATTAAGT	3838
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D3	3839	GCTGGTCCCTACAAAGCCCAAGGGGATCCGGAGACAGAGAGCTGGGCCCTTACCTCTTA	3898
QY	3777	tatcttcctccctcaagtaagggttctgctccatgctgtaacccgagatcatcacccaaga	3836
D3	3839	CTCTCTCTCCCAAGAACGGGTTCGGGCTCTCTCGGCAAGAGGTTCATCACACAAAGAT	3958
QY	3837	gtttgacatgtygtctcgtcatcatcttctctcaactgataccatcgctagagcg	3886
L3	3959	GTTTGATACAGTGGTCTCTGCTTCATCTTCCTCAACCTCGTACACATTCGCTGAGAG	4018
QY	3897	cccccaattgagcccccaacgcgtatgagcatcttctcagaccctcccaatacatct	3956
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QY	3957	cacgycagcttctctgctgctgaaatgacagtaagtgtygtgcacgtggctgctgttg	4016
D3	4079	CACGGCCATCTTGCTGGCGAGATGATGTGAAGGGTGGCGCTCGCTGCTCCGG	4138
QY	4017	ggaacagagctacctgcgcagcagcagcagatgtgctgtaacgctgcgtgctcatctc	4076
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Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS 1 (bases 1 to 6740)  
TITLE Mitman, S., Guo, J., Emerick, M.C. and Agnew, W.S.  
Structure and alternative splicing of the gene encoding alphaII, a  
human brain gamma calcium channel alpha1 subunit  
JOURNAL Neurosci. Lett. 269 (3), 121-124 (1999)  
MEDLINE 99381950  
REFERENCE 2 (bases 1 to 6740)  
AUTHORS Mitman, S., Agnew, W.S. and Guo, J.  
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FEATURES  
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ORIGIN

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 REFERENCE 1 (bases 1 to 1344)  
 AUTHORS Perez-Reyes,E., Cribbs,L.L., Daud,A., Daud,A., Lacerda,A.E., Barclay,J., Williamson,M.P., Fox,M., Rees,M. and Lee,J.H.  
 TITLE Molecular characterization of a neuronal low-voltage-activated T-type calcium channel  
 JOURNAL Nature 391 (6670), 896-900 (1998)  
 MEDLINE 98154730  
 REFERENCE 2 (bases 1 to 1344)  
 AUTHORS Cribbs,L.L., Yang,J., Daud,A., Lee,J.-H. and Perez-Reyes,E.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-OCT-1997) Physiology, Loyola University Medical Center, 2160, South First Avenue, Maywood, IL 60153, USA  
 COMMENT IMAGE Consortium clone #50902 (GenBank Accession Number H19230).  
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ORIGIN				

Query Match	Score	DB	Length
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KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Taxonomy: Chordata: Vertebrata: Mammalia:  
Taxonomy: Mammalia: Primates: Hominidae: Homininae: Hominini: Homo

**REFERENCE**

Eutheria; Primates; Catarrhini; Hominae; Homo.  
1 (bases 1 to 135259)  
Birren, B., Fasmann, K., Linton, L., Nussbaum, C. and Landier, E.  
*Molecular Systematics* 17 Clon. hctm 22 k 21

JOURNAL  
Unpublished  
REFERENCE  
2 (bases-1 to 135259)  
AUTHORS  
Birren, B., Fasmann, K., McKernan, K., Nusbaum, C., Richardson, P.,  
Sattler, N., Sattler, T., Sattler, J., Sattler, I., Sattler, R., Sattler, M., Sattler,  
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Benn, J., Boatin, C., Boutwell, C., Brown, A., Byrne, S., Cantu, C.  
Castle, A., Cerny, J., Cooke, P., Daly, M. J., Depayre, E., Devon, K.  
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Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Gray, D., Hagos, B., Harris, K., Horton, L., Howland, J. C., Hul, L., Jacotot, K., Linton, L., Macdonald, P., Marguis, N., McEwan, P., McGowan, J., Mella, M., Morris, W., Morrow, I., Murchalkevskij, J.,

Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rollins, G., Rossello, R., Shyam, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, J., Sutherland, K., Tansley, A., Torneilla-Miller, T.,

**TITLE** Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W. J., Zhao, J. and Zody, M.  
**Direct Submission**  
Submitted: 10 Apr. 1999, Whitehead Institute/MIT Center for Genome Research

REFERENCE  
AUTHORS

Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 135259)  
Birren, B., Fasman, K., Linton, L., Nusbaum, C., Tander, E., Allen  
Baker, N., Beckwith, R., Benn, J., Boatin, J.,

Boutwell, C., Brown, A., Byrne, S., Cantu, C., Castle, A., Cerny, J.  
Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durelle  
Etemad, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R.,  
Gilmartin, T.

Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hul, L.  
Jacotet, L., Kann, L., Macdonald, P., Margus, N., McEwan, P.,  
McGuirk, A., McKernan, K., Meldrum, J., Molla, M., Morris, W., Morr  
Navarro T

Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, J., Shyam, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, Shyam, R., Torruella-Miller, I., Vassiliev, H., Vo, A., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., and Zhao, T.

TITLE  
JOURNAL  
Direct Submission  
Submitted (09-MAY-1998) Whitehead Institute/MIT Center for Ge

Submitted (09-MAY-1998) Whitehead Institute/MIT Center for Genome

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 9, 1998 this sequence version replaced qt:3116418.  
 All repeats were identified using RepeatMasker: Smit, A.F.A. &  
 Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

## FEATURES

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Wed Jan 19 08:14:55 2000

pct-us99-19675-1.rge

Page 43

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Oy 1681 tggcacttgag 1692  
Db 32588 TGCCACATAGAG 32599

Search completed: January 16, 2000, 00:18:40  
Job time: 4322 sec



GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 16, 2000, 00:07:18 : Search time 22.58 seconds  
(without alignments)  
6440.206 Million cell updates/sec

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Perfect score: 12469  
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Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database: SPTREMBL\_11:\*

Word size: 0

Number of hits that pass the threshold: 199794

1: SP\_Archaea:\*

2: SP\_Bacteria:\*

3: SP\_Fungi:\*

4: SP\_Human:\*

5: SP\_Invertebrate:\*

6: SP\_Mammal:\*

7: SP\_Mhc:\*

8: SP\_Organelle:\*

9: SP\_Phage:\*

10: SP\_Plant:\*

11: SP\_Rodent:\*

12: SP\_Virus:\*

13: SP\_Vertebrate:\*

14: SP\_Unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID     | Description        |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1          | 7392   | 59.3        | 1555   | 4  | 094770 | 094770 homo sapien |
| 2          | 6247   | 50.1        | 2353   | 4  | 095802 | 095802 homo sapien |
| 3          | 5348.5 | 42.9        | 1835   | 11 | 0920Y8 | 0920Y8 rattus norv |
| 4          | 3546.5 | 28.4        | 1657   | 5  | 018840 | 018840 caenorhabd  |
| 5          | 1709.5 | 13.7        | 1810   | 5  | 044930 | 044930 alptasia pa |
| 6          | 1706.5 | 13.7        | 2333   | 11 | 089089 | 089089 rattus norv |
| 7          | 1657   | 13.3        | 1891   | 5  | 097017 | 097017 stylophora  |
| 8          | 1636.5 | 13.1        | 1993   | 5  | P90670 | P90670 aplysia cal |
| 9          | 1622   | 13.0        | 1984   | 6  | 028644 | 028644 oryctolagus |
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| 14         | 1589   | 12.7        | 1688   | 13 | 057483 | 057483 rana catesb |
| 15         | 1585.5 | 12.7        | 1783   | 5  | 017050 | 017050 caenorhabd  |
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| 23         | 1564.5 | 12.5        | 2169   | 11 | 092305 | 092305 cavia porce |
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|----|--------|------|------|----|--------|--------------------|
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| 29 | 1539.5 | 12.3 | 2007 | 13 | 09YGN7 | 09YGN7 cynops pyr  |
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## ALIGNMENTS

RESULT 1

IN 094770 PRELIMINARY; PRT; 1555 AA.

EC 094770;

DE 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

RP [1]

RA SEQUENCE FROM N.A.

RA KISHI F.;

RT "Human NBR13.,"

PL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB012043; BAA36409.1; -

SC SEQUENCE 1555 AA; 171385 MW; 73884065 CRC32;

|                       |                       |                                      |           |              |
|-----------------------|-----------------------|--------------------------------------|-----------|--------------|
| Query Match           | 59.3%                 | Score 7392;                          | DB 4;     | Length 1555; |
| Best Local Similarity | 95.8%                 | Pred. No. 0;                         |           |              |
| Matches 1414;         | Conservative 17;      | Mismatches 43;                       | Indels 2; | Gaps 2;      |
| QY 1                  | MDEEDGAGAEESGQPRSF    | TOINDLSGAGRGPGSTEXDPSADSEAGLPPALAVY  | 60        |              |
| DB 1                  | MDEEDGAGAEESGQPRSF    | MRINDLSGAGRGPGSAEDPSADSEAGLPPALAVY   | 60        |              |
| QY 61                 | FHYISQDSRRSMCLRTVCNPF | ERYSMVLVILNCVTIGMFPCCDIDCSORCHLOAF   | 120       |              |
| DB 61                 | FHYISQDSRRSMCLRTVCNPF | ERYSMVLVILNCVTIGMFPCCDIDCSORCHLOAF   | 120       |              |
| QY 121                | DDFIYAFVAVVVMVMAALGIF | GKKCYIGDTYNAKDLDFVIAGMEYSLDLQNVFSAVR | 180       |              |
| DB 121                | DDFIYAFVAVVVMVMAALGIF | GKKCYIGDTYNAKDLDFVIAGMEYSLDLQNVFSAVR | 180       |              |
| QY 181                | TVAVLRPLRAIRNVRSMRLIV | TLDTLPMLGNYLLCFEYFIFGIYGVOLMGLRNR    | 240       |              |
| DB 181                | TVAVLRPLRAIRNVRSMRLIV | TLDTLPMLGNYLLCFEYFIFGIYGVOLMGLRNR    | 240       |              |
| QY 241                | CELPERFSLPLSVLEPIYQI  | ENDESPTICQPRENCRSCRSVPTLRGGGGPPCSTL  | 300       |              |
| DB 241                | CELPERFSLPLSVLEPIYQI  | ENDESPTICQPRENCRSCRSVPTLRGGGGPPCSTL  | 300       |              |
| QY 301                | DEYFNSSNTTCVMMNOYITNC | SGEHNPKGAINPQNTICATIAIFOVITTEGWDIM   | 360       |              |
| DB 301                | DEYFNSSNTTCVMMNOYITNC | SGEHNPKGAINPQNTICATIAIFOVITTEGWDIM   | 360       |              |

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DB 421 STLASFSEPGSCYEELLYIYIILKARLAQVSRAGVRAGLSSPVARSGOEPGSG 480
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DB 481 SCTSRSHRLSVHNLVHHHHHHHHHNLGTLNVPASPEIQRDANGSRRLMPPSTP 540
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DB 541 TPSSGPPRGAESVHSFYHADCHLEPVRCOAPPRCPSPASGRVSSGVYTVHTSPPE 600
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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE LOW-VOLTAGE ACTIVATED CALCIUM CHANNEL ALPHA 1H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=MODULARY THYROID CARCINOMA;
RX MEDLINE: 99127945.
RA WILLIAMS M.E., WASHBURN M.S., HANS M., URUTIA A., BRUST P.F.,
RA PRODANOVICH P., HARPOLD M.M., STAUDERMAN K.A.;
RT Structure and functional characterization of a novel human
RT low-voltage activated calcium channel."
RT J. Neurochem. 72:791-799(1999).
DR EMBL: AF073931; AAD17668.1;
SQ SEQUENCE 2353 AA; 259141 MW; 28D150E3 CRC32;

Query Match 50.1%; Score 6247; DB 4; Length 2353;
Best Local Similarity 55.3%; Pred. No. 0;
Matches 1386; Conservative 212; Mismatches 550; Indels 360; Gaps 66;

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DB 27 GASPESEGAGRAERAGSELGVPSPSPAERGAELGABE-QRVYPALAATVFFCLGO 85
OY 67 DSRERWCLTVCNPMWERYSMLVILLNCYTLGMRPCEDDIADSORCILLAFDFTFA 126
DB 86 TTRPRSMCLRLVCNPMFEHYSMLVIMLNCYTLGMRPCEDVEGSRCHILFAFAFTA 145
OY 127 FFAYEMVKKVVALGIGKCKGCGYLDGTNRRLDFFIVIGMLEYSLDLOVSESAVRYTVLR 186
DB 146 FFAVEMVKKVVALGIGKCKGCGYLDGTNRRLDFFIVIGMLEYSLDLOVSESAVRYTVLR 205
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DB 266 FVRNNNLTFLAPYQYOTEGEGENPFICSRDNGMOKSHIP--GRRELMPCTLGWEAY 322
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DB 443 NDSTLASFSEPGSCYEELLYIYIILKARLAQVSRAGVRAGLSSPVARSGOEPGSG 501
OY 479 SGSCYRSHRR-----LSVHNLV-HHHHHHHHHHNLGTLNVPASPEIQRDANGSR 530
DB 501 -----GHRORAGRHRHSAVHNLVHHHHHHHHHNLGTLNVPASPEIQRDANGSR 548
OY 531 RLMT--PPSTPSPGPPRGAESVHSFYHADCHLE--PYRCOAPPRCPSPASGR-TVG 585
DB 549 RLVRAAGAPSPSPGPPRGAESVHSFYHADCHLE--PYRCOAPPRCPSPASGR-TVG 607
OY 586 SGKV-YPTV-----HTSPPEILKXKALVEVAPSP-----GPPLTSTFNIPPGP 628

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Db      608 LGTMVYPTILPSGVSGKSTSPGPK-----GKNMAGPGPGTGGHGPLSLNLS-----PDP 656
Qy      629 BSSMKHLELTOSTGAC--HSS-----CAISSPCKADSGACGPDSCYCYCART--GAGEPES 660
Db      657 YKIFHVYGEHGLGQAPHLISGLSVPCPLPSP--PAGTLICELKSCPCYCTRALEDPEGEL 714
Qy      681 ADHVMPDSDSEAVYEFTODAOHSDLRDP-----HSHRROBSLGPDAEPS 724
Db      715 SCSSEGDSDGRVYEFETDVRHGDMDPTPRPRATDTPGPGPSQORRAOORAP--GEFG 773
Qy      725 SYLAFWRLICDTERKIVDSKTFGRGIMAILVNTLSMGIEYHEQPEELTNALISNIVFT 784
Db      774 WNGRLMVFYSGKLRIVYSKYFSRGINMALLVNTLSMGVEYHEQPEELTNALISNIVFT 833
Qy      785 SLEFLEMLKLVLVYPGFGIKKPNYIFDGYIVYISVMEYVQGGGGLSVYRTFELMRVLK 844
Db      834 SMFALEMLKLACGPPLGIRNPNYIFDGIIVYISVMEYVQADGGLSVYRTFELMRVLK 893
Qy      845 LVREPLALQROLVLMKTMNVATFCMLMLLFIIFSLGMLHFGCKFASERD--GDTLPD 903
Db      894 LVREPLARQROLVLMKTMNVATFCMLMLLFIIFSLGMLHFGCKFASERD--GDTLPD 953
Qy      904 RKNFSLMAIYVFOIITLOEDMNVLYNGMASTSNALFYALMTFGNVYLENLVAI 963
Db      954 RKNFSLMAIYVFOIITLOEDMNVLYNGMASTSNALFYALMTFGNVYLENLVAI 1013
Qy      964 LVGEFOAEIGKREDASQOLPLVNSGGDATKSESEPDFSPSVYDGGDRKKRLAL 1023
Db      1014 LVEGFOAE-----GDANRSDTDEKTSVHEEDFHLRELQOT 1050
Qy      1024 VAL-----GEHAELRKSLPLLIHTATPMSLPSKSS--TGVEBALGSGSRRTSS 1073
Db      1051 TELKMCSLAVPTNGHLEGRGSLSPPLIMCTAATPMPYTPKSSPFLDAPSLDPSKRSGSS 1110
Qy      1074 GSAEGGAHHEKSPSPARSHPFWSAASSWTSRRSSRNLGRAPSLKRRSPGERRSL 1133
Db      1111 GPPPLG---DQKPPASLRSPFCAPWGPSMSRSSWSLSGRAPSLKRRGCGERRSL 1166
Qy      1134 LSGEQSGODEEESSEEDRASPA--GSDHRHRSGLERAKSSFLPDLT-----QYPL 1185
Db      1167 LSGEQSGTDDP--AEDGRAAGPRATPLKRAESLDPPPLPALPPLCKCRDROGVVAL 1224
Qy      1186 R-----RTASGRSSASEHODCKGSKASGRRLARTLTDPPOLDGDDDEGNLSKGRITQA 1240
Db      1225 PSDFLRIDSHREDAAELDDDESDCCLRLKHLPEYKQ----- 1265
Qy      1241 WYRSRLPACCRERDSWMAIYPPPOSERFLCHRIITHKMPHYVLYIIFLNCITIAMER 1300
Db      1265 W-----CRSERMALYLFSPONKFRVSCOKVITHKMFHVLYVLFILNCVITALERP 1316
Qy      1301 KIDPHSAERIFLTSNYIFTAVFLAEMTVKVALGWCFGEOAYLRSSMNVLDGLLVISY 1360
Db      1317 DIDPSTERVFLSVSNYIFTALFEVEMKVKVALGILSGEHAYLQSSMNLDDGLLVYSL 1376
Qy      1361 IDLIWSMVSOGTKILGMLRVILRLTLPRLVYSRAQGLKLYVETLMSLSKPIGNVVI 1420
Db      1377 VDIIVAMASAGAKILGVALRVLRLLTLPRLVYSRAQGLKLYVETLMSLSKPIGNVVI 1436
Qy      1421 CCAFFIIFGILGVOLEFKGFYVCGEDTRNTLNKSDCAEASRYWRHRYKYNEDNLQALMS 1480
Db      1437 CCAFFIIFGILGVOLEFKGFYVCGEDTRNTLNKSDCAEASRYWRHRYKYNEDNLQALMS 1496
Qy      1481 LFLVLSKOGWMDIMYDGLDVAVGOQPTLMNNPMLLYFIFLLIYAFVYLMFVYVVE 1540
Db      1497 LFLVLSKOGWMDIMYDGLDVAVGOQPTLMNNPMLLYFIFLLIYAFVYLMFVYVVE 1556
Qy      1541 NFHKCRQOHEEERARRREKRLRLERKRRMLLDVYIASGSSASASEAQCKPYSDYS 1600
Db      1557 NFHKCRQOHEEERARRREKRLRLERERRR-----STFPEPEQORRYIVADYS 1604
Qy      1601 RRLVHLHCTHYLDLFTIGYIGLVVYTMAMERYOQPOLDEALKNICNYIFVYVVEFS 1660

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Db      1605 PTRSHSLCTSHYLDLFTIIFICVNVITMSMEHYNOPSLSDEALKYCNVYFIVEFEA 1664
Qy      1661 VFKLAVGFRREFDORNNODDLAIVLLSINGITLEIEVNASPIPIITIRIMRYLIRAR 1720
Db      1665 ALKLVAEFERREFDORNNODDLAIVLLSINGITLEIEVNASPIPIITIRIMRYLIRAR 1724
Qy      1721 VLKLLKMAVGRALLDVTMOALPOVNGILGMLLFEIFALGVELFEDCEDETHPCBG 1780
Db      1725 VLKLLKMAVGRALLDVTMOALPOVNGILGMLLFEIFALGVELFEDCEDETHPCBG 1784
Qy      1781 LGRHATFENEGMALTLIFRSTGDNWNGIKDTLRDC---DDESTYNTVISPITYVSV 1837
Db      1785 LSRHATFENEGMALTLIFRSTGDNWNGIKDTLRDC---DDESTYNTVISPITYVSV 1844
Qy      1838 LTAOFVNVYVIAVLMKHELESNKEAKEAEALAELEKTLSPQPHSPLGSPFLMPGV 1897
Db      1845 LTAOFVNVYVIAVLMKHELESNKEAKEAEALAELEKTLSPQPHSPLGSPFLMPGV 1885
Qy      1898 EGVNSPDSFKGAPHTTAHGAASGSLERPTWVPHPEEYVPVLPGLDLTVKSGVSRTH 1957
Db      1885 --AGP-----GSARVDADRP---PLPOESPGARDAPNLVARKVYSRML 1925
Qy      1958 SLPNDSYCMRNGSTA-----ERSLGRGGLCPKAQSGSLISVHOPADTSCILQD 2008
Db      1926 SLPNDSYCMRNGSTA-----ERSLGRGGLCPKAQSGSLISVHOPADTSCILQD 1982
Qy      2009 KDVR-----YLQPHGAPTWGAIPKLPPEGRSPLAORPLRQAIRTDSDLVQGLG 2059
Db      1983 LAVSSPARSGEPHLALSPRGT-----ARSPSLRLLCROEAVHTDLSLEGR-ID 2029
Qy      2060 SREDLSEV---SGPSCPLTRSSSFWGSSIOVQORSGIOSKV---SKH-----IRLPA 2107
Db      2030 SPRTOLDPAEGERETVPARYTQ-----GSLQSPRSPAPAVYRIRKHTFGCHYCSSNP 2083
Qy      2108 PCPLGPSMAKDPETRSSLELDELTSWISGDLPL--SSOEPLSP-----RDLLKC 2157
Db      2084 KAPGGEAEASDP-----ADEVEHSITSSACPMQPTAEHPGAPSPVAGGERLRL 2135
Qy      2139 YSVENQSRRRRGSWLDQORRHSAVSCLDGSGOPLRCPSPSSLGQPLGPR--GSRPK 2215
Db      2136 YSVDAQGLDKPGR--ADEQWBPASAE---LQSGE-----PEAKAWG--PEAEPLGARRKK 2185
Qy      2216 KLSPPSISIDPP--ESQGS--RPPCSPG--VCLARRAPA-----SDSKDPSVSPDLSTAA 2265
Db      2186 KMSPCISVEBPADDEGASARPSAEGSTTLRRTTRPCCATPRDLSLEPTEGSAGAGDPA 2245
Qy      2266 S-----PSPKDTLSLSGSSDPTM-----DP-----VLPTLP 2294
Db      2246 AKGERWGOASCRALHLPVPSFAFEPDLGLVPSGDPPLDGSHTVPESRASSSGATVLEP 2305
Qy      2295 HHLSP--PGADPSSASMAAFLKSPTAASSHEAPHLPSV---AGDDE 2337
Db      2306 PSEPEPMVGDPPPEKRRGLYTVQCPPL--EKGPSASATPAPGAGDD 2351

RESULT      3
Q320Y8      PRELIMINARY;      PRT; 1835 AA.
AC      Q320Y8;
DT      01-MAY-1999 (TREMblrel. 10, Created)
DT      01-MAY-1999 (TREMblrel. 10, Last sequence update)
DE      01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE      LOW VOLTAGE ACTIVATED T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.
GN      CACNA1L.
O3      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      11
FE      SEQUENCE FROM N.A.
RC      STRAIN:SPRAGUE-DAWLEY; TISSUE: BRAIN.
RA      MEDLINE; 99165796.
RA      LEE J.-H., DAUD A.N., CRIBBS L.L., LACERDA A.E., PEREVERZEV A.,
RA      KLOCKNER U., SCHNEIDER T., PEREZ-REYES E.,

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"Cloning and expression of a novel member of the low voltage-activated  $I$ -type calcium channel family."

RT J. Neurosci. 19:1912-1921(1999).

DR EMBL: AF086827; AAD17796.1; -

SO SEQUENCE 1835 AA; 205207 MW; 01C7F69 CRC32;

Query Match 42.9%; Score 5348.5; DB 11; Length 1835;

Best Local Similarity 55.3%; Pred. No. 0; Mismatches 364; Indels 347; Gaps 47;

Matches 1143; Conservative 214; Mismatches 364; Indels 347; Gaps 47;

27 GAGGAGGPGSTKEDKPGSADSEAE---LPYPALAPVFFYLLSODSRPSCWCLRTVCNFM 82  
 19 GTPGPRSPRPSPGPLEEPLBGTNDPDPHPLDAPAFGLKOTSPRMWCIKMCNFM 78  
 83 FERVSMVLINCYLTGMRPCEDICDSQCRILQAFDFEFAFVENVVAVLALGIF 142  
 79 FECSMVLINCYLTGMRPCEDICDSQCRILQAFDFEFAFVENVVAVLALGIF 138  
 143 GKCYLGDPTNRDLDFEYIAGMLEYSLDLQVNSFAVTVKVLPRALNRVPSMRLVT 202  
 139 GKCYLGDPTNRDLDFEYIAGMLEYSLDLQVNSFAVTVKVLPRALNRVPSMRLVT 198  
 203 LLLDTPMLGNVLLCFEVEFFIEGIVGQVAGLLRNKCLPENFSLPLVDLEPYQTE 262  
 199 LLLDTPMLGNVLLCFEVEFFIEGIVGQVAGLLRNKCLPENFSLPLVDLEPYQTE 258  
 263 NEDESPFICSPRENGMSRSPVTLRGEGGGPPCSL-----DYETVSSNTT--CV 314  
 259 EDDDEPFICSLTGDNGLNGCHEIRPLKQ---GRECLSKDDVDYDFGAGNOLNASLGV 315  
 315 NMNYYTNCAGENHNFKAIFDNIGYAMIAFOVITLEGWDMYFVMDASHFYFIY 374  
 316 NMNRYNVCRTGMNPHKAIINFDIGYAGIVFOVITLEGWDMYFVMDASHFYFIY 375  
 375 FILLIIVSFMINICLVIAIATOPSETKORSOQLREORVLEFNASTLASFESPGCYE 434  
 376 FILLIIVSFMINICLVIAIATOPSETKORSOQLREORVLEFNASTLASFESPGCYE 434  
 435 ELTKLYLVLRKAARLQVSRALGVAGLLSSPVARSQGPPOPSGCTSRHRLSVHHL 494  
 435 ELFOVYCHILKRAK---RALGLYQAL-----ONRROA----- 465  
 495 VHHHHHHHHHNGTLEVRPASPEIODRANGSRRLMLPPSPPTPSGGPRPGASVH 554  
 465 -----MGPGT-----PAPAKPG----- 478  
 555 SFYHADCHLEPYRCQAPRCPSEASGRTVSGKYVPTVHTSPPEILKDKALVEVAPSP 614  
 478 ---HAK---EPHCKLCRPHSLD-----PTPH-----LVQ----- 504  
 615 GPPLTISFNIPGPFSSMKHLELTOSTGACHSSCKISSPCKADSGACGPPSPCYC--- 671  
 504 -----PISALH-----ASDPSCPRCHQHEA 523  
 671 -----ARTGAGPESADHVPDSDSEAVYEFTODASHDLDPHSRRRQSLG 718  
 524 GRPRLSGSTDSGGEGSGGSAE---AANGDGL-OSSEDEVSSD-----LG 567  
 719 PDAEPSSVLA-----FWRLICDTFRKIVDSKYFGKGMIAILVNTLSMGIEYHEOPELT 773  
 568 KEEDQEDGAARLCGDVWRTRKRLKGIIVDSKYFENGIMAILLVNVMGIEHEOPELT 627  
 774 NALFISNIVTSLFALEMLKLVGPGFINKPNIIFGVGVVIVSWETVQOQGGSLV 833  
 628 NIEIENVFTSMFALEMLKLVGPGFINKPNIIFGVGVVIVSWETVQOQGGSLV 687  
 834 LRFERLMRYLKIYRPLALOROLVVMKTMNVAFKMLLFIFFISLIGNHLRCKFA 893  
 688 LRFERLMRYLKIYRPLALOROLVVMKTMNVAFKMLLFIFFISLIGNHLRCKFA 747  
 894 SEED-GDLPDRKNSDLMAIVTFOILTOEDMNKLYVNGASTSSWALYFIALMTFG 952

Db 748 LRTDTGDTVPDRKNFDSLMAIVTFOILTOEDMNKLYVNGASTSSWALYFIALMTFG 807  
 953 NYVLFNLLVALLVGEFOAEIGKREDASGQLSCIQLPVNSOGDATKSESEDPFSPVD 1012  
 808 NYVLFNLLVALLVGEFOAE-----GDANNSCDEDOSSSNE 844  
 1013 G-----GDGRKRLALVALGEMHAKLSLPLILH--TATPMSPKSSSTVGEA 1062  
 845 EFDKLPEGLDMSRDLKCLPMPNGHLDPSL--PLGAHLGPGAGTGTAPRLSLQDPVL 902  
 1063 LGSGRRRTSSGSAEPGAHHEKSPSARSPPSWASASWTSSRSNLSGRAPSLK 1122  
 903 VALDSKRSVNSL---GMSVDQRSLSRSSSYGPMGRSGTVASRRSSWN-----SLK 953  
 1123 RSPSGERRLSLSEGOES--ODEESEE--DRASPAGSDH-----RHR 1163  
 954 HKPSEAHESLSSGCGGCVACAGEAREEAPTATLAPHAHHAHGHPLAHRHRHR 1013  
 1164 GSELEAASSPDLPDTLOVPLHRTAS--GRSSASEHODCGKASGRLARTLTD--DPQ 1220  
 1014 RLTLSDTSDVDLGEVYVGAHSAARAGAGAPGHEDCGRPN--IAKDVFTKXDDR 1071  
 1221 IDGDDNDENGLSKGERLQAWVRSLRACREDSWASAYIFPPSRRLLCHRTITHKMF 1280  
 1072 RRGDEDEIDYTLQFRVKMIDYKPDWCVRREDWSYILFSPENKFRILCOTIIAHLF 1131  
 1281 DHVAVIIFLNCITTAMERPKIDHSARITLTSNYFTVFLAEMTVKVALAGWCFGE 1340  
 1132 DVYVLAFLFNLCITTALRPPIDEGASTERIFLTVSNYFLTAIFGEMTLKVASLGLYFE 1191  
 1341 QAYLRSSNMVLDGLVLLSVLSDIIVASVSDSGTKILGMARVLRLLRPLRVISRAQGL 1400  
 1192 QAYLRSSNMVLDGLVLLSVLSDIIVASVSDSGTKILGMARVLRLLRPLRVISRAQGL 1251  
 1401 KLAVETLMSLKPIGNIVVICOAFFIIGIIGVOLFKEKFEVCOGEDTRNTKNSDCAEA 1460  
 1252 KLAVETLMSLKPIGNIVVICOAFFIIGIIGVOLFKEKFEVCOGEDTRNTKNSDCAEA 1311  
 1461 SYRWVHKHKNFNLGALMSLFLVLSKDGWVDIMVGDGAVGVDDQPTMNNPMLLYFI 1520  
 1312 NTRWVHKHKNFNLGALMSLFLVLSKDGWVDIMVGDGAVGVDDQPTMNNPMLLYFI 1371  
 1521 SFLLIYAFVLMFVGVVVENHFKCROHEEABRREKRLRLLEKRRMLDDVYAS 1580  
 1372 SFLLIYAFVLMFVGVVVENHFKCROHEEABRREKRLRLLEKRR----- 1422  
 1581 GSSASASEAOCKPYSDXSRLVNHLCSTHYLDLPTTGIGIGANVTMAMEHYOQOI 1640  
 1422 -----KAORLPYATCPTRLIHSWCISHYLDLPTTGIGIGANVTMAMEHYOQOI 1473  
 1641 IDEALKICNYIFVIFVESFVKLVAFGRFRFODRWNOLDLAILVLSIMGITLEEIEVN 1700  
 1474 LETAALKCNMFTYVLEAVLAKIVAFGRFRKRWMDLDAIYLLSMGITLEEIEIN 1533  
 1701 ASDLPNTIIRIMVLRIRARVLRKLMKAVGALLDVTQOALPOVGNIGLLFMLEFIFA 1760  
 1534 AALPINTIIRIMVLRIRARVLRKLMKAVGALLDVTQOALPOVGNIGLLFMLEFIFA 1593  
 1761 ALGVEFLGDLDETHPGCGIGHATERNFGMAFLTLFVSTGDMNNGIMKOTLIDBC--DQ 1819  
 1594 ALGVEFLGDLDETHPGCGIGHATERNFGMAFLTLFVSTGDMNNGIMKOTLIDBC--DQ 1653  
 1820 ESTCYNTV--ISPIFYVSFVLAQVYLVNVVAVLAKRLHESNKEAKEBALEAELEEM 1877  
 1654 ERCTLSLQVSPFLYFVSFLTAQVYLVNVVAVLAKRLHESNKEAKEBALEAELEEM 1713  
 1878 -KTLSPQHPSPDSSPLMP---GVEGVNSPDSKPRAPRTTHAIGASGSELEHPTMYH 1933  
 1714 AHGIGPCP--GPCGPGPCPCPCACAPRLPTS--SPAG-----GSGG----- 1755  
 1934 PEVVPVLPGLDPLVLRKSGVSRTHSLPNDYSYCRN--GSTAERSLGHGRLPKRAGSIL 1992  
 1755 -----GAGAGD-----TESHLCHRCYSRAQETL-----W-----LDSVSLI 1786



QY 1993 SVHSQPADTSCLOLPKDY-HYLLOPHG 2019  
DB 1787 IKDSLEGELTIDNLSSGFHHYASPD3 1814

RESULT 4  
018840 PRELIMINARY: PRT: 1657 AA.

ID 018840  
AC 018840  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
DE SIMILAR TO DIHYDROPRYRIDINE-SENSITIVE L-TYPE.  
GN C54D2.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 94150718.  
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN T., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RA MINX P.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN (3)  
RP SEQUENCE FROM N.A.  
RA WATERSTON R.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U37548; AAA79201.1; -  
DR PFAM: PF00520; Ion\_trans. 4.  
SQ SEQUENCE 1657 AA; 190370 MW; AB3670CD CRC32;

Query Match 28.4%; Score 3546.5; DB 5; Length 1657;  
Best Local Similarity 41.8%; Pred. No. 1; Le-256;  
Matches 810; Conservative 240; Mismatches 450; Indels 439; Gaps 45;

QY 9 GAESGQPSFTQNDLSCAG-----GROGPGSTKDGASDSEAGLPYPALAPVVEFY 63  
DB 74 GSKETQLSEHRILASSSSASPSRWEGROIENGNE--QIEESE-LPYGFAEPALRC 129  
QY 64 LSGDSPPRSWCLRTVCNPFERVSMLVLLNLCVTLGMRPCED-IACDSQRCLQAADD 122  
DB 130 FTQARPERKMAQWMSPFDRITMAVIMINCVTLGMRPCEDGDCQTYRCQILIDIDN 189  
QY 123 FFAFAVAVMVKVALGFFGKKCYLGPTMWNLDFFIYIAGALEYSDLDQ---IVSFAV 179  
DB 190 CIFVYAFEMVAKIMALGFGYPAAYMSDTRNRLDFIYMAAGIAEVLHREYGININTAI 249  
QY 180 RTVAVLRPRAIRAVPSMRILVTLTLLDLPMLGNVLLCFVFFLFGIVGQVLAGLLRN 239  
DB 250 RTVAVLRPRAIRAVPSMRILVTLTLLDLPMLGNVLLCFVFFLFGIVGQVLAGLLRN 309  
QY 240 RCF--LPEKFS-----LPLSYDLPEPYQOTENDESPIQSPRENGMSCSVPTLGG 292  
DB 310 KCVINLPKTISENQSLFNNVAKLIRFYLP-DTSLFTICSDPANGLHTCENLPPYVD- 368  
QY 293 GGGPGCSLDYETYNSSSTTQVNMNVOYTYNCSAG-----EHNPFKAI 335

DB 368 --GVKCNLTIDEDYDKYTNDSICIMNNIYNEQVNIYPSLMTIASCFIKVMQNPQGSV 425  
QY 336 NEFNIGVAMIAIFQVYITLEGVMDIMFTVMDASHFYNFYIFILLIYGSFFMNLCLVYA 395  
DB 426 SEDNIGFAMVAIFLVISLEGMTIDIMYVQDAHSFMWYFVLLIVIGAFEMNLCLVYA 485  
QY 396 TQSEFKQRESQLMREORVRLFNASTIASFSEPG-----SCYEELKLYVILRK 446  
DB 486 TQFAETKRERFERMLQERKMLNDSISCTGSELGASKEEDYVYAFVFRIGFTFR 545  
QY 447 AARLIAQVSAIGVRAGLLSPVARSQEPQSGCTRSRRLVHHVHHHHHHHHYH 506  
DB 546 TKRAKKKRYTAY-----NEERAKKSSERQORRSKL- 578  
QY 507 LGNGTLRVPRASPEIODRDANGSRRLMPPSPITPBGCPGPGCAESVSHYADCHLEPV 566  
DB 578 --DMKATLSRIEKADEE-----DETITTRNGDDQLEQN- 612  
QY 567 RCQAPPPRCPSSEASGRVYSGKYVPTVHTSPPEILKALVEADPGPPLTSFNIPP 626  
DB 612 -----GDGVRIKRYKIEDEPKI- 629  
QY 621 GPFSSMHLFTQSTGACHSCKISSPCSKADGACGDCPCYCAPTAGEPESADHVP 686  
DB 629 -----KIGNNSGPRYKKS 643  
QY 687 DSDSEAYEFTQDAHSDLRDPRRRORSIGPDAEBSVLAFWRLICDTFRKIDSKYF 746  
DB 644 SDEDS-----DEDEEQQVYGGEEKARR-----STPSKL--WV--FREKIQFYCHID 689  
QY 747 GRGIVATLVNTLSMGIETHYHOPPEELNNALEISNYVTSFALMLTKLIVGPEFYIN 806  
DB 690 TRGIVATLVNTLSMGIETHYHOPPEELNNALEISNYVTSFALMLTKLIVGPEFYIN 749  
QY 807 PYNIEDGVIVISWEIIVGQGGGLSVLRTFLMRVLKLVLPALORLVLMKTMNV 866  
DB 750 GPNLEFDGIVALSVLELFQEGKGLSVLRTFLRLIKLVRFAPALRYOLVYVLMNDV 809  
QY 867 ATFCMLMLFFITFISILGMHLFGCKFASERD---GDTLP--DKKNDLSLMAIVTYFOLL 921  
DB 810 TVFGLLVLFIFISILGMHLFGCKFVEKFLGGLAKCKERKNDTLLMALITYFOLL 869  
QY 922 TQEDNNKLVNMASTSWALYFIALMTGNYVFLNLAIVVEGFOAEIQRDASG 981  
DB 870 TQEDNNKLVNMASTSWALYFIALMTGNYVFLNLAIVVEGFOAEIQRDASG 924  
QY 982 QLSCIQLPVNSQGDATKSESEPFESPVYDGDGDKKRLALVALGEHAEIKSLPLI 1041  
DB 924 -----KROLEEDARRQAVEEDERRRELEI-----IAKTTSP-- 957  
QY 1042 IHTAATPMSLPKSSSTGVGEGALGSGSRSTSSGSAEP---GAAHHEMKSPSPARSSPHSP 1098  
DB 957 -----AFNNQVAPAECTQCPSSPEESPRILLNAYH----- 990  
QY 1099 KSAASWTSRRSSSRNSGRAPSLKRSPSC-----EERSLISEGGSODEESSEDRA 1153  
DB 990 -----PSPERKHSANLDAIIDRLVY-----RNSAPFDRF 1019  
QY 1154 SPAGSDHRHRSGLERAKSPFDLPLOVPLHRTASGRSSASEHODCNKSGSLART 1213  
DB 1019 SPV--SEGDDSLRNHA--SLVLPVANGV-----YRORVHMKRSQSLKA 1063  
QY 1214 LRTDDPOLDDGDDNDEGNLSKGERIQAMVSR--PACCRSDSWSAVIPPQSRFLLOH 1272  
DB 1064 LAEEERKREARON-----TFVRKLKTKTLHRTFSFLIMGPKNPLRIKOL 1110  
QY 1273 RITTKMDHYVLYVIFNCTIAMEBKIDPASHAEIFLTINNYFTAVFLAEMVYKV 1332  
DB 1111 OTQOKWMDYVLYVIFNCTIAMEBKIDPASHAEIFLTINNYFTAVFLAEMVYKV 1169  
QY 1333 ALGWCFGQAVLRSSWNLGLLVLVISVIDLVMSWSDGKTIILGNLRYLRLTLRPLR 1392  
DB 1169 ----- 1169

1393 VISRAOGLKLVETIMSLKPIGNIYVICAFFIIFGILGVOLFCKGFEVCOGEDTRNIT 1452  
1169 -----VSRITPLKPIGNIYVICAFFIIFGILGVOLFCKGFEVCOGEDTRNIT 1217  
1453 NKSDCAEASR--WVRKRYFNEDLGOALMSLVFLASKDVNDIMTDLAVGVDOOPIMN 1510  
1218 TKADCE-DYRKNKVRNRYNEDNLGOALMSLVFLASKDVNDIMTDLAVGVDOOPIMN 1276  
1511 HNPMLLYFISFLIYAFVYVNMFGVGVVNEHRCROHOEEEARREERLRR----- 1565  
1277 YNEWRMYFISFLIYAFVYVNMFGVGVVNEHRCROHOEEEARREERLRR----- 1336  
1565 -----LEKRRHMLMDVIVASGSSASAASEOCPYSDYSRRELLVHNLCTSHYDLFT 1619  
1337 FEESMAGKRRKNR--VMAGSAIKSIFSVERNPYHYDGHTRFLGHGIVTSKYEDLAI 1393  
1620 TGVIGLVNVTYMAEHYQOPLDALKICNYITVIVFESVFLVAFGRREFODRWNQ 1679  
1394 AAVGINIVASMEFYMPGLKYLKALNEFTAVFTLEAMKLALGKREFIEKMR 1453  
1680 LDIVLSTINGITLIEIEVNASLPINPTIRIRNVRIRARVILKLMXAVGRALLDTVM 1739  
1454 LDMFVILSTINGITLIEIEVNASLPINPTIRIRNVRIRARVILKLMXAVGRALLDTVM 1512  
1740 QALPOVGNILGLFMLFFIFALGVLEFGLDECDTHPCBGLGRHATFRNGAFLTLFR 1799  
1513 EALPOVGNILGLFMLFFIFALGVLEFGLDECDTHPCBGLGRHATFRNGAFLTLFR 1572  
1800 VSTGNNNGIMKDLR--DCC-----QESTGNTYISPIFYEFVLTQOVLVNVAVIAM 1853  
1573 IATGNNNGIMKDLR--DCC-----QESTGNTYISPIFYEFVLTQOVLVNVAVIAM 1632  
1854 KHLESNKAKEAELEAE 1872  
1633 KHLESN---KRDAGPAE 1648

196 SMRLVTLTDLTLPMLGNVLLCFEVEFIEGIVGOLMAGLNRCELPENFSLPLVDL 255  
214 GIKTVNALLKSMKMLDLVLTFTFLCVLGMOLVGLSKNKCYLKRPLPLTTIDYDS 273  
256 -----EPYOTENEDESPEFISQPRENGMRSCRSVPTLRGEGGGPCSLDIETYNSSNT 311  
274 FVNESHHYHPDIDTITC-----GNSTAGPCPLNY----- 307  
312 TCVMNNOYTTGSCAGHNPFKGAINEFNGICAMIAIQTIVITLSEWVDIMFVMDHSEFN 371  
307 TGL-----ANG--NPNNGYTNLDNFGWAVTAAQVLTLDWENVYVTVLSMGSWY 357  
372 FTYEFTLLTIVSFPINCLVIAVTOFSETKORESOALREOYRFLSTNASTLASFSEGS 431  
358 IFTFEMVITFSGSFILNVLAVAVSY-----QOEVLALDREYVNNLNGVASTSYFEG 412  
432 CYELLKYLYILKRAARLAQVRAIGVAGL--LSSPVARSQOEPQSSGCTSRHRLS 450  
413 C-----VPRKLNRSKSKTKSLASKMSFCVPCFSIGQPHSNG----- 454  
491 VHLVHHHHHHHHHNGTLRVPRAPE--IQDRDANGSRRLMTPPSTPPSGGP 547  
454 -----HASNDSHASTG-GTIRVDSTAIEKMLNDKNEVATNGHSLPERKT----- 500  
548 RGAESVHSFYHADCHLEPVRCAAPPPOCPSEASGRTVSGKRYPTVHTSPPELIKDAL 607  
500 -----SSEF-----SVASDN---SIH-----IRNMS 518  
608 VEVAPSGPFTLTSF--NIPPEPSSMHKLETOSTGACHSCCKISPCSKADGAGCP 665  
519 TEVMPQ-----TSKEDDNI-----LTKTLDVKS-----SFLKSLAISQSS----- 556  
666 SCPCARTGAGPESADHMPDSDSEAVEFEFTODAQSHDLDPHSRRORSRIGDAEPSS 725  
556 -----TDCVDNNENINNTQPOKSYFTARV-----LIPROSLAQSTGSAITHKT 601  
726 VL--AFWRLIODTFRKIYDSKYFGRGIMAILVNTLSMGIEYHOPELTNALEISIV 782  
602 ITRKOTKMRIRRMISKIVLHGYNDFITFCMYNTLFLSEYHMDSNYLVLVEIGKV 661  
783 FTSPLAEMLLLVYPPGYIKNPNIFDGIYIVISWE-----YVQGGGGLSLRTF 837  
662 FTWVLEMLLITLAFEGEYKYSKRNIPDFGIYIVISWDLMAVELLVDDHSGLSVLTFT 721  
838 RLMRYVILKIVFPLAQOLVLMKTMNVATPCMLMIFIFSLIGLHFGCKFASERD 897  
722 RLRYVKLQASQNMMLISTARSGOGLNLTIVIGIYVLAVGOLPDQYTTKNE 781  
898 GDTLPDKKNEFSLMAIVTVFOILTOEDMKNKVLVNGMASTSMALYFTALMTFGNYLTF 957  
782 NGDVP--RNNFTFQWHSFMMIFRYLGE--WIEPLVOCMASTSMATLFTLVIGNEFLVL 839  
958 NLLVATLVEGFOEIEGKREDASGOLCQLPVNSOGDPATSESEPPFFSPSYVDGDDR 1017  
840 NLLVATLVEGFOEIEGKREDASGOLCQLPVNSOGDPATSESEPPFFSPSYVDGDDR 874  
1018 KRIALVALGEHAELKRS--LLEPLLIHTAATPMLSPKSSGTGVBALGSGGRTSSGS 1075  
874 -SKLSR-ALFRSTVSKTQVLTIRVHD-----GENATDGDK----- 910  
1076 AEPGAHHEMKSPSARSSHPWMAASSMTSRSSRNLGRAPSLKRRSPGE----- 1130  
910-----APTOUNGLESTSDASTSSTSMANAMISAVTFAOQNKKGKGLNRDTF 957  
1130 RSLLSGEGQESODEBSESPEDRASPGSDHRRGSLEREAKSSFDLPDTLOVGLHRTA 1189  
958 RRLSLATE-----TANDSNTSNVLAMAAST----- 985  
1190 SGRSSASEHODCKGASGLARTLRTDDPOLDDGDNDEGNLSKGERQIAVYRSRLPAC 1249  
985 -----SITGR-----QDHGTSDDPPDPPTVEVDECCPACMKMKMTG 1019  
1250 CREDSMSATY-FPPQSRFLLCHRIITHKMPDHVVLVLIIFLNCIITAME-----RPXI 1302

Query Match 13.7% Score 1709.5; DB 5; Length 1810;  
Best Local Similarity 25.4%; Pred. No. 4,7e-119;  
Matches 512; Conservative 344; Mismatches 684; Indels 473; Gaps 66;

78 VCNPFERYSMVILLNVTGLGFRCEDIADSOQRILQAFDFIF-AFAVEMVYKM 136  
110 ITNQFEEFILLTIYVNCIFLAL-----RDAPQEPVEFAIYTFEMLIKI 155  
137 VALG-IFGKKYIGDTWNLDFPIYAGMLEYSLDQNSFSVAVRYRLRLRAINRP 195  
156 IAGLVHHEVAYLRDPMNMLDFEVVILGYVTLVNVANL--SGIRFVRLALRTISAVE 213

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Db 1020 CILTR--WKASDGYRSMRNLRLAVKFKVHKFFETLAIIMASSIALTFEDINIPSPKL 1077
Qy 1303 DPHASERIFLILSNYIFLAVFLAEMTVKVALGWCFCBOALRSSMNVLDGLVLISVID 1362
Db 1078 -----KEYLOQINIFFAVTFEIEFLKVLGL-----GVASYFRKCMNCLDLVLIVFV- 1126
Qy 1363 ILVSNVSDSGCT--ILGMLRVRLRLRTLRPRVRSAGGLVAVETLMSLSKPIGNVVI 1420
Db 1126 ---SSVAYLSDNODSLSSIRSLRLTRALRPLRLAISRMGEMRVVNSLFLPILGIVGLV 1183
Qy 1421 CCAFFILIFIGLVDFKRFVFCGEDTRN-----ITKSDCAEASRYRWVHKYFNPNLG 1475
Db 1184 CMVFMILIFISMGVCFEGFECVGNKKERLPISIVQNRSEICIOGYRWVNSDINFDNSL 1243
Qy 1476 QALMSFVLASGDVNDIMVGDVAVGDOOPIMNHNPMMLLYTISFLIYAFVLMFV 1535
Db 1244 NGPMALFOVAITEGMIYVNRDAVAREVDQPSDGINFSAYVYVFLIVSGFTLLFLFI 1303
Qy 1536 GVAVENFKRCRHOEEEA-----RRREKRLRLKRRN--LMLDD 1576
Db 1304 GVLIDNFKLQYEDFGALDVLTPRSORAMGTRKAAKPKKPKVSRPENSFMALFD 1363
Qy 1577 VIASGSSASASEACKRPIYSYSRFLLVHHLCTSHLDFTIGVIGLVNVTYAMHQ 1636
Db 1364 VHS-----SRFETLI-----MFF--ICLMLVMKIOHYG 1391
Qy 1637 QPQILDEALKICNYIFTVIFVESVFKLVAFGFRFQDMMNOLDLAILVLSIGITLEE 1696
Db 1392 QKPAVQALMINTLVFTGIFLEALIRIVLRL-HYFREPNNVDEVIVLVLSIGITLH 1450
Qy 1697 IEVNASLPNPIITIRMYRLARVLLKXAVGRALLDVTVMQALPOVNGMLLMFLF 1756
Db 1451 LEXEFLTPSP--VAARFRIGRLRLRYKGAKIRRLIFLALISLALLIGALLFLIM 1507
Qy 1757 FIFALGVLEFDLCEDETHPECEGRHATFRNFMAFLTFRTVSTGNNMGKIDFL- 1815
Db 1508 FIYALIGMSFGYK-----KTGALDSVNPETFGNSMLLFRISTSGMWDVAKPLIK 1562
Qy 1815 -RDCDOE-----STCYNTVISPITVFSFVLTAQFVLVNVAVIAMKHEESKEAEEA 1867
Db 1563 PPDCKMLKCIENGCSFPMALVYFTFIFLFIILIMYALILELSQLH-EOEEVG 1621
Qy 1868 ELEAELELMKTLSPQPHSLPGSPFLMPGVEGVNSPDSKGPAPHTAHIGAAGCF--SL 1925
Db 1622 VDDDLDMY-----YHMERFD-----PGAIQIYTH-SALSDYFDGL 1657
Qy 1926 EHPYVPHPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRN--GSTAERSL 1976
Db 1658 DHELRIPOKFKACINLINPIKQ-----DRVHCFDVMQALVRVLGDIEDGL 1706
Qy 1977 GHRGWLPRKAGSGSILSVSPADTSCILQLPK 2009
Db 1707 G-----SSVATYLLKMSKMEQHCISTEPK 1730

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RESULT 6
089089 PRELIMINARY: PRT: 2333 AA.
AC 089089:
DT 01-NOV-1998 (TREMBLrel. 08. Created)
DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10. Last annotation update)
DE PORE-FORMING CALCIUM CHANNEL ALPHA-1B SUBUNIT VARIANT A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-NEURONAL;
RC MEDLINE: 97163393.
RA LIN 2., HAUS S., EDGERTON J., LIPSCOMBE D.;
RT Identification of functionally distinct isoforms of the N-type Ca2+

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RT Channel in rat sympathetic ganglia and brain."
RL Neuron 18:153-166(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-NEURONAL;
RC SCHORGE S., GUPTA S., LIN Z., LIPSCOMBE D.;
RT "Stabilization of the N channel alpha1b message by calcium entry
RT through L channels."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF054477; AAC29043.1; .
DR PFAA: PF00520; Ion_trans; 4.
SC SEQUENCE 2333 AA; 261928 MW; D6E05C95 CRC32;

Query Match 13.7%: Score 1706.5; DB 11; Length 2333;
Best Local Similarity 24.1%: Pred. No. 1,1e-118;
Matches 649; Conservative 363; Mismatches 817; Indels 859; Gaps 96;

Qy 27 GAGRGPGSTKEDGSDASEAGLPPALAPVF-----FYLSQDSRP 70
Db 25 GAGGAGGCGGGLPPGQRLVKQSIQARATMALNPIPVKQCFYVNSLFEVSEDNV 84
Qy 71 RSMCLPTCNPFERSVSLVLLNCVTLGFRPCEDLACDSQCRILQAFD--FIFAF 127
Db 85 KRYARITWEPPEEYMLATIANCIVAL---EQLHPGDKTPMSERLDTEPIFTGI 140
Qy 128 FAVENVVMAVG-IFGKCYLGDTRNRLDFFIYAGMEYS--LDLQVNSFAVTRV 183
Db 141 FCEAGIITIALGFVHKGSYLRNGMVMDFVVLGTIATGTDPDRL--TLRAVR 195
Qy 184 VLRPRLAIRNRPRIYLTLLDTLPMGLNVLLCFVFFIETIVGVQVMAGLLRRCL 243
Db 196 VLRPLKLVSGIPSLQAVLKSIMKAMVPLDQIGLLEFALIMFALILETYMGFHRACF- 255
Qy 244 PENFSLPLSVLEPYCYOTENEDESPFICOSPRENMGSRSPVTLRGEGGCPCLDE 303
Db 255 -----PNSTAEAPV-----GDPCKCKEAP 273
Qy 304 TYNSSNTCYVNMNOYITNCAGSHNPKALINFDNIGVMIALFOVITLGVNDIMTV 363
Db 274 ARLCSIDEC--REYV-----GNFGITNEDNLFIILVFCITMEGTDLTYNT 323
Qy 364 MD-ASFPNFYFILLIIVSGFEMINCLVIVATOFSETGORES-----QLMREQVRFF 416
Db 324 NDAAGNTNMMLTFLIPLIIGSFPMNLVGLVSGEPRKEREENRRARLKLRRQOIE- 383
Qy 417 LSNASTLASFSEPGSCYEELLYVYLIRKARRLAQVSAIGVRAGLLSSPVARSQGP 476
Db 383 -----RELNGYLEWIFKAEVLAED-----KNAEEK 410
Qy 477 QPSCGCTSHRRLSVHHVYHHHHHHHHYHNGTGLAVPRASPEIODRANGSRRLMP 536
Db 411 SPLDYLKRAATKSRNDLIR-----AEEGEDR----- 438
Qy 537 PSTPPSGPPRGAEVSAHSFYHADCHLEPVRCQAPPRCPSEASGRVYSGKYVPTVHTS 596
Db 438 ----- 438
Qy 597 PPELTKDALVEVAPSGPPTLSPNIPROPFSMKLLETOSTGACHSCKISSPCK 656
Db 438 -----FVLDL-----CAAGSPFAR 450
Qy 657 ADGACGPDSCPYCARTGAGEPESADHVMPDSSEAVEEFTQAOHSDLRDPSRRSROS 716
Db 451 AS-----LKSGETESSYF-----RRKEK- 470
Qy 717 LCPALPSSVLAFWMLIDTFRKIYDSKTYRGIMAILVNTISMGLEYHEQPEELTNAL 776
Db 470 -----MREFL--IRRVKQASFYWVWLVVALNTLCVAMVHNVQ-- 514
Qy 777 EISNIVFTSLFALEMLLKLAVYGPGFYIKPNYNIFDGVIVISVWETVQO--OGGGL 831
Db 515 YRADEVFGLTLTMSLKMVGLGPPSYFRSSFCDFGIVAGSIFVYMAIMKPGISFPI 574

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QY 832 SVLRTFRLVRLKLVLPALOROLVLMKTMNVATFCLMLFLIFISILGMLFGCK 891  
 575 SVLPALRLRFRKTKYKWNLSRLNVLVSLNMSKSIISLFLFLFVALLGMOJFGGQ 634  
 QY 892 FASERDGLPDRKNFDSLMAIVTVFOILQJEDMKVLYNGM-----ASTSSMALYFI 946  
 635 FNFODEFTPT-----TNFDTFPAAILTVFOILGEDMNAVMHGLESGOGVSKGMSFYFI 690  
 QY 947 ALMFNGVNLVFLNLVAILVEGF-QAEIEGK-----REDASGOLSCIQ----- 988  
 691 VLLFNGTLLNVLALAVDMANAOELTKDEEMEPANOKLALQAKAVAVSPMSAA 750  
 QY 988 ---LPVNSOGG-----DATKSESEPD----- 1006  
 751 NISIAAQNSAKAKRSVWEQASOLRLQNLASCEALYSEMDPEERLYASTRHVRPDMK 810  
 QY 1006 -----FFSPSVDG-----DDRRKRLALVALGHEALRKSLLPRLIIH-----TAA 1046  
 811 THMDRPLVVEGRDGLRGPAGNKS-----PGTEATEADPPRRHHRDRBDKTSAS 863  
 QY 1047 TP-----MSLPKSSSTGVGEALGSGSRRTSSGSAEPGA-----AHHEKMSPP 1089  
 864 TPAGEDORTDPCRAESTETGAREERARRSHSKEA-PGADTQVRCERSRHHRRGSGPE 922  
 QY 1090 SA-----RSSPHSPWSAASMTSRSSRNSUGRAPSILKRSPSGERSLSGEOES 1141  
 923 EATEREPRRHRRHRAOOS-----SKEGKEGTAFVL---VPERERRARRHGRPTGP 970  
 QY 1142 ODEESSSEDRASPAGSDHRRHRSLEAKSSFDLPDTLOVPGYLH-----RTASGRSSA 1195  
 971 RETENSEEPT-----RHR-----AKHYRPTLEPPERERVAKESNVVEGKET 1014  
 QY 1196 SEHOD-----CN-----GKSASGRILARTL-RDDPOLGDDDDND----- 1229  
 1015 RHHQKREPCDLEALAVGVGSLHMLPSTCLOKVEDPEDADNONGVYRMGSOQSDPSTT 1074  
 QY 1229 -----EGNLSKGR-----IQAWYRSMLPACCRBDSMS 1257  
 1075 VHVPTLTGPGEATVVPASANTLEGO-AEGKKEADVDLDRGPRPLVPS-----S 1126  
 QY 1258 AYIFPPOSRFLRILRHITHKMEDHVVLYIIFLNCITIAMERPKIDPHSABRIFLTSNY 1317  
 1127 MCCLSTNLRLRFRCHYIVMRFEVILVIALSSIALAEDP-VRTDSFRNMLKMYDY 1185  
 QY 1318 IFTAVFLAMTVKVALGWCJEGEOALNSSNANVDGLVLISYDILYSMV-SDSGTIL 1376  
 1186 IFTGVTFEMVIMKIDILGILLHPGAYFRDLMNILD-----FIYVSGALVALFAFSGSGKDI 1241  
 QY 1377 GMLRVILRLRLRPLRVLISRAGLKVUETLMSLKPIGNIVVICAFIIFIGILGOVF 1436  
 1242 NTKSLRVLRVLRPLTKTRLPKLVKAVFCVYNSLKNVNLIVLMFMFIFAVAVOLF 1301  
 QY 1437 KGFVYCOGE-----DTBN-ITNKSDECAEASYSR-WVRHKYFNDLGOLMSLFVYLSK 1487  
 1302 KGFVYCTDESKLERDCGOYLDEYKEVEAOPQMKYDHYDNVLMALLTLTFTVSTG 1361  
 QY 1488 DGVNDIMTDLAVGVDOORPIMNHNPMMLLYFISFLIYAFVLMFVGVVENHKKRO 1547  
 1362 EGMPLVKLSVDAITYEEOGSPGFRMELSYFYVVFVVEFFVNFVFAVALLITP----- 1417  
 QY 1548 HOEEEARREERKRLRLRLEKRRNLMDVVIASGSSASASEAOCKPYUSDYSRFRLVH 1607  
 1417 -QOGGDKVME-----CSLENER-ACIDFAL-----SAKPLTRYMP-QNKOSPOYKIV 1462  
 QY 1608 HICTSHYLDLFTIGVIGLVNVTAMHYYOQPOLDEALKICNTIFVIVVFSVETKIVAF 1667  
 1463 TFFVSPPEFEYFIAMIALNTVLMKFEYDAPYEELMCLNIVFTSMFSLCIIKILAF 1522  
 QY 1668 GFRFPDDRNQDLAIVILSINGITLEE-EVNASLPINPITIRIMARLIRAVYKLK 1726  
 1523 GVLNVEFDANVDEYVTLGSLIDILVTEIAETN-----NFIWLSRLRFRARLILKLR 1577

QY 1727 MAYGBALDTVMQALPOVGNLGLLFMLFEIFAFALGVEFLGDECEDETRPCBGLGRHAT 1786  
 1578 OGTYIRILLMTFVOSFRALPVCLILMTEPIYALITGMOJFGNALDDG--TSINRHN 1634  
 QY 1787 FNFEGMAFLTERVSTGDNWNGIMKDTL--RDGD-----OESTCINVTIVSPIYFVSUFLAQ 1841  
 1635 FRTFLOALMLLFRSATGVAWEIMLSLGNRACDPHANASQC-GSDFAVEYFVSFIPLCS 1693  
 QY 1842 FYLVAVVAVIAMLKHEENKEAK-----EEALELEALE-----LEM-KTL 1880  
 1694 FLMLMLFAVAVINDNEEYTLRDSLSLGRPHHDEFTIRWAEIDPRAACGALSYNDMEMLKHM 1753  
 QY 1881 SPQPSPLG-----SPILMPGVEGVNSPDSKPGABRTTAHIGAAGFSLE----- 1927  
 1754 SP-----PLGLKCKCARAYAKRIVAMNPNINEMDTVHTSTLMAILRTALEIKLAPAGT 1809  
 QY 1927 --HPTWVRPHEVP-----VPLGDELTV-----RKGV 1954  
 1810 KOHOCDAELRKEISSVMANLPQKTLDLLVRPHKRDPMYGVKVALMIFDEYKONKTRTD 1869  
 QY 1955 RTHSLPNDSYMONGNSTARSLGNRWGLPRAOGSILSVHOPADTSCILDPKDVHYL 2014  
 1870 QTHQAPG-----GL--SOMQPVSLFPIKAT-----L 1894  
 QY 2015 LOPHGAPTWGALPKLPPRGSPPLAQR---PLRQALIRTDLDVQ-----GLGSRDILLS 2066  
 1895 EOTAPAVLNGA-----RVFLRQKSATSLSNGALIOGIESGIKESLSMGTORTDVLX 1946  
 QY 2067 EYSGRSCPLTRSSFW-----GSSSIYOQRS-----GIOS-KVSKHILP 2106  
 1947 EA---RAPLERHSAEIPYGOFGALAVDVMONMTLRKPDGEPORGLEDSOGRAASMPRLA 2003  
 QY 2107 A---PCGLEPS-----WAKDP----- 2122  
 2004 AETQPRNAPSARKRISTLARPHGTOLCNYLDPRPSQVSHHHNRCHRRDKQKSL 2063  
 QY 2122 ETRSSLELDETE--LSWISGDLIPSSOEPLSPRDLKCYSVETOSCCRPRGSMWDEQRH 2179  
 2064 EKGPSLVDTEGAPSTAAGSLPHGEGSTGCRERKROERGSQE--RQPPSSSSEKORF 2121  
 QY 2180 STAVSCLDGSOPRLCPSPS-----SLGQPL----- 2207  
 2122 --YSCDRGSRPPOPKPSLSHPISPLALPEPHRPGSSVAGSPLMSTSGASTGR 2178  
 QY 2207 GGPSPRKKLSP-PSIS-----IDBPESQGSRRPSPG-----VCLRRAPA 2248  
 2179 GGRROLPPQPLPRPSTITKTANSSPVHFAEGOSGLPAPSPRLSRGLSEHALLQKEPL 2238  
 QY 2249 SD-----SKDPSVSPUDSTIASPSFKOTLSL-----SGLSS 2281  
 2239 SOPLASGSRIGSDPYLGORLDEASAHNLPEDTLTFEEAVATNSGRSS 2286  
 RESULT 7  
 097017 PRELIMINARY; PRT; 1891 AA.  
 AC 097017;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, last annotation update)  
 DE L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT.  
 GN STPCACHL.  
 OS Stylophora pistillata.  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;  
 OC Pocilloporidae; Stylophora.  
 RN [1]  
 RE SEQUENCE FROM N.A.  
 RX MEDLINE; 99148007.  
 RA ZOCCOLA D., TAMOUTTE E., SENGAS-BALAS F., MICHIELS J.F., FAJULA J.P.,  
 RA JAUVERT J., ALLEMAND D.,  
 RT "Cloning of a calcium channel alpha1 subunit from the reef-building  
 coral, Stylophora pistillata."  
 RL Gene 227:157-167(1999).

DR EMBL: U64465; AAD1470.1;  
SEQUENCE 1891 AA; 213240 MW; DC226908 CRC32;

Query Match 13.3%; Score 1657; DB 5; Length 1891;  
Best Local Similarity 24.4%; Pred. No. 4.3e-115;  
Matches 548; Conservative 343; Mismatches 640; Indels 712; Gaps 69;

QY 11 EESGPR-SFTQND-----LSGAGRGPGSTEDKPCSDSEAEGLPYR 54  
DB 2 EONGYRAFTGSKIFWNGTDMOTARLNGHGKRAKVAAROKKSGNTNR--PKR 59  
QY 55 ALAPVFFLSDSRPSKCLRTVCNPW--FERVSMYLILNCYTLGMPEDDIADSO 112  
DB 60 AL-----LCISLGNPIRMAINLV--EWKPEVMTLITIFANCALAFEPLE--KDS 110  
QY 113 RCRILQAFDDIF-AFEAVEMVVKVAVG-IRGKCYGDTMNRDLDEFIVAG---MLE 166  
DB 111 EINDNEVAEYFLAVFTMEANLKIIAGFLFHPGAYLRNGNILLDFYVVGATILVK 170  
QY 167 YSLDQNVSAFVTRVLRPLRAINRVPMSRLVTLDDLPMIGNVLLCFEVEFIG 226  
DB 171 AILSSGSPFVKALRAFVRPLRLVSGVSLQVLSIKALILPLFHALLVFEVLIYA 230  
QY 227 YGVOLMAGLLNRCLPNEFSLPLSVLEPRYQTEDESPFICSPRENGMSRCSVP 286  
DB 231 IIGVELFMGRILKTCY--DNTGASFE-EPH----- 260  
QY 287 TLRGEGGGPCSLDETYSNSSNTCYNMNQYTNCSAGEHNPKAGINEDNIGYAMIA 346  
DB 260 -----PCS-----SGSSGFCQDKAAGV--CEGKMGKPGNHGITTNDGLACMT 301  
QY 347 IFVITLEGVIMYFVMDA-HSFNYFIYFILLIVGSEFMNCLVYIATQFSETOR- 405  
DB 302 VQCILTEGTVLYINDAVGNSMPWYFVLLIWGSEFVLNLVGLVSEPEKARR 361  
QY 405 -----ESQLEOR-----VRLSNASTLASFEGSCYELLLKYILKKAARL 451  
DB 362 OKSGEFOKREKQVEDAYNGYLDWITQAEIDEGSESGDES-----KASKK- 411  
QY 452 AQVSRALIGVRAGLISPVARSQGEPOPSGCSRSHRLSYHNHLYHHHHHHYHLNGT 511  
DB 411 -----TSRSQRT-----EDLEMDRNERQDSI-----SCHDTNHT- 442  
QY 512 LRVAPRAPEIODRANGSRRLMPPSTPTSPGPPGAEVSHFYHADCHLEVRQAP 571  
DB 442 ----- 442  
QY 572 PPRCPSEASGRIVSGKYVPTVHTSPPEILKDALVEVAPSPGPTLSFINIPGPSS 631  
DB 442 ----- 442  
QY 632 MRLLETOSTACHSSCKISPCSKADSGACGDCPYCARTAGEPESADHVMPDSE 691  
DB 442 -----GMCHEKRY----- 451  
QY 692 AYVEFTQDAQHSRLDRPHSRQRORSIGRPAESSVLARMLICTFRTKYVSKTFGAGIM 751  
DB 451 -----LKKWHRROTE-----LRAVFTQAEFWYVI 476  
QY 752 IAILVNTLSMGLEYHEQPELINALESINIVTSFALEMILKLVLVRFYKIPYIE 811  
DB 477 VVVFELSLTLEHYPOLMKFLPDANKRLGLFTIEMIKYKMCIGFHHYFASLRF 536  
QY 812 DGVIVY-----ISVWEIVQGGGSLVLTFTFLMRYLALVRLPRLQQLVYLAKTMDV 866  
DB 537 DCVLVATSSLELATLALOPPLGISLVLCILRIFFVTRWSSLSLVLASLNSMSI 596  
QY 867 ATPCMLMLFIFISILGMLFGCKFASERDGTLPDRKNFSDLSLMAVTVFQILTOR 926  
DB 597 AGLLLSLSTFMLCSLGMQIFGK--NTDDDEIP-RSNFESFRALITYFQILIGDM 653  
QY 927 NKVLYNGMAS-----TSSMALFIALMTGNTVLENLVAILVEG-----QAE 971

DB 654 NAYMVDGIRAGGIGEGSALAILYFELVYGVNLYILLNFVLAIVDNLADAEINTEME 713  
QY 972 ELGRKEDASGQLSCIQ--PYNOSGQATSESEPPDFSPVGGDDRKRRLALVALGHE 1029  
DB 714 EKKRKEARERKELAKMGKSVDSQ-----RIODG----- 745  
QY 1030 AELRSLPLPLIHTAATPMSLPKSSST---GVGALGSGSRRTSSGSAEPGAHNEM 1085  
DB 745 -----AIVPN---HSSABRSNVLTKSTQELHSGTLNGVAFYA----- 783  
QY 1086 KSPPSARSSPHSPMSAASWTSSRSRNSLGRAPSLKRSPSGERSLSLSCGQESODE 1145  
DB 783 -----SHDV 787  
QY 1146 ESSEDRASPAGSDRRHRSLERAKSSFDLPDTLQVPLHRTASGRSASEHODNGKS 1205  
DB 788 EAQSTDISEIVGS-----KSAVSN---NNES 810  
QY 1206 ASGLARLRTDDPOLQODDYNDEGNLSKGERIOAWYRSLPACCRERDSWAIYPPQS 1265  
DB 811 ASA-----SSSDID-----RAEP-----PESALFIFSPN 837  
QY 1266 RPLCHRIITHKMDVLYVLIIFLNCITTAEMERKIDPSPAERIFLTSNYFTAVFLA 1325  
DB 838 IFRVYCKIANTYTFVNFILCLIVSSITLAEDEP-LNASKARQVNTFYFTSVTF 896  
QY 1326 EMTKRVVALMGCEQVAYLRSSMNVLDGLVLSVIDLVSWSDSGTKILGMLRVRL 1385  
DB 897 ELIVFISYGLILHKSFCRSRFAFNLDDLVAVSVISISLR-----TSQFSVRLIRVL 950  
QY 1386 RILRLPLRYSROGLKLVETILMSLKPIGNIVYICAFPIIGILGVOLEFKFVCOG 1445  
DB 951 RYLRPLRLAIRAKGLKRVYGVSAVAVKTIGNIKVYMLRQELRAVIGQLEFKFTFSCND 1010  
QY 1446 EDTRNITKSDCAEASY-----RWBRHKYFNLGQALMSLEVLASKDG 1489  
DB 1011 E---KILTAEEC--QGNVYIDFKGPELSNPVYKEREMRHDDFNVDGAMLLTFVTMFE 1066  
QY 1490 WYDIDWDGIDAVGPOOPIMNHNPMILYFISPLIYAFVLMVGVVVENHKKRQNH 1549  
DB 1067 WGLIENSIDSTEDVKGQNNRPMVAIYITITITIAFPMLEVGFTVLT----- 1120  
QY 1550 EEEEARREERKRLRLERKRRNMLMDVYASGSASASAEQKPYYSIDYRRELLVHNL 1609  
DB 1120 ---OSEGREEFECBLEDKNOQCI-----EPALAKAPLKRYIPENRLOFHTMPY 1165  
QY 1610 CASHLDLEITVIGLVNLYTAMMEHYQOPOLDEALNICYFIVIVFESVKIYAFG 1669  
DB 1166 VTSQAFETLITAFVTCNVLMQYVDEPKLYTRVLDGFNIGFAVFLLECILKLTAEPK 1225  
QY 1670 RYFODRNNOLDLAVLLSINGITLEEIVNASLPIMPTIIRIVRYLRIARVLLKMAV 1729  
DB 1226 KNYFTDRWNLFDLIVGVSIIIDITMNEVSSQMFAG-----FRLERALRLKLLNQS 1280  
QY 1730 GMRALLDYM---QALPYGMLGILMLIFITFALGVELFGDLECDETPCGLRHAT 1786  
DB 1281 GIKTLMTFISFQALPRV---ALLIYMEFTIYAVIOMEGRAINSQ---TAIRNNNN 1334  
QY 1787 FNFQGAELTFEVSSTGNMNGIM-KDILRD---CDOE-----STCYNTVISPFIYFS 1836  
DB 1335 FQTPQSLMVFERSATGEMWQIMLACTHNRDVKCDQNDAPQDEPSGUGSDFAFYFVS 1394  
QY 1837 VLTQGVLYNVVYIYALMHNDESKKEAELELALELEKTLSPGPHPLQSPPLWPG 1896  
DB 1395 YSICSEFLINLEVAIYIMNFYLTLD-----WSILPHNHIDEX 1432  
QY 1897 VEGVNSPDSPPKPGADHTAHGAASGEFLEHPTM---VPHPE---VPRVLCPLDILT 1947  
DB 1433 VAVWSEYD---PDAICVKKHDIYTVLKLRLPRLGPFKPCFHRAKCRLYTMNG----- 1485  
QY 1948 VAKSGV-----SRTSLPNDSTYMCNGSTAESNLGHRGKGLPKAOSGSITLV 1994

Db 1485 LTKDGVDFNATLFGILRSSINIKRPGKSIDKANEVRNIIIRTW--PKT-SMELLDK 1541  
 QY 1995 HSOPADTSCILQJPK-DVHYLLO-----PHGAPTWGAIPKLPP-PGR 2034  
 Db 1542 VVOSSGVDRDVTYKFKATYIIIOYFRFRKAROKAKONQANEPHGNSTMALQALRTHGL 1601  
 QY 2035 SPLAORPLRQMAI-----RTDSLVOGLSREDLSEVS-GPSCPLTRSSSF----- 2082  
 Db 1602 GPQLRRRAISGGLSDDEDLFLKEDDSOKRAHDKGFWSLKAIVSVPRHSFRSARLSA 1661  
 QY 2082 ---WGSSIOVQOQRSQISQSKYSK 2101  
 Db 1662 FLGRNNGLETKKRSSMSNLSE 1684

RESULT 8  
 ID P90670 PRELIMINARY: PRT: 1993 AA.  
 AC P90670:  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE SODIUM CHANNEL ALPHA-SUBUNIT SCAP1.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 OC Aplysiidae; Aplysia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-NEUROUS SYSTEM;  
 RX MEDLINE: 97238630.  
 RA DYER J.R., JOHNSTON W.L., CASTELLUCCI V.F., DUNN R.J.;  
 RT "Cloning and tissue distribution of the Aplysia Na<sup>+</sup> channel  
 alpha-subunit cDNA."  
 RL DNA Cell Biol. 16:347-356(1997).  
 DR EMBL: U66915; AAC47457.1; -  
 DR PFM: PF00520; Ion\_trans; 4.  
 KW Ionic channel.  
 SQ SEQUENCE 1993 AA; 225896 MW; 4344A9E3 CRC32;

Query Match 13.1%; Score 1636.5; DB 5; Length 1993;  
 Best Local Similarity 25.2%; Pred. No. 1.6e-113;  
 Matches 542; Conservative 348; Mismatches 718; Indels 545; Gaps 75;

QY 4 EEDGAGAESGPRSTQGLDLSG-----AGRGSGSTEXDPSGADSEAE 49  
 Db 28 EEEAAHKAAPESDDDEDELDEPSHEENIKPNKLEAGKLPDSLEDP-----REYV 83  
 QY 50 GLPYPAL-----AFVFFYLSODSRPRSACLRTVCNPFWEERV 86  
 Db 84 GRLPELDEFYNNKTFVVLKKDKAIFRSATDAIFLLSPFIRIAIYILVHIFSL 143  
 QY 87 SMVLILLNCVTLGM--FRPCEDIACDSQRCRLQAFDEDFI-AFAVEMVYKAMALGIFG 143  
 Db 144 VMMTILVNCVFMAIISYTP-----PAFEHIFLGITVEAVKVLISRGFVL 189  
 QY 144 KK-CYIGDMNRDLDEFIV-IAGMLEYSLDLQNVSSAVTVLRLRAINVPMSRLIV 201  
 Db 190 KPTTYLRDMNMLDFEIVISAIYTKTVKSGNL--QALTFYVLAALKIISYIPLKTIIV 247  
 QY 202 TLLIDTLPMLGNVLLCFEVEFFIGIVGVLAMGLLRNCPLEPNSPLS----- 253  
 Db 248 GALLEAVRRLRDVMIITVFLSIFALIGMQLYSGALRCQVLPVDELGTINTHDEWMDW 307  
 QY 253 VDELPYVQIENEDSEPFISQPRENMGRCRSVPTLRGGGGGPPCSLDIETYNSSNT 312  
 Db 308 VNNESSHOKDFYDEWO--VC-----GNGTGAGCG--NGTIINGTAEL 346  
 QY 313 CV-NMNOYATNCAGHENPFKAINPDNIGYAWIAIFQVITLEGWDIMYFMDAHSFYN 371  
 Db 347 CLPNIGO-----NPNHDTSFDFNGMALCAFLMTQDFWSTLHLVRAVGAH 396  
 QY 372 FIFILLIIVGSPFMNLCLVIAIATQPSSETKQRESQLMREQRYRFLSNASTLASSEPS 431

Db 397 CLIFVLILGSLFYIVNLLIALIVAMSDEI-QKDDQADAEAEA-----AEQD--- 444  
 QY 432 CYELLKLYVILKRAARLA-QVSAIYVAGLSSPVARSQOEPOPSGSCRRSRHS 490  
 Db 444 --EERKEALISIMKSPSNSMNNDFEAGVR-----TAGDKAEERLSLTSDSATS 494  
 QY 491 VHHLVHHHHHHHHYHLGNGFLRVBPASPEIQQDANGSRRLMPPSTPPSGGPRGA 550  
 Db 495 AHLKPSRLNOKRH-----SLSLP-GSPYIHRNNSGSOYMWKRPVPTAKRS----- 540  
 QY 551 ESHVSFYHADCHLEPVRCAAPPPCPSEASGRVYSGKVPYVHTSPPELIDKALVEV 610  
 Db 540 -----PYCPDR-----QPLVHHTLENLPLP-FADDSAAV-- 568  
 QY 611 APSGPPPLTSE-----NTPPG--PESSMKLLTQSTGNCHSSCKISSPCSKDAGC 663  
 Db 568 --TPSEEDICNFSFLRNPNGRFSFASQRPDGTGRSGSRSS--FASNHSRASRTSRG 623  
 QY 664 PDSCTYCARTAGE-----PESA-DHVAPDSSEAVYEFTQDAQHSDLRD 707  
 Db 624 -----SGGDDTKTQTLINFEKKGVPPVLDKSLDDQDSV--SSGSGCHCEKD 672  
 QY 708 PHSRRR---QSLCPDAEPSSVLA-----FWLIC 734  
 Db 673 KASESNPFLSHSPGPPVEMKDVWLKDLDOAGSHRRSFVSMYSIHQRTKMDIMMYFC 732  
 QY 735 -----DTPKRI-----VDSKYFGRGIMAILVNTLSMGIEYHEOPELTNALEISNIV 782  
 Db 733 TWDCHNPFQKIORLVSLEFMDAFVDLFTTICILVNTAMAEHDMEDDLAAVNAALV 792  
 QY 783 FTSLEFLEMILLVYGPFGYIKNPYIFDGIYIVISWEIVGOGGSLVLFTRLMRV 842  
 Db 793 FTAIFVEAFILILASPIYFKDGMNIFDSIIVALSMELSMKLPGLSVLRAFLRLRV 852  
 QY 843 LKIVRPLALQOLVYLMKTDONVATFCMLMLFFITFSIILGMHFGCKFS-ERD----- 898  
 Db 853 FKLAKSMPLNMLIIVGTMGALGNLITVLGITLIFRAVMOQLFSSDYTYEREIDAM 912  
 QY 898 -----GDTLPBRKNFDSLMAIVTVFQILTOEDMNKVLVYNGMASTSSMAL-YFIALMT 950  
 Db 913 GNVTTIKDKMP-RMNPNDLHSMIVFRLCGE-WIESMW-GCYLVSGMACVPFLLTYV 969  
 QY 951 FGNVYLFNLVAILVEGFAEIEIGKREDASGOLSCITLPVNSOGDAKSEEPFSPS 1010  
 Db 970 VGNLYVNLFLAILLSSFSESISQSE-----SODEPSKIEA 1007  
 QY 1011 VDDGGRKRRLA-----LVALGEHAEILKSLPLLIHTATPMSLPKSSSTGVGAL 1063  
 Db 1008 I---DREKRFGNWVKITVICIKYAKLQKQKMRPP-----PTQGOSEVN 1046  
 QY 1064 GSGSRRTSSGSAPEGAHHEMKSPPSARSSPHSPWASAASWTSRRSSNLSGRAPSLKR 1123  
 Db 1049 G-----KQPAVVDITVSMEXTPDPPDPCCPQAQIIC----- 1083  
 QY 1124 RSPSGERRSLSEGOESODEESESSEEDASPAAGSHRGRSLEREAKSFLDPTLQVP 1183  
 Db 1083 -----SARKDLKSPGS--HSNBS----- 1101  
 QY 1184 GMRHTAGRSSASEHODCNKASGRLARTLRITDDQLDGDNDNGLSKGERIOAWVR 1243  
 Db 1101 -----SHCSGSSLSAOTKTD--LEADHEINVEL-----VYVK 1135  
 QY 1244 -----SRLPACCREDS-----WSAIFPQSFRLCHRIITHKMFHVAIVYI 1287  
 Db 1136 EPDDCFYMTKRCPCVCKEYKSGIRAWMA-----VRCFFYRLTENKKFDSFIIM 1187  
 QY 1288 IFLNCITIAERKIDPHSARIFLILSNITFAVLAETVAVVLAIGMCFGOALRBS 1347  
 Db 1188 ILASCALADEDYILHAKRPLKLELVDVFAITIEELIKWLH-----FGKITYFTTA 1243  
 QY 1348 MNVLDGLVILISVDIVSVS-VSDSGTKILGMLRVRLRLRTIAPLVISAQGLKLVET 1406

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Db 1244 MCMLEDTIVMLSIYMLVADLTASEEGGSGMSMKSMTLRALRPLRAYSREMGKRVYNA 1303
Qy 1407 LMSLKLPGINIVICAFIIIFIGILGVLFGKGFVCGE-----DIRNITNKSDCAEAS 1461
Db 1304 LKRALPISICNVLLVCLFWLFLFINGVOLFNKGFACDEKGDYPREEPYNNKVCIDKG 1363
Qy 1462 YRMVRHKYFNFDMLGOALMSLFVLASKDGMVDIMYDGLDVAVDOPIMNHPMLLYFIS 1521
Db 1364 YMMTANQINFDHVLASAYLALFOVATYKGMIDIMNNAIDSTELIGQPSSEENVIMLYEVL 1423
Qy 1522 FLIIYAFFVLNPFVGVVVENFHKQHOEBEAREKRLRLREKRRNMLDDVYASG 1581
Db 1424 FIVFCSFFTLNLFIVITLENFS-----OKK-----AGG 1453
Qy 1582 SSASAASEACKPRYSKDSR-----FRL-LVHHLCTSHYDLFTTGYGL 1625
Db 1454 SLEMFTEEQ-KKYNNAMKRMQSKSPQKSIRPKKYLGLJFDITTOGKPIALMIVITL 1512
Qy 1626 NYVTNAMEHYQOPILDEALKICNTIFVIVFESVFELVAFGR-REFODRNQDLAI 1684
Db 1513 NMLTMEFHGMSAQMKNLIGFNLIFTITFAECVLKI--GLRWYFKIPMWVDFPV 1570
Qy 1685 VLLSTIGLIEIEVNASLPINPTIIRMLRILARVLKLMVAGMRALDVTWQALPQ 1744
Db 1571 VVLSIASLSFEF--DSFFISPTLLRIVRFRVGRVLRVKSAGITLILFSAVSLPA 1628
Qy 1745 VGNLGLLMLFFITPAALGVELGDLCEDETHPCBGLRHATFNFEGMAFTLFRVSTGD 1804
Db 1629 LENIGLILGLIMFIYALMGMMNF--MGAEOK--GLDANFNFTFLNLSFTLLRQMTSA 1683
Qy 1805 NNNGIKMDLRDCDOESTCYNTVISPITYFVSFLVLAQVFNVYVAVMLKLESENKAK 1864
Db 1684 GMSDVINGIACARBGCTKDNVATITLTYLVSVLVNMTAVILENFSQATED-- 1742
Qy 1865 EBALEAELEEMKTLSPQSPPLSPPLMWEGSVNSPDSKPGAPHTTAHIGAASGF- 1924
Db 1742 EDOGLLPD-DFDMYXEKMEKYPKASKYI-----PLQLDFV 1778
Qy 1924 SLEHPTVPRPE-----EVPVLP-----DLTVRKSGVSRTHSLP 1960
Db 1779 DYLEPFLRPKNHFLVKLDIPICENDRCROLDLALTNFGLGTGSDIP 1831

RESULT 9
Q28644 PRELIMINARY: PRI: 1984 AA.
ID 028644
AC 028644
DT 01-NOV-1996 (TREMELREL 01, Created)
DT 01-NOV-1996 (TREMELREL 01, Last sequence update)
DT 01-NOV-1996 (TREMELREL 08, Last annotation update)
DE SODIUM CHANNEL ALPHA-SUBUNIT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE-SCIENTIFIC NERVE;
RX MEDLINE: 96074641.
RA BELCHER S.M., ZERILLI C.A., LEVENSON R., RITCHIE J.M., HOWE J.R.;
RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
cells."
RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
DR EMBL: U35238; AAA89159.1;
DR PFM: PFM0020; Ion.trans: 4.
DR PFM: PFM0612; IO: 1.
KW Ionic channel.
SQ SEQUENCE 1984 AA; 225748 MW; EF89D962 CRC32;

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Query Match 13.0%; Score 1622; DB 6; Length 1984;  
 Best Local Similarity 25.6%; Pred. No. 1.9e-112;  
 Matches 532; Conservative 356; Mismatches 73; Indels 458; Gaps 73;

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Qy 54 PALAVVEFYVLOSRRPSMCLRTVCNPMFEERYSMVLINCYTLGMRPCE---DIACD 110
Db 104 PAL-----YILSPSPRLRISIKLVLSLSMLIMCITILNCFMNMNPAEYTKV---- 156
Qy 111 SORCLLAEDDFIF-AFAVENVYKVALGI-FGKKCYGDTWNRDLDFPIYIAGLLEYS 168
Db 156-----EYFTGTGYTFEESLVKIFARGFCVGEFTFLRDMNMLDFIVIFAYLTFF 204
Qy 169 LDIQVNSAVRYTVLRPLRINRVPMSRLIVTLIDTLPMGIVLLCOEFVFFGV 228
Db 205 VMLGV--SALTRFVLRALATISVIPGLKTIVGALQSKALSDVILITFELSFALI 262
Qy 229 GVQLMAGLRRNRCFLP-EN-----FSLPSVLDPEYTOTENEDSPFICSPRENGR 280
Db 263 GLQFLTGLHKRLKLTLENETLESIMSSIESEEDYKKFYFLLGSKDALCGRSTGSD 321
Qy 281 SGRSVPTLRGGGGGPPCSLDIETYNSSNTTCVNMNQYTCNSAGEHNPFGAIFMDI 340
Db 321 QC-----PRG-----YI--CVKGRNDYGYTSFDTF 345
Qy 341 GYAMIAIFQVITLGGWVDIMYFVADASHFYNYFILLIIVGSEFMINCLVIAIQSE 400
Db 346 SVALFALRMLTMDQWENLYOQTLRAAGKTYMIFEVVIFLGSFYLINLILAVVAAE 405
Qy 401 TKQRSQMLRQQRVRLSNASTLASFSEPGCYELLKYLIVILRKAARLAQV--SRAI 458
Db 406 QMANIEAKKQELFQOMDLRLKQDEADA-----IAAAAEYISGRSRIM 454
Qy 459 GV-----RAGLSSPVAR-----SGQEPQSGSCTRSHRLSVHNLVHHH 498
Db 455 GLSESSSTKSSKSAKERANRRKKKQKKLSGEEKGDXELKSSESEST----- 508
Qy 499 HHHHHYLG-----NGTLRVPRASPEIORDA-----NSRRLMLPPESTPTPSCG 545
Db 508 --SRQFHLGVGHRLAREKRLSAPNOSP--LSIRGSLFSARRSSRSLSPFKRGKDIDS 564
Qy 546 PRGSAESHYHADCHLEPRCAQPPRCPSEASGRVYSGKYVPTVHTSPPEILKDK 605
Db 565 EIEFADDSHIFGDN--ESRRGSLFVQRQRRSSNLQA----- 604
Qy 606 ALVEVAPSPGPTLTSTNIPPGPSSMHKLLLETOSTGACHSCKKISSPGKADSGACGD 665
Db 604 -----SRSPML-----QMNKMSAVDCNGVSLVD-----GPS 633
Qy 666 S-----CPYCARTAGGEPESADHYWPDSDSEAVVEYFQDQHSPLRPHRRRORS 717
Db 634 ALMLPENGOLLEPVILIDKATSDDSCTQIRKKRRSSVLSLSDM-----LNDPILRQAM 689
Qy 718 GPDAEPSSVL-----AFWRLICDT-----FRK-----YVDSKYF 746
Db 689 -----RASILNTVEELEESRQKCPMSWYFPAHFFLIWNCSPWIKFKFYIIVADPV 743
Qy 747 GRGIMAILVNTLSGIVYHQPEPELNNALIEISIVTSLFALMLKILLYVPEFYIN 806
Db 744 DLATITCIVLNTLPMAMHNMTEEPKNLVYVGNVYVTGTGFAEDMLKLIADPIYFQV 803
Qy 807 FYNIDGVIVIVISWEIVGQGGSLVLTFRRLMRVLKIVRLPALOROLVLMKMTDNV 866
Db 804 GNNVDSILVILSTLDELPLADVEGLYSRFRILRYEKLAKSMPTLNMILKIKINSVGL 863
Qy 867 ATFCMLMLFIFISILGMHLFG-----CKFASBDDGTLTLDKRNPSLMAIYTVQ 919
Db 864 GNLITVLIAIYIFAYVGMQLFGKSYECCKT---NDQSLP-RHMANDFRISFLIVR 919
Qy 920 IITJEDMKNVLYNGW-ASTSSMAALYFALTMTGQNVYLFMLVAAILVEGFOAEIKR 978
Db 920 VLCGE-WIETMDCMEVAGQAMCLIVMMVIGNLVNLFALLISRPSDNLSAIBE 978
Qy 979 ASGQLSCIQLFVNSGGGATSESEDPFSPVDGCGDKRRLATVALGHAELRSLP 1038
Db 979 -----DTDN--NLQIAVIRIKGINVYQTLR 1004
Qy 1039 PLIHITAATPMSLPK-SSSTGVCEALGSG-----SRRTSSSGSAEFGAAHHEKSPSPAR 1092

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Db 504 IIAVFLNSLAVEHYDOPDYITMELDRANYFGLFTFEMLLKIKYCLGIGYVLSNFKR 563  
 Qy 811 FDGVIVIVISWEI-----VGOQGGGLSVLRTFRMLRVKLIVRELPAQLOLVLMKTMON 865  
 Db 564 FDLVLVSSLLLEAVITVPTGPIGIVLRCVRLRLFXKTRWESLSNVOGLVSNIS 623  
 Qy 866 VATFCMLMLFIFIPSLIGHFEGCKFRASERDGTLPDRKNFDSLMAIVTVFOILTQED 925  
 Db 624 IGSLLILFLIFLIFSLGMOIFGGRFNLD---EQAPPRIINFSFMRSLITVFOILTQED 680  
 Qy 926 MNKVLVNGMAS-----TSSMALYFALMTFNGVYLFNLVAVLVEG-0AEELKRE 977  
 Db 661 MNKAVVYVIGSWGKIKNPSSIIATYVAVYVGNITLNLVFLAVDNLADENMKR-- 739  
 Qy 978 DASGLSCIOLPVNSOGDATKSESEPDFFSPVYDGGDRKKRLALVALGHAELKRSLL 1037  
 Db 739 -----VNEEEKRKK-----DAKIMKLT- 757  
 Qy 1038 PRLIHTATPMSLPKSSSTGVGALGSGNRITSSSAPRGAHHEKSPSARSSPHS 1097  
 Db 757 -----ARKKK-----DLSABGKKTETESTIDG---KDPISGSEGED 793  
 Qy 1098 PMSAASWTSRRSSRNSLGRAPSLKRRSPGERSLLSGEOESQDEESSEEDRASPAQ 1157  
 Db 794 V-----ELGNP-----KSKNGTLRHM-----GETSTEMSGKEARIRPLR 829  
 Qy 1158 SDHRHSLEREAKSPDLPTLOVPGIHRASGRSSASEHQCNGKSASGRALRLTRD 1217  
 Db 830 LS-----ELNLLKIPDM----- 844  
 Qy 1218 DPOLDGDDNDGNLSKGERIOAWVRSLPACRERDSWASATPEPSPRLLCHRIITH 1277  
 Db 844 PPES-----SPEISANKRLRYLCRLAVN 868  
 Qy 1278 KMFDBVVIIFLNCITAMERPKIDPRISARITLTSNIITFAVFLAETVAVVALGMC 1337  
 Db 869 KIFINSILVILIMSSVALAEDP-IGRDVLRNKLIGYFDIEFTFMFTEVYVMAIFGVY 927  
 Qy 1338 FGEQVLRSSNMVLDGLVLIVSIDILVSWVSDGSKILGLARVLRILTRILPRVISA 1397  
 Db 928 LHKRSFCRFFNOGLDVLIVANMAIMSRGSAI-----SVRLRLRLRLRLRALINRA 962  
 Qy 1398 OGLKIVETLMSLSEKIGNIVYICAFILIFGLVOLFKGKFFVCGEDJTRNIT----- 1453  
 Db 983 KGLKHVOCVPLAKRSIGNIMIVLLFQFPAVIGIDLFQGTFFYC--TRSRMTEBECK 1040  
 Qy 1453 -----NKSDCAEASYRWVRKRYNDNLGQALMSFLVSLASGDGVDIMYGLAVGY 1503  
 Db 1041 GFENSYEPVNLANPVYARTKHTFRDNYFOAYLSLFVYMTREGPSILHSIDSTYV 1100  
 Qy 1504 DQOPTMNNPMLLYFISFELLIVAEVYLMFVGVVENFKCRHOHEBARREKRLR 1563  
 Db 1101 NOGPFFNNRPFAIYVYIILIAFFMINIVGVIVTF-----ONEGESEFADCE----- 1152  
 Qy 1564 REKKRRLMLDDVYASSSSASASEACQKRYSDYSRFLYV--HLCSSHLDLFTIG 1621  
 Db 1152 -LDKQKR-CVEYVLT-----VKTYTFVPKRRQIHWIRVVSRLFEIWIIFG 1197  
 Qy 1622 VIGLNVYVAMEHYQOQILDEALKICNYITFVIFVESVFKLVAFGFRFODRNNQD 1681  
 Db 1198 FLIGNTIYLAQYHASKLYERVDGFNIGTAVFLDECVLKMAFNKRYFDPNNIIFD 1257  
 Qy 1682 LAIVLSTMGITLIEIEVNASLPIPIIRIMRYLARIYAKLLKMAVGRALLDPTM-- 1740  
 Db 1258 FVIYVGSJADIILIGLISDGSIKVNA-----FRLFRALRLKLLSOGDGIKTLMTWFMKS 1312  
 Qy 1740 -QALPOVNGILFEMLFFIPALGVELGDEDETHPCGELGRHATFNFNGAFPLTF 1798  
 Db 1313 FQALPFFV---GLLILFLFIAVIGMOVFGIRLDSG---TVINSNNNFTQFPQALVLF 1366  
 Qy 1799 RYSTDGNNNGIMKOTLR-----DQDOSTCYNIVISPIYVSVVLAQVYLVVAVYAVL 1852  
 Db 1367 RSATGENMOQIMMACVNSESKCEVDPSKTC-GTDFAVLYFMSPYMICFLLINLFAVAVI 1425

Qy 1853 MKHLEESNKE-----AKEEAELELELEMKTLSPQPHSLGSPFLMPGEVGNSPD 1904  
 Db 1426 MDNFNDYLRDMSILGAAHHELEEVYRIMAEVDPE----- 1458  
 Qy 1905 SPRKGAHPHTAHICANSGSELEHPYVPHPEVVPVGLDPLTVKRSQVSRHSLPNDST 1964  
 Db 1458 -----ASG-FMKHVDIVSMLEPPLGFGKCCPHREACKRLVSM---NM 1498  
 Qy 1965 MCRNGSTAE-----BSLGRGWLKPKAOSGSLSVSHQPADTSCILQPKDVHL 2014  
 Db 1499 MNANDGYDFATLFAVLRISLNLK-----KPADTEITLIANNELKRI 1541  
 Qy 2015 LQPHGAPLWGAIRK-----LPPRGSPLAORPLRQOALRTDLSLDVQIGSREDLL 2065  
 Db 1542 LK---HLM---PRTNENLPDKLIPPDYA-----EGI----- 1568  
 Qy 2066 SEVSGSPCPLRSSSFWGSSIO-----VOORSGIOSKYSKHIRLPAPCPGLEPSMA 2117  
 Db 1568 -----TVCKFATPLIDIEYFRKFKKROEERKKKNADSVIALKA---GLRTLOE 1613  
 Qy 2118 KDPETRSSLELDTLSWISGDL-PSQOEPLSPDLKCYSVETQSCRRRGSWLDEQ 2176  
 Db 1614 LGPKIKRA-----ISGLIMEEGTKEEKEKEKPMKRHSFMGLKGIISFAGK 1663  
 Qy 2177 RRHSTAVSLDSSQ-PLCPSPSSLOGOPLGPGSRPKKLSPPSISIDPESSQSR- 2235  
 Db 1664 KRSTYVALDPTPKOTKQPTSSV---SHLAAPNTQ-GKRISLPSLQTKTNSOODNIPR 1719  
 Qy 2235 -----PCSPGYCLRRRAPAS-----DSKD---PSVSSPLDSTAASPSPKD 2272  
 Db 1720 GALHEGSPIMQRLSPRLKRGQRKSTPEFIHHDSDALAPQIVLSQSDVSNPSK-- 1778  
 Qy 2273 TLSLSGLSDPTDMDPVLPLPHLSL-PCADPSS 2306  
 Db 1778 -----DRDNRSSSTPOHASSIPGADLNS 1800

RESULT 11  
 008562 PRELIMINARY; PRT; 1984 AA.  
 AC 008562;  
 DT 01-JUL-1997 (TREMBLER, 04, Created)  
 DT 01-JUL-1997 (TREMBLER, 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBLER, 08, Last annotation update)  
 DE VOLTAGE-DEPENDENT SODIUM CHANNEL PNI (FRAGMENT).  
 O: Rattus norvegicus (Rat).  
 O: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97188502.  
 RA TOLEDO-ARAL J.J., MOSS B.L., HE Z.J., KOZLOWSKI A.G., WHISENAND T., LEVINSON S.R., WOLF J.J., SIIOS-SANTIGO I., HALEGOUA S., MANDEL G., "Identification of PNI, a predominant voltage-dependent sodium channel expressed principally in peripheral neurons".  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).  
 RL [2]  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97007982.  
 RA KOZAK C.A., SANGAMESWARAN L., "Genetic mapping of the peripheral sodium channel genes, Scn3a and Scn10a, in the mouse".  
 RL Mamm. Genome 7:787-788(1996).  
 RL [3]  
 RN RP SEQUENCE FROM N.A.  
 RA SANGAMESWARAN L., FISH L.M., KOCH B.D., RABERT D.K., DELGADO S.G., TUNICKA M., JAKEMAN L.B., NOVAKOVIC S., WONG K., SZE P., TZOUIMAKA E., STEWART G.R., HERMAN R.C., CHAN H., EILEN R.M., HUNTER J.C.; J. Biol. Chem. 0:0-0(1997).  
 RL EMBL; U79568; AAB50403.1;-.  
 DL EMBL; AF000368; AAB80701.1;-.  
 DL PFM; PF00520; ion\_trans; 4.

PFAM: PF00612; IQ; 1.  
 FT Ionic channel.  
 NON\_TER 1984 1984  
 SEQUENCE 1984 AA; 226037 MW; CA080891 CRC32:

Query Match 12.9%; Score 1612.5; DB 11; Length 1984;  
 Best Local Similarity 25.2%; Pred. No. 9.9e-112;  
 Matches 514; Conservative 351; Mismatches 714; Indels 461; Gaps 67;

2 DEEDGAGAEESGQPRSTQLANDSGAGRGPR--GSTKEDGSASAESEGL-PY----- 54  
 37 DEKXD--DEEGPKRSS-----DLE--AGKQLPITYG--DIPGEMVSEPLDIDPIYADK 85  
 54 -----PALAPVFFYLSDQSRPRSMCLRTVCNPFEEVSMVLILNC 95  
 86 KTFIVLNKGAIFRNATPAL-----YMLSPFSLRISTIKILVHSLFSLMIMCTILITNC 140  
 96 VTGNEFPCF--DIACDSQRCRLQAFDDFI-F-AFRAVENYVMAVAGT-FGKKCYLGD 150  
 141 IFMTLSNPETWKV-----EYTFGIYTFESLILKILARGFCVGEFTLRD 186  
 151 TWRNDFEIVLAGMLEYSLDQNSAFRTVRLPLRAINRVPMSRIITVLLDITPM 210  
 187 PNMWLDFFVIVFAITTEFVNLGNV--SALRTFRYLAKITISVPLGKTIYVAGLISQVK 244  
 211 LGNVLLCFEVEFFIGIVGOLMAGLNRGCF--LPENFSLPLSV-----DLEPIYQ 260  
 245 LSDVILVFCISVAFALIGLQFMGNLKHCFKRELEENETLESIMTAEESEELKRYFY 304  
 261 TENDESEFICQPRENMRCSRVPYTLRGSGGPGCSLDYETYNSSNTTCVNMNOY 320  
 305 YLEGSKDALCGFSTDSQ-----CPEGI-----ICV----- 332  
 321 TNGSAGENPFKGAIFNFIAGYMAIAFOVITLEGWDMFVMDASHFYNFIFILLI 380  
 332 ---KAG-RNPDDGYTSFDFSMALFALFRIMQDWMENLYOQLRAAKTYMIFVYIF 387  
 381 VGSFMINCLVVIATQSEYKQRESQLMREORVAFLSNASTLFSFGSCYEELKYL 440  
 388 LGSFYLINILAVVAMAYEEQONANIEEKQELFEQOMDLRKLKEQDEAA----- 440  
 441 VYILKKAARLAQV--SRAGV-----RAGLSSPYAR-----SCOEP--- 477  
 440 ---IAAAAEFTSIGRSRIMGISESSSETSRLSSSAKERRRRKKKKOKXSSGEKDD 496  
 477 ---OPSGCTSRSHRLSYHNLVHHHHHHHHHNGTLRVPRASPEIODRDA-----NG 528  
 497 EKLKSGS--EESIRKKSFLHGEVGHRTREK-----RLSTPNQSP--LSIGSLFSARS 548  
 529 SRRLMPPRSTPPSGPRGASVSHFYHADCHLEPRVCAQAPRPGSEASGRVYSGK 588  
 549 SRTLSFSGRGLDSETEFADDEHSIFGDN---ESRSGSLFVDRPERRSSNISQA- 605  
 589 VYPTVTPSPPEILKALVEVAPSPGPTLTSFNIPPGFSSMKLLETOSTGACHSSC 648  
 605 -----SRPPVL-----PVGKMHSAV 621  
 649 KISSPCKADSGAGPDCPYCARFAGGEPESADHVPDSSEAVYETQDAQHD----- 705  
 622 DCGVAVSLVD---GPSA--LMLPNCQLPEVILDKATSDSGTTNOMKRLSSSYFLS 675  
 705 ---LRPHSRKRRSLGPRAPSSVLA-----FMRLICQ----- 737  
 676 EDMLNDPHLEQRAMS-----RASILTNTVEELLESROKCPRMWRFAATFLIMNCSPW 729  
 737 --FRK-----IVDSKYFGRGIMAILVNTLSMGIEHEOPEELTNALEISNIVFTSLFALE 790  
 730 IRRKLLIYFVMDPYDATTICIVLNTLFMANEHHPMEEFKRVNLAVANGLETGFAAE 789  
 791 MLKLKLVGGEGTINKPNYITFDGVIYVIVSWELVGGGGLSLKTRFLMRVLAFLRFP 850  
 790 MVKLIMADPYEYFOVGMNIFDSLIVTSLIDELADVEGLSVLRSFRLRFLAKSWP 849

851 ALQRLVVIAMTMDNNATFCMLMLFIFIFISILGMHFG-----CKFASERDGTLPD 903  
 850 TLNMLIKIIGNSVAGLNLTLVLAIVIFRAVGMOLFSGSYKECVCTI---INDCKLP 905  
 904 IRNPDLSLMAIVTFOILTOEDMKNVLYNGM--ASTSSMAIFYIATMTFGNYVLFNLVA 962  
 906 RHMNDFFHSLIYFRVYLCGE-WLETMDGMEVAGQIMCLIVMMVAVGNLVNLFLA 964  
 963 ILVEGFOAEIIGKREDASGQLSCIQLPVNSGGDATSESEPFDFSVDGDRK-RL 1021  
 965 ILLSFSSDNL-----TAIEDDANNLOI 989  
 1022 ALVAAGEHAELKSLPLPLIHTAATPMSLPKSSSTGVGEALGSGSRRTSSGSAEBGA 1081  
 990 AVARIKRGINVYQTLREFILKFS--KKRKS-----KDTAKTA----- 1028  
 1082 HHMKSPSPARSPPSWAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLSGE--GQ 1139  
 1028 -----DPNNKKENYISNRTLAE 1044  
 1140 ESQDESESEEDRASPAGSDHRHRSLEREAKSSFDLPDLOVPGIART--ASGRS-- 1194  
 1045 MGRDNFLKENDRIGYGS-----SLDKSEMDENDYQSFTHNSLVYVPIAAGESDLE 1098  
 1194 -----SASEHQDNGKSASGRLARTLRDPPOLDGDDDEGNSKGERIQAWBS-- 1245  
 1099 IANTELSDSQSDYSKERNSSSECSYDNP.LPGEAEABEVNADDEACFTGCV 1158  
 1245 -RLPACCREDSMSAVIEPPQSEFRLCHRIITRKMPDHVVLVIFLNCITIAERKID 1303  
 1159 RRPCCQVAVDSGKRWV--WTIRKTCYRIEHSWFESFVLMILLSSGALAEEDYIE 1215  
 1304 PHSARIFITLNTYFETANFLAEMTVKVALGWCQGEQAYRSSWNVNVDGLVLSVIDI 1363  
 1216 KKKTIILLEYADKIFTYIFIMELKLWYA---YGYTYTFNACWLDLIVDS----- 1268  
 1364 IYMSVSDS--GTRILGLRYLRILRLPLRYSRQGLVETLMSSLPKIGNIVIC 1422  
 1268 LVTLVANTIGYDGLPIKSLRFLRALRALSREGRRVYNALIGAIPIIMVLLVCL 1327  
 1423 AEFIIFGLIGVOLFKGFEVCOGE-----DTRNTKNSDC-----AASRWVHKKNF 1471  
 1328 IFWLIIFISMGVNLFAKFEVCVNTDGSRRFPYSOYANSECCALMNVSGNRWKKLVNF 1387  
 1472 DNLGQALMSFLVASKDGWDVMDYDGLDAVGYDOOPIMNHPMLLYIFISFLIYAFVL 1531  
 1388 DNVGLGSLLOYATITKGMMDIMYAVSVNNQEPKYYSIXMYIYEIFIIFGSFTL 1447  
 1532 NMFVGVVVENFHKCRQHOEEEARREERLRLEKRRRLMLDVIYASGSASASEAQ 1591  
 1448 NLFITGLIDNFQKKLGGDIFMTEE-----OKKYANM-----KLGSKRP 1491  
 1592 CKPYSDYSKFLVNLHLCSTSHLDLFTIGVIGLVNVTAMHYOQOLIDELAKICYVI 1651  
 1492 QKPIPRGNKFQCIQDLYTNOAFDITIVLCLNNVYTMVKEGOTEMDVLMIMNV 1551  
 1652 FTVIEVESYFKLVAFGRFRFQDRNNQDLAIVLISIGITLEE--IEVNASLPINPTII 1710  
 1552 FIILFTGEVYKLISLR-HYFTVGNNINDFVVLISYIGMLAEIE--KYFVSPLE 1607  
 1711 RIMVLIARVILKILKAVGMRALDVTQALPQVGNLCLLMLLFTIFALGVELFGDL 1770  
 1608 RVIRLIRIGIRLIRLIKAGKIFRLLFALMMSJPALEINIGLLFLVVIYIAGMSFAV 1667  
 1771 ECDETHCEGLGHAFTRNGMAFLFLFRVSGDMNGIMKDTLR---DCDO----- 1820  
 1668 KKE-----AGINDMFEITFGNSMILCFQITTSAGWDGLAPILNSAPDCPKYHPS 1722  
 1820 --ESTCYNTYISPIYFSEVFLTAQFVLVNVVIAVLKKHLEESKKEAEAELELEM 1877  
 1723 SVEDDCNPVSGVIGIFYYSIIISFIVVNMVIAVILENFSVATEESTEPJ---SEDDFEM 1779



Db 1276 YAVIGMOWFKVALODGTQ-----INRNNNFOTPEQAVLLIFRCATGEAWOIMLASIPGN 1331  
 QY 1816 DCDDES-----TC-YNTYISPIYVSVFLTAQFLVWVAVIAVKHLEESNKEAKEE 1866  
 Db 1332 RCDPESDGPGEFTGCGNFAIA--YFISFPMCAFLINIFAVINDND----- 1381  
 QY 1867 AELEAELEKKTLSPPHSPSLGSPFLW-----PGVEGVNSPSPKPGAPHTAHIGAAG 1922  
 Db 1381 -----YLIRDSIILG--PHHIDEFKRIWSEYDPGAKG----- 1411  
 QY 1933 FSLHEPIWPHPEVYPVLPGLDLYTKRSGVSRHSLPNDSYMGNGSTAEKSHGHGWG 1982  
 Db 1411 -RIKHLDVALLRRIQPLGKLCOPHRVACKRLVAM-----N 1447  
 QY 1983 LPKAGSGSI-----LSVHSQPADTSCILQPKDVHLLQPHGAPTGAIPK- 2029  
 Db 1448 MPLNSDGIYTFEATLFAIVRTSLKITE-----GNLEQANQELRIYIK---KIKRMRKOK 1499  
 QY 2029 -----LPPPGRSPLAQ-----RPLRRO-----AALRTDLDVQGLGR 2061  
 Db 1500 ILDEVIPLPDEEETVYKGYATFLIQDYFRFRKRRKREKGLLGNDAAPSTSAIQAQLRSL 1559  
 QY 2063 EDLLSEVSGSPCLTRSSSFGSGSSIOYQSGISQVSKHILRLPAPCPGLEPSMAKDP 2121  
 Db 1560 QDLGEMKQALTCDEEEBEEBQEBEEDKEDLETNKATVSOAPSARG----- 1610  
 QY 2122 ETRSSLELDTLWSIGDLPLSSQEPPLSPDLKCYSVETQSCRRRPSWLDORRHSI 2181  
 Db 1610 ---SGISVSLPY---GDRLPDLS--FGPSDDRGFTPSQPSVQAQS---NTHRR--- 1656  
 QY 2182 AVSCLDGSGQPLCPSPSSLGQPLGSGESRRKRLSPSPSIDPPEGSGSRPSPGVC 2241  
 Db 1656 -----GSGALIFTIPEBGNQPKGTQKQNKQDEDEVPDLSTYLDQAGTPCS--VL 1706  
 QY 2242 L-----RRAPASDKSPSVSSPLDSTAASPPKDKTSLSGSSDPTD 2285  
 Db 1707 LPPHRAQRMQDGLVPRKRLP-----PPTAGKRPFTTIOQLQROGSC 1749  
 QY 2286 MDVPLFTLPHLSPPGADPSSASMA 2310  
 Db 1750 EDLPFGTYHGRNGSPNRAQGSMA 1774

RESULT 13  
 Q15858 PRELIMINARY; PRT: 1977 AA.  
 AC Q15858;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
 DE SODIUM CHANNEL ALPHA SUBUNIT.  
 GN HNE-NA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYROID;  
 RA MEDLINE: 95237189.  
 RX KLUGAUER N., LACINOVA L., FLOCKERZI V., HOFMANN F.;  
 RT "Structure and functional expression of a new member of the  
 RT tetrodotoxin-sensitive voltage-activated sodium channel family from  
 RT human neuroendocrine cells.";  
 RL EMBL J. 14:1084-1090(1995).  
 RL EMBL: X62835; CAAS8042.1.;  
 DR PFAM: PF00520; Ion\_trans. 4.  
 DR PFAM: PF00612; IQ. 1.  
 KW Ionic channel.  
 SQ SEQUENCE 1977 AA: 225195 MW: 062DCE60 CRC32:

Matches 548; Conservative 386; Mismatches 790; Indels 491; Gaps 81;  
 QY 3 EEDDAGAEESGQPRSTQINDLSGAGRGCP---GSTEDPGSADAEAL-PY----- 54  
 Db 36 KEKKDDDEAPKPS-----DLE--AGKQLPIYTG--DIPPGVSEPLEDLDDYADKK 86  
 QY 54 -----PALAPVVEFLYSDSRPSRSMCLFVCPMPFERVSMYLILNCV 96  
 Db 87 TFLVINKGTFIFRNATPAL-----YMLSPSPRLRISIKLIVSLSLMILMCIILNCI 141  
 QY 97 TLGMFRP---CEDIACDSORCRLIADFDTF-AFAVENVKNVAGI-FGKKCYIGDT 151  
 Db 142 EYTMNPPPMWNTNV-----EYTFGTGYTESLVKILARFCVGEFTFLRDP 187  
 QY 152 WNLDFEYIAGMLESLDLQVNSAVRYVRLPLAIRNVSMTLYLTDLTLM 211  
 Db 188 WMLDFVVIYFAYLFEFVNLGNV--SALRTFRVLAKTISVIGLKITVIGALLQSKKL 245  
 QY 212 GNVLLCFEVEFIFGIVGVLWAGLIRNCF--LPENFSLISV-----DLEPYQT 261  
 Db 246 SDVMLITVCLVFPALIGQLFMGLMKHKCFRNSLENNETLESIMNTLESEDEPRKYFY 305  
 QY 262 ENEDESPTICOPRENGMRSRVPFLRGGGGGPPCLDIETIYSSNTCYVMNQYIT 321  
 Db 306 LEGSKDALCGFSTDSGQ-----CEGY-----TCVKIGR-- 336  
 QY 322 NCAGAHNPKKALNPNDNGVAMIAIFOVITLEGVNDIMYFMDAHSFYNYFILLIIV 381  
 Db 336 -----NDYGTSTFTDSMAFLFLRLMTQDYENLYQQLTRAAGTYMFFVYVFL 388  
 QY 382 GSEFMNLCLVATQFSTKQRESQIMREQVRFLSNASTLASFEGSCYEELKLYV 441  
 Db 389 GSFFYLNLIAVYAMAYEQNQANIEAKQKELFQOMDLRKKQBEAEALIAAAAEYT 448  
 QY 442 YLRKARRLAQVSAIGVAGLLSPVAK-----SGQEPQSSGCTSH 486  
 Db 449 SIRSRIIMGISESS-----ETSKLSKSAKERNRNRKKKQKLSGEGKDAELTSE 504  
 QY 487 -----RLSVNHLVHNHNNHNNHNGTLRVPRASPEIORDA-----NGSRRLMDP 536  
 Db 505 SEDSIRKSHLGEVGHRAHEK-----RLSTPNQSP--LSIRGLSFARSRSRTLSF 557  
 QY 537 PSTPTSGGPPRGAEVSHFYHADCHLEPVRCQAPRPPCPSASGRTYGGKGYVTVHTS 596  
 Db 558 KGRGRDIGSETEPADDEHSIFGDN--ESRGLSEFVPHRPOERSNSISQA-----SR 607  
 QY 597 PPEPILKDKALVVAASPPPTL---TSPNTPPGFSSMHLLLEQSGACHSSCKISS 652  
 Db 608 SPPMLPVNGRMHSAVDONGVSLVDRSALMLPNG-----QLPREGTINQIHKKRCS 661  
 QY 653 PCSKADGACGDCSPFCARTGAGEPESADHWVPDSSEAVYEFTODACHSLDRPHSHR 712  
 Db 662 -----YLSEDM-----LNDPNIHQ 676  
 QY 713 RQRLSGDAPSSVLA-----FWRLICD-----TFKR----- 740  
 Db 677 RAMS-----RASILTNTVELEESROKCPMWYRPAHKLINW--CSPYWKIFKKCIYE 728  
 QY 740 IYDSKYGRGIMAILVNTLSMGIEVHEQPEELTNLEISNIFVTSFLFLEMLKILVYG 799  
 Db 729 IYDPEFLAITICIVANTLPMANHEHPMTEERKNVLAIGNLFTGIFFAEVLKILAND 788  
 QY 800 PFGYIKRPNYIFDVIYIVISVWEIVGQGGSLVLTFRMLRVYKLVRLPALQRLVVL 859  
 Db 789 PVEYFGVGMNIFDLSLYTLSELVELADVEGLSVLSERFLRVFKLAKSWPTLNMILKII 848  
 QY 860 MKNVDAVATFCMLMLFIPIFSILGHLFG-----CKASRSDGDTLPDRKNFDSLLM 912  
 Db 849 GNSYGALGNLILVLAIVLFIYFAVVGQOLFQKSYKECVCKI--NDCCITLP--RWNHNDPEH 904  
 QY 913 AIVTVEQLIODEMKNKVLVNGM--ASTSSMAALYFIALMTGNYLVLFNLVAILVEGFOAE 971  
 Db 905 SFLIVFRVLCGE-WIETIMDCMEVAGQACLIYIMAMVIGNLVNLFLALLLSFSSSD 963

QY 972 EIGKREDASGOLSCIOLPVNSOGGATKSESHPDFSPVGDGDRKRLALVALGEHAE 1031  
 Db 964 NL-----TAIEDPD-----ANNLOIVTRIKGIN 989  
 QY 1032 LRKSLPLLIHTAATPMSPKSSSTGVGALGSGRR---TSSGSGAPGAHHEKSP 1088  
 Db 990 YKQTLREFILKA---PSKKPKISREIROADLTKENTISNNTLAKEMKGNFLKEX 1045  
 QY 1089 PKRRSSPHFMAASWTSRRSSRLGRA---PSLKRSPGGRKSLGEGEODE 1144  
 Db 1046 DK1-----SGFGSSVDKHLMESSDQSFHNLSLTVTP-----IAGE-----SDL 1087  
 QY 1145 EESSEDRASPAGSDHRHSGLERAKSSFDLPDLOVGLHRTASGRSSASEHODCNKG 1204  
 Db 1088 ENNMNEELSSDSEY-----SKRLNMSSE-----CS-- 1118  
 QY 1205 SASGRILARTLTDPOLODDNDENGLSKERRIQAWRS---RLPACRRR-DSWSAVI 1260  
 Db 1118 -----TVDNPLPEGEAEAPMNSDEPEACFTDCVRFSCCOYNIESGKGI 1166  
 QY 1261 FPROSRLLCHRIITHKMEHVIVITLNGITIAMERPKIDPHASRIELTSNYFT 1320  
 Db 1167 W---WIRKTCYKIVHSFESFIVMLILSGALAFEDITYERKTKITILEYADKIFT 1223  
 QY 1321 AVFLAEMTVKVAALGWCFGEOAYLSSNMVLDGLVILSVIDLIVSNVSDS-GTKILGML 1379  
 Db 1224 YIFLEMLKMLIA---YCKTYFNAMCWDIFLVDVS---LTVLVAANLGVSDLGPI 1275  
 QY 1380 RYVRLRLTRPLRPLVSRAGGLVYETLMSLKPIGNIVICAFITIFGLGVOLRKCK 1439  
 Db 1276 KSLRLRALRPLRALSRFGEMRVNVALIGALPSIMNVLCLLFWLTFSTMGVNLKAGK 1335  
 QY 1440 FVFC-----OGE--DFRNTINKSDC-----AEASYRMVRHKNFNLGOALSLVYASKD 1488  
 Db 1336 FYECITTTGSRFPASQVNRSECFALMNVSONVRKMLKAVFMDVGVIGYLSLOVATFK 1395  
 QY 1489 GAVDITVLDGLAVGDOQPIHNNHNMMLIYFISPLIYAFVLANFVGVVFNHCKROH 1548  
 Db 1396 GWTIIMYAVDSVNDKQPKREYSYLMYIYEFVFIIFGSEFTLNFILVIIDNNQOKKK 1455  
 QY 1549 QEESEARREKRLRLEKRRNLMDVDIASGSSASASEOCPPYSDVSRRRLVNH 1608  
 Db 1456 LGGQDLFTME-----OKRYNAM-----KKLGSKPKQKPIRPNCKKIOGCFD 1499  
 QY 1609 LCTSHYLDLFTGVIGLVNVTAMETHYQOPQILDEALKICNYIFTVIFVESVRYAVFG 1668  
 Db 1500 LVNNAFIDISIMVLCNNVTVWVEKEGQSHMEVILWVINVFIILFTGCVLKLISLR 1559  
 QY 1669 FRFPDORNNODLAVLSTINGITILEEVNASLPINPTIIRIKRVIRIARVYKLKMA 1728  
 Db 1560 -HYFVGNITIDEVVAIISIVGMELADL--IETVFSPTLFRVIRIARIRIIRIYKGA 1616  
 QY 1729 VGMARALDVMQALPOVNGILGLFMLLFFIFALGVLEFGDECDETHPCGGLGHATER 1788  
 Db 1617 KGRITLFLFMAVSLPLALFEGILFLVMTIYAFGSMNFAYVKKR-----GJINDMNEFE 1671  
 QY 1789 NFGMAFLFRVSTGDNMNGIKDKTLR---DCDQ-----ESTCYNTVSPITFVS 1835  
 Db 1672 TFGNSMICFOITTSAGMGLLAPILNSKPCDKVHPGSSVAGDGNPSVGFJFVS 1731  
 QY 1836 FYVLAQFVLYNVYIVAMHLEESNKEAKE--ALELELELEMKLTSQPHSPISLSPITW 1894  
 Db 1732 YIIISLVVNMATIVILENFSVAIEESTEPISSEDFEATF-----VW 1775  
 QY 1895 PGEVGVNSPDSRPGAPHTAHIGAAGF--SLEHPITVPHDEEVVPLGDLITVRKSG 1952  
 Db 1776 EKRD-----PDATQ-----FIEFSKLDPAALDPLLIATKPKVOL--IAMDLPKV--SG 1822  
 QY 1953 VSRTHSLPDSYKCRNGSTARSLSHGKGLPKAOSGSLVSHSPADTSCIOLOPDDYH 2012  
 Db 1823 -DRHCL--DILF-----AFTKRVLG-----ESGEMDSLRSQ--MEERMSANPSKVS 1865

QY 2013 YLLOPHAGAPTWGA/PKLPBGRSPLOAPRLRQARITDSLDVGL-----GSRED 2063  
 Db 1866 Y-----EPITTLKROEDVSAIYIORARRY-RLQONKNKISSIYIKGDPRD 1913

RESULT 14  
 ID 057483 PRELIMINARY; PRT: 1688 AA.  
 AC 057483:  
 AT 01-JUN-1998 (TREMblrel. 06, Created)  
 E 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DE 01-AUG-1999 (TREMblrel. 11, Last annotation update)  
 DE VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL, ALPHA-1S SUBUNIT (FGLAPHA1S).  
 OS Rana catesbeiana (Bull) frog.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Raninae; Rana.  
 PN (1)  
 KP SEQUENCE FROM N.A.  
 RC TISSUE=SKLETAL MUSCLE;  
 RX MEDLINE: 98411359.  
 RA ZHOU J., GRIBBS L., YI J., SHIROKOV R., PEREZ-REYES E., RIOS E.;  
 RT "Molecular cloning and functional expression of a skeletal muscle dihydropyridine receptor from Rana catesbeiana.";  
 RL J. Biol. Chem. 273:25503-25509(1998).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH.  
 CC THE ISOFORM ALPHA-1S GIVES RISE TO L-TYPE CALCIUM CURRENTS.  
 CC LONG-LASTING  
 CC (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED (HVA)" GROUP.  
 CC THEY ARE BLOCKED BY DIHYDROPYRIDINES  
 CC (DHP), PHENYLTALAMINES, BENZOTHRIZAPINES, AND B  
 CC (OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA).  
 CC THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE (BY SIMILARITY).  
 CC -1- PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL FUNCTION (BY SIMILARITY).  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO.  
 CC THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT.  
 CC IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY.  
 CC THE AUXILIARY SUBUNITS, BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC AN ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE CHANNEL (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS  
 CC (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4).  
 CC S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.  
 CC EMBL: AF037625; AAC36126.1; -.  
 CC PFAM: PF00520; Ion\_trans; 4.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;







```

Db 457 KLNRCRRA----- 466
QY 709 HSRROSLCPDPAEPSSVLAFWLIDOTFERKIDSKYFGGIMAILVNTLSMGIEHQ 768
466 -----C---RRLVKSQFFYVLVLVLTNTLVLSHYQ 497
QY 769 PEELTNALEISNIVFTSLFALMELMLKLVYGPFGYIKNPYNIFDGVIVISWEIV----- 825
498 SEMLDHQTMANLEFVILFSEMLKMYSLGFTYTSQNFREDCEFYISSILEFVLVYF 557
QY 825 -GQGGGLSVLTRRLMRVLKIVRFLPALOROLVLMKTDVNATCOMLMEFIFSTI 883
558 DLMPLGVLSVRSARLIRKVRKWTSLRNVLSSILNLSRSTISLLFLFTIVFALL 617
884 GMLFGCKFASERDDTLPRKPNFDSLMAIVTFQILTOEDMKNKVLNMGASTSSMAL 943
618 GMOVFGGKF--NFPQOPKPRANDTFVQALITVFOILTGEDMNTVMYHIESFGVGT 675
QY 944 -----YFIALMFGNVLEMLVAILVEGFQAEIGKREDASQLSQILPVNSQOGDA 997
676 GVIYCIYIYVLFICGNVILLNVFLAIVDNL----- 707
QY 998 TKSESEPPFSPVDGODGRKRLALVALGHAELRKSLLPILIHATPMSLPKSSST 1057
707 -----ADAD----- 711
1058 GVGELGSGSHRTSSGSAEPGAHHEMKSPPSARSPHSPWASAASSWTSRRSSRLGR 1117
Db 711 ----- 711
QY 1118 APSLKRSPSGERSLSLSCGEOBODEPESSEEDRASPAGSDHHRGSLEREAKSSFDLP 1177
711 -----SLTNAKEEEOQELIEGDE-----FE-- 733
1178 DTLQVGLHRTASGRSSASEHODNGKASGRRLARTLTDPOLDGDDNDENGLSKGER 1237
733 -----EGEDBEGBEH-----GMDP--EGD--EMTSARPRR 759
QY 1238 IQAWVRSLPACCRER---DSNSAIYPPQSRFLCHRITTHKMFHVIVITFLNCIT 1294
760 M-----SEVPASIVKPIPKASSLFLSHNTSFVFCMMVNHSTFNAVLECLVSSAM 814
1295 IMERPCKIDPHSAERILPLISNIFTAVLEMTVKVVALGMCFGEOALYLRSSMNVDGL 1354
815 LAAEDP--IQANSTRMILNYPDYFTSVFYETITLKVIFGLVPHKSGFCNNAFNLIDL 873
QY 1355 LVLSIVIDLVSMSVDSGTLIGMLVRLRLTLRLPRLVISRQGLKLVETLMSLKP 1414
874 VVAVSLTSFLR-----TDMSYVKILRVLRPLRALINRAKGLKHVOCVIAVAKTI 927
QY 1415 GNIVVYICCAFFIIEGLVQVLFKGFVC-----QGEDTRNITNKS 1455
928 GNIMLVTFMLOMFALIGVLFKGFELCNDISKTEACRGEYIHYEDGDTKVSCKR 987
1456 DCAEASVYRWARKYFNEDNGQALMSLEVLASKDGVNDIMYDGLDVGVDOPIMNHNPM 1515
988 -----VMSNDFENFNDGDMISLFVSTFEGMPQLLYAIDSNEEDKPIHNSRQAV 1040
QY 1516 LLYFISFLIIVAFVLMFVGAVVENFHKRQHOEBEARREKRLRLREKKRNLMD 1575
1041 ALFEIATFIVIAFMMINIEVGEIVTF---ONEGEREYENCE-----LDKNORCKI-- 1089
QY 1576 DVIASSSSASASEAQCKRYGSDYSRFLVHLHLCSTHYLDLFTIGVIGLVNTMAMEHY 1635
1089 -----EFAKKAPHRRIYPRNLOYRWMMFVTSRAFEYVITLIIYMNIVSLACKHY 1139
QY 1636 QOPQIDALKICNYLFTVIFVESYFKLVAFGRFFQDRNODLAVLLSINGITILE 1695
1140 PSSRGEDFLDVNLFITGVFAEVLKIVALPNKVIYISDRMNVFDLAVVGSFIDITYG 1199
QY 1696 EIEVNASLPINPTIIRIMVRLIARVLLKKAIVGMRALLDVM---QALPOVGNLGLLF 1752
1200 KLNPGGT---NLISINFRLFRVRLVLLKSREGIRTLIMTFMKSFOALPVY---ALLI 1253

```

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QY 1753 MLLFFITPAALGVELFGLDEDETHPCBGLGRHATFRNFGMAFLTRFVSTGDNWNGIM-- 1811
Db 1254 VILFFIYAVIOMQFFGVVALDSS--TSIHRNNHSHFPALIVLFRSAGEWMDIMLS 1310
QY 1811 ---KDLRDCD-----OESTCYNTVISPITYFVSFVLTAQFVLVNVVIAVLMKHL 1856
Db 1311 CSDEEDVY--CPMADDYHKGLNBSRCGNFPAYP-YFISFMLCSFLVIMLFAVIMDNF 1368
QY 1857 BESNKEAKEAELEAELEKNTISPQPHSPLGSPFLMPGVEGVNSPDSKPCAPHTTAH 1916
Db 1369 D-----YLTRDWSILG--PHLLEFVRMLSEYD--PD----- 1397
QY 1917 IGAASGFLEHTPWPHHEEVPVPLG-----PDLITVRSKGVSRHSLPNDYSYCRNGST 1971
Db 1397 --ANG-RIKHLDVYTLRLKISPLFGKLCPLHLACKRL-VSNMPLNDGTYVCEFATL 1451
QY 1972 AERSLGHGWCGLPKAOSGSLSVHSPADTSCILQLEPKDVHYLLQPHGAPTWGAIPKLP 2031
Db 1452 -----FALVTRN---LKITYE-----GNIDEANE 1472
QY 2032 PERSPLAOPPLRKOALITDSIDVQGLSREDLSEV---SGPSCPILRSSFPWGSSTIQ 2088
Db 1473 QLRSAI--KRIMR-----THKDLDEVPPRAGKEDDYV--VKFYATFLIQ 1515
QY 2089 VOQRSGIOSKYSKHIRLPAPCPGLEPSWAKDPPTRSSLEIDTFLS--WISGDLPSOQE 2147
Db 1516 DYFR---RFXKKKEAEAGVLPACQTPQAMALQAGRLTHELGPRLKRAISNLETDFND 1572
QY 2148 PLSPDLKRCYSVETQSCRRRPGSWLDEORRHSLAVSCLDSSG-----QPLCFSPSLG 2202
Db 1573 EPEPOH--RPHSLFNNLVRLSLGAGSKSPTEH---ERIEKGSYLLPQOPRFSFPTSLA 1627
QY 2203 GQPLGPGSRPKKXLSPPSISIDPESQSRPSPGVCLRRRPA 2248
Db 1628 GAE--GSPVPSQMHGAPINQSLNLPVNGS-----ARRLPA 1662

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Search completed: January 16, 2000, 00:11:30  
Job time: 252 sec

Wed Jan 19 08:15:02 2000

pct-us99-19875-2.rpt

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2000, 00:55:03 : Search time 148.95 Seconds  
(without alignments)  
11974.618 Million cell updates/sec

Title: PCT-US99-19675-1  
Perfect score: 7129  
Sequence: 1 atggacgagagagagatg.....gtccgcacacagagatg 7129

Scoring table: IDENTITY\_NNC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36.\*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 909.8 | 12.8        | 5562   | 1 V57542  | Human calcium chan  |
| 2          | 279.6 | 3.9         | 567    | 1 V57544  | Rat calcium channe  |
| 3          | 262   | 3.7         | 567    | 1 V57543  | Human calcium chan  |
| 4          | 145.6 | 2.0         | 6524   | 1 T77803  | CDNA encoding wild  |
| 5          | 144.2 | 2.0         | 7555   | 1 081328  | Cardiac sodium cha  |
| 6          | 144   | 2.0         | 7052   | 1 T77805  | CDNA encoding vari  |
| 7          | 144   | 2.0         | 6527   | 1 T77806  | CDNA encoding vari  |
| 8          | 138.8 | 1.9         | 6556   | 1 V58419  | PN4 sodium channel  |
| 9          | 138.8 | 1.9         | 5977   | 1 V58420  | Tetrodotoxin-sensi  |
| 10         | 138.8 | 1.9         | 6007   | 1 V58421  | PN4 sodium channel  |
| 11         | 138.8 | 1.9         | 6586   | 1 V58423  | PN4 sodium channel  |
| 12         | 136.4 | 1.9         | 5975   | 1 N91778  | Rabbit skeletal mus |
| 13         | 136.4 | 1.9         | 5975   | 1 087978  | Rabbit skeletal ca  |
| 14         | 136   | 1.9         | 7555   | 1 005831  | Cardiac sodium cha  |
| 15         | 135.8 | 1.9         | 5904   | 1 037813  | Sequence encoding   |
| 16         | 135.8 | 1.9         | 6575   | 1 084555  | Human neuronal cal  |
| 17         | 135.8 | 1.9         | 6725   | 1 087834  | Human neuronal cal  |
| 18         | 135.8 | 1.9         | 5904   | 1 V42681  | DNA encoding human  |
| 19         | 134.8 | 1.9         | 5975   | 1 T70328  | Rabbit calcium cha  |
| 20         | 134.8 | 1.9         | 5975   | 1 T96811  | Rabbit skeletal ca  |
| 21         | 132.6 | 1.9         | 6048   | 1 V09829  | Human hhl sodium c  |
| 22         | 127.6 | 1.8         | 7175   | 1 037818  | Sequence encoding   |
| 23         | 125.6 | 1.8         | 7860   | 1 T44380  | Stretch-activated   |
| 24         | 124.4 | 1.7         | 6232   | 1 029269  | Human calcium chan  |
| 25         | 124.4 | 1.7         | 7362   | 1 037817  | Sequence encoding   |
| 26         | 124.4 | 1.7         | 7362   | 1 084557  | Human neuronal cal  |
| 27         | 124.4 | 1.7         | 7175   | 1 084558  | Human neuronal cal  |
| 28         | 124.4 | 1.7         | 7266   | 1 V29059  | Human calcium chan  |
| 29         | 124.4 | 1.7         | 7362   | 1 V42685  | DNA encoding human  |
| 30         | 124.4 | 1.7         | 7175   | 1 V42686  | DNA encoding human  |
| 31         | 122.4 | 1.7         | 7635   | 1 037811  | Sequence encoding   |
| 32         | 122.4 | 1.7         | 7635   | 1 V42679  | DNA encoding human  |
| 33         | 122.4 | 1.7         | 7635   | 1 V42697  | DNA encoding human  |
| 34         | 122.2 | 1.7         | 7635   | 1 084553  | Human neuronal cal  |
| 35         | 122.2 | 1.7         | 7635   | 1 084554  | Human neuronal cal  |
| 36         | 117.2 | 1.6         | 2980   | 1 029270  | Human calcium chan  |
| 37         | 113.6 | 1.6         | 6452   | 1 T330193 | Peripheral nervous  |
| 38         | 109.6 | 1.5         | 6513   | 1 T33238  | Drosophila para vo  |
| 39         | 109.6 | 1.5         | 6513   | 1 T18986  | Drosophila para vo  |

|    |       |     |      |          |                    |
|----|-------|-----|------|----------|--------------------|
| 40 | 103.6 | 1.5 | 6519 | 1 V82500 | Calcium permeable  |
| 41 | 108.6 | 1.5 | 6789 | 1 V29372 | Calcium ion channe |
| 42 | 107   | 1.5 | 7808 | 1 084659 | Human neuronal cal |
| 43 | 107   | 1.5 | 7791 | 1 084660 | Human neuronal cal |
| 44 | 102.8 | 1.4 | 6922 | 1 083735 | Calcium channel al |
| 45 | 102.6 | 1.4 | 7089 | 1 084563 | Human neuronal cal |

## ALIGNMENTS

| Result ID | Score | Query Match | Length | ID        | Description         |
|-----------|-------|-------------|--------|-----------|---------------------|
| 1         | 909.8 | 12.8        | 5562   | 1 V57542  | Human calcium chan  |
| 2         | 279.6 | 3.9         | 567    | 1 V57544  | Rat calcium channe  |
| 3         | 262   | 3.7         | 567    | 1 V57543  | Human calcium chan  |
| 4         | 145.6 | 2.0         | 6524   | 1 T77803  | CDNA encoding wild  |
| 5         | 144.2 | 2.0         | 7555   | 1 081328  | Cardiac sodium cha  |
| 6         | 144   | 2.0         | 7052   | 1 T77805  | CDNA encoding vari  |
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| 8         | 138.8 | 1.9         | 6556   | 1 V58419  | PN4 sodium channel  |
| 9         | 138.8 | 1.9         | 5977   | 1 V58420  | Tetrodotoxin-sensi  |
| 10        | 138.8 | 1.9         | 6007   | 1 V58421  | PN4 sodium channel  |
| 11        | 138.8 | 1.9         | 6586   | 1 V58423  | PN4 sodium channel  |
| 12        | 136.4 | 1.9         | 5975   | 1 N91778  | Rabbit skeletal mus |
| 13        | 136.4 | 1.9         | 5975   | 1 087978  | Rabbit skeletal ca  |
| 14        | 136   | 1.9         | 7555   | 1 005831  | Cardiac sodium cha  |
| 15        | 135.8 | 1.9         | 5904   | 1 037813  | Sequence encoding   |
| 16        | 135.8 | 1.9         | 6575   | 1 084555  | Human neuronal cal  |
| 17        | 135.8 | 1.9         | 6725   | 1 087834  | Human neuronal cal  |
| 18        | 135.8 | 1.9         | 5904   | 1 V42681  | DNA encoding human  |
| 19        | 134.8 | 1.9         | 5975   | 1 T70328  | Rabbit calcium cha  |
| 20        | 134.8 | 1.9         | 5975   | 1 T96811  | Rabbit skeletal ca  |
| 21        | 132.6 | 1.9         | 6048   | 1 V09829  | Human hhl sodium c  |
| 22        | 127.6 | 1.8         | 7175   | 1 037818  | Sequence encoding   |
| 23        | 125.6 | 1.8         | 7860   | 1 T44380  | Stretch-activated   |
| 24        | 124.4 | 1.7         | 6232   | 1 029269  | Human calcium chan  |
| 25        | 124.4 | 1.7         | 7362   | 1 037817  | Sequence encoding   |
| 26        | 124.4 | 1.7         | 7362   | 1 084557  | Human neuronal cal  |
| 27        | 124.4 | 1.7         | 7175   | 1 084558  | Human neuronal cal  |
| 28        | 124.4 | 1.7         | 7266   | 1 V29059  | Human calcium chan  |
| 29        | 124.4 | 1.7         | 7362   | 1 V42685  | DNA encoding human  |
| 30        | 124.4 | 1.7         | 7175   | 1 V42686  | DNA encoding human  |
| 31        | 122.4 | 1.7         | 7635   | 1 037811  | Sequence encoding   |
| 32        | 122.4 | 1.7         | 7635   | 1 V42679  | DNA encoding human  |
| 33        | 122.4 | 1.7         | 7635   | 1 V42697  | DNA encoding human  |
| 34        | 122.2 | 1.7         | 7635   | 1 084553  | Human neuronal cal  |
| 35        | 122.2 | 1.7         | 7635   | 1 084554  | Human neuronal cal  |
| 36        | 117.2 | 1.6         | 2980   | 1 029270  | Human calcium chan  |
| 37        | 113.6 | 1.6         | 6452   | 1 T330193 | Peripheral nervous  |
| 38        | 109.6 | 1.5         | 6513   | 1 T33238  | Drosophila para vo  |
| 39        | 109.6 | 1.5         | 6513   | 1 T18986  | Drosophila para vo  |



Db 2723 TGGAGATGATCTGTAAGTGGCTGATTTGGGGCTTTCGATTAAGTACTGCGTAACTTCA 2782  
Qy 2426 acatcttgaatgagtgatctggtgcatcagtggtggaagtgtggaagcaaggag 2485  
Db 2783 ACATCTTGGAGAGATCATTTGTCAATCAACATCTGGAGATGATGGGAGCGAGC 2842  
Qy 2486 gtggcctgtggtgtggtggaacctccggcgtgagcggtgtgtaagtgtgtcttc 2545  
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Db 2663 TCTGCATGCTGCTCATGCTCTTCACTTCATCTTCACATCTTGGGATGCATATTTTG 3022  
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Db 3143 TCGTCTCTCAATGGATGAGTGGCTCCACTCTCCCTGGGCTCCCTTACTTGTGGCCC 3202  
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Qy 2903 tccaaggaaggaagaaatcgcgaacgggaaga----- 2934  
Db 3263 TCCAGGGGAGGTGACTGTGTCTTGGCAGAGAGAACCCCAAGAGGCTCGAAGA 3322  
Qy 2934 --tgaggtggaagatgaaatcgtatcagtcgtcgtcaactc----- 2976  
Db 3323 CTGGGCGAGGAGAGGTGGCTGTGATGGGAGAGGCTGCATTTCAACTTTCAGAGCA 3382  
Qy 2976 -----tcaaggggagagatgcacaaagtctgaagtc-- 3006  
Db 3383 ACCTATCCCTAAGAGAGGGGTGTGATGAGGTGGGTGAGGCCAATCGCTCTACTCG 3442  
Qy 3006 -----agagctgattcttcttcgcccagtgatg 3037  
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Qy 3038 gtgatgggagcagaagaagcgcttgccccgtgtgtgttggttggaagacagcgaaactac 3097  
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Db 3563 GTCTCCACTGGGTGGGCACTAGTCTGCTGGGCTGGGAGACTGCCCCCGACTCT 3622  
Qy 3157 -----aagaagctc 3164  
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Qy 3225 cgtgtg-----agcctgagctgtccc 3244  
Db 3743 TGCAGCTGCTTTGGGCACTGGTCCCGAGCGGTGGGTGTGCTGTGGGCGCTGAC 3802  
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Db 4283 AATGAGCTAGCTAGTGGGGGCGGGCGGAGGAGGAGCTGACCTGCTTCGCGCTCC 4342  
Qy 3716 aagccttgatagatcccggtctcgtgtgtgacagagcagatctcgtgagcgct 3775  
Db 4343 GCAAGATGATGAGTGTATTAAGCCCGAGCTGTGCGAGTCCGGAAGACTGCTGTCT 4402  
Qy 3776 atatcttccctcctcagtaaggttgcctc----- 3810  
Db 4403 ACCTTCTCTCCGAGAGAGGCTCAGGGATCTGGGCTGGTAAAGCTCGAGTGCAGG 4462  
Qy 3810 -----gtgcacggagta 3823  
Db 4463 GAAAGTGGGAGCTCTGT 4522  
Qy 3824 tcaaccagaagatgttgaacatgtgttccgtcatcatcttccatctgatacca 3883  
Db 4523 TTGCCCAAACTCTGAGTACTGCTGCTGCGCTTCACTTCTCACTGATGATGCA 4582  
Qy 3884 tgcgtatgagagcgcccaaaatgtgaccccaagcgctgagcgaatcttctgaacctc 3943  
Db 4583 TCGCCCTGAGCGGCTTCAGATCGAGGCGCGGAGCCAGCAACCATCTTCTCACCGTGT 4642  
Qy 3944 ccaactacatctcaagcgagctcttctagctgaatgaaggaaggtgtgtgacgtg 4003  
Db 4643 CCAACTAATCTTACGGCCCACTTCTGTGGCGGAGATGAATGAAGTGTCTCTCGTGG 4702  
Qy 4004 gctgtgcttlttggaagcagcgctacactgtgcagcagctgtgaaatgtgtgagcgttcg 4063  
Db 4703 GCTGTACTTCCGCGAGCAGGCGTACTACGAGAGCTGGAAGTGTGATGAGCTTTC 4762  
Qy 4064 tgtgtcatcttcgtcatatgacatcttcttccatggtctcgcgaacgagcgaacaaga 4123  
Db 4763 TTGCTTGTGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4822  
Qy 4124 tcccttgcatgtgaaggt 4183  
Db 4823 TCTTGGGGGTCTCCGAGT 4882  
Qy 4184 ggcgggcccaggaagcgtggt 4243  
Db 4883 GCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4942



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OY 4244 gcaacattgtgcatcttctgctccttctcattcatttttgaattctcgggtgagc 4303
DB 4943 GCACATGTGCTCTACTGCTGCTGCTCTTCAATCATCTTGGATCCTGGAGTGCAGC 5002
OY 4304 tcttcaaaaggaaagttcttctgtgtcagggtgagacacaggaacatcattacaat 4363
DB 5003 TCTTCAGGCGAAGTTCTACACATGCTGCGGCGTGACACCCGCAACATCCACCGCT 5062
OY 4364 ccgactgtcgtgaggccagctaccagatggtccggacaaagtacaaacttaccactg 4423
DB 5063 CGGACTGCATGCGCCCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5122
OY 4424 gccaggtctgagtcctctgttgtgtcgtgctcccaaggatggttgggttgcacatgt 4483
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OY 4484 atgagtgctgagatgctgtgtgtgtgtgagatcagagcccatatgacacacacccctgga 4543
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OY 4544 tctgtctactcattcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 4603
DB 5243 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5302
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OY 4664 ggcggcgtagagagagagagagagagagagagagagagagagagagagagagagagag 4723
DB 5363 GCGGCGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5411
OY 4724 acgagttaattgtcttcgcgcagctcagccagcgtcgtcagaaagccagtgagagccct 4783
DB 5411 -----AGGCCCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5428
OY 4784 actactctactactcagatcgcgtctcctgtgcacacacactgtgtccagacactacc 4843
DB 5429 ACTATGCCACTTATGTCACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5488
OY 4844 tggacctcttcaactggtgtcagctcgcgtcgaagctgtgtgtgtgtgtgtgtgtgtgtgt 4903
DB 5489 TGGACATCTTCATACACCTTATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5548
OY 4904 accagcagccc 4914
DB 5549 ACAATCAGCCC 5559

RESULT 2
V57544
ID V57544 standard; cDNA; 567 BP.
AC V57544;
DT 20-NOV-1998 (first entry)
DE Rat calcium channel subunit alpha-1 partial sequence encoding DNA.
KW Calcium channel subunit alpha-1; recombinant; alpha 2 delta;
beta calcium channel; agonist; antagonist; alpha-11 calcium channel;
histological assay; tissue distribution; rat; ds.
OS Rattus sp.
FH key
FT 1.567
FT CDS
FT /tag= a
FT /product= "Rat calcium channel subunit alpha-1
partial sequence"
PN WO9838301-A1.
PD 03-SEP-1998.
PF 27-FEB-1998; CA0173.
PR 25-FEB-1998; US-030482.
PR 28-FEB-1997; US-039204.
PI (NEUR-) NEUROMED TECHNOLOGIES INC.
PI Baillie DL, Snutch TP.
DR MPI; 98-481203/41.

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DR P-PSDB: W79163.
PT Newly identified calcium channel subunits alpha 11 and alpha 1H
PT for development of cell lines which express the novel calcium
PT channels, useful for screening channel (ant)agonists
PT Claim 13; Pages 35-36; 45pp; English.
CC This represents a cDNA encoding a partial sequence of a rat calcium
CC channel subunit alpha-1. The invention provides isolated DNA fragments
CC coding for novel mammalian calcium channel subunits alpha-11 and
CC alpha-1H. An eukaryotic cell transiently or stably transformed with an
CC expression vector containing the calcium subunits encoding DNA fragments
CC can be used for expressing the calcium channel. The cells are optionally
CC further transformed to express alpha 2 delta or beta calcium channel or
CC both the proteins. The transformed cells are useful for identifying
CC compounds capable of acting as agonists or antagonists for the alpha-11
CC calcium channel. The nucleic acid sequences can be used in histological
CC assay to determine the tissue distribution of the novel calcium channel
CC subunits.
SQ Sequence 567 BP; 118 A; 164 C; 150 G; 135 T;

Query Match 3.9%; Score 279.6; DB 1; Length 567;
Best Local Similarity 70.1%; Pred. No. 2.2e-50;
Matches 397; Conservative 0; Mismatches 154; Indels 15; Gaps 1;

OY 589 atgcgcatctcgtcacattactcgtgacaccttgctcctatgtctgtggaagctcctgtg 648
DB 1 ATGCGCATCTGCTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
OY 649 ctctgttcttcgtcttcttcaactcttgatcgtgtggtcgtcagctctgtgagagagatg 708
DB 61 CTCTGTTCTTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
OY 709 ctctggaacagatgctctcctcccggaacttcagctccctcctgagcgtgtgagagctgag 768
DB 121 CTACGGAACCGCTGCTCTTCTGTAAGAACTTACCATTCAGAGGAGATGCTGCTGCTG 180
OY 769 ccttattacagagagagatgagagagagagagagagagagagagagagagagagagagag 828
DB 181 CTTTATTAACACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
OY 829 aatgagatgagatcctcgcagagagatgtgcccacactgcgtgtgagagagagagagagag 888
DB 241 AATGGAATCATGCGCTGCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
OY 889 cctcgcagctgagactatga-----gacctatacaagttccagcaacacc 933
DB 301 CTGTCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
OY 934 acctgtgtcaactgtgacagatcattacacactgctcgtgtgtgtgtgtgtgtgtgtgtgt 993
DB 361 CTGTGCTCAACTGGAACCGCTCTACTCAACGTCGTGCGGACGCGCAACGCCCAACCTTCA 420
OY 994 aaagggccatcaacttgcacacattgacattgctatgctgtgagtcgcatcctccaggtatc 1053
DB 421 AAGGGCCCATACACTTTTGAACAACTTGGCTATGCTGATGATGATGATGATGATGATGATG 480
OY 1054 aacatgagagagctgggtgcagacatgacttctgtatgtgagcgtcactcctctacaac 1113
DB 481 ACTGTGAAGAGCTGGGGAGATCATGTATGTATGTATGTATGTATGTATGTATGTATGTATG 540
OY 1114 ttcatctacttacttctcctcatc 1139
DB 541 TTCACTACTTCACTCCGCTTATCAT 566

RESULT 3
V57543
ID V57543 standard; DNA; 567 BP.
AC V57543;
DT 20-NOV-1998 (first entry)
DE Human calcium channel subunit alpha-11 encoding DNA.
KW Calcium channel subunit alpha-1; recombinant; alpha 2 delta;
beta calcium channel; agonist; antagonist; alpha-11 calcium channel;

```

KW histological assay; tissue distribution; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..567  
 FT /\*tag= a  
 FT /product= "Human calcium channel subunit alpha-11"  
 PN MO9838301-A1.  
 PD 03-SEP-1998.  
 PE 27-FEB-1998; CA0173.  
 PR 25-FEB-1998; US-030482.  
 PR 28-FEB-1997; US-039204.  
 PA (NEUR-) NEUROMED TECHNOLOGIES INC.  
 PI Ballie DL, Snutch TP;  
 DR WPI: 98-481203/41.  
 DR P-PSDB: W79162.  
 PT Newly identified calcium channel subunits alpha 11 and alpha 1H -  
 PT for development of cell lines which express the novel calcium  
 PT channels; useful for screening channel (ant)agonists  
 PS Claim 1; Page 34; 45pp; English.  
 CC This DNA encodes a human calcium channel subunit alpha-11 (a partial  
 CC sequence of the calcium subunit alpha-1). The invention provides isolated  
 CC DNA fragments coding for novel calcium channel subunits alpha-11 and  
 CC alpha-1H. An eukaryotic cell transiently or stably transformed with an  
 CC expression vector containing the calcium subunits encoding DNA fragments  
 CC can be used for expressing the calcium channel. The cells are optionally  
 CC further transformed to express alpha 2 delta or beta calcium channel or  
 CC both the proteins. The transformed cells are useful for identifying  
 CC compounds capable of acting as agonists or antagonists for the alpha-11  
 CC calcium channel. The nucleic acid sequences can be used in histological  
 CC assay to determine the tissue distribution of the novel calcium channel  
 CC subunits.  
 SQ Sequence 567 BP; 106 A; 165 C; 157 G; 139 T;

Query Match 3.7%; Score 262; DB 1; Length 567;  
 Best Local Similarity 68.2%; Pred. No. 1.2e-46;  
 Matches 386; Conservative 0; Mismatches 165; Indels 15; Gaps 1;

QY 589 atggcagcttcgctcacatctactgtagacacgtgctgctgtagcagcgtcgtgag 648  
 DB 1 ATGGGAGATCCGCTGACACCTGCTCTGACACACTGCCCTGCGGAGATGCTCTGCTG 60  
 QY 649 cctgttcttcgtctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 708  
 DB 61 CTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120  
 QY 709 ctctgcaacgagctgctctctcccgagaaacttaagctccctcctgagcgtgagc 768  
 DB 121 CTGGCTAACCCGCTCTCTCTGAGAGACCTTCACTAAGAGGGATGGCTTGGCC 180  
 QY 769 ccttattccagacagagaaatgagagagagcccttcttcttcttcttcttcttctt 828  
 DB 181 CCATACCTACACCGCGAGAGATGATGATGCTTCACTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 829 aatggcagagatctctgagagagtggtccacactgctgtgagagagcgtgtgtgtcc 888  
 DB 241 AATGGGATTAAGGGCTGCGATGAGATCCCGCTCAAGAGAGGCGCCGTGAGTCTG 300  
 QY 889 cccctgacgtcgtgactatgagact-----ataacagttccagcaacacc 933  
 DB 301 CTGTCCAGAGACGCTCTAGACTTTGGGGCGGGCGCCAGAGACCTCAATGCGACGGC 360  
 QY 934 accgtgtcaactggaacagactactatacaactgctctgagggcgagcaacccttcc 993  
 DB 361 CTCTGTGTCACCTGAGACCGCTTACTACATGTGTGCGCGCACGGGCGACGCCCCAC 420  
 QY 994 aaaaagcgcacacacttggacaacattggtcgtgagtcgacatcttccaggtcagc 1053  
 DB 421 AAGGATGTCATCAGCTTTGACAAACATGGTTATGCTTGGATTGTCTCATCTTCCAGG 480  
 QY 1054 aacactggaaggtcgtgctgacatcatgactcgttaatggaagcctcaactccttcaac 1113  
 DB 481 ACTCTGAAGGCTGGTGGCGATCATGTACTAGTGTGATGATGCTGCTCTCTTCAAC 540

QY 1114 ttcatctactcatctcttccatcat 1139  
 DB 541 TTGCTCTACTTCACTCCGCTTATCAT 566

RESULT 4  
 ID T77803  
 AC T77803  
 DE 09-OCT-1997 (first entry)  
 DE cDNA encoding wild type rat DRG (SNS-B).  
 KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;  
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;  
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;  
 KW enteric nervous system; central nervous system; dorsal root ganglia;  
 KW cranial ganglia; ss.  
 OS Rattus rattus.  
 EN Rattus rattus.  
 FT Key Location/Qualifiers  
 FT CDS 204..6077  
 FT /\*tag= a  
 FT /product= Rat\_DRG(SNS-B)  
 PN MO9701577-A1.  
 PD 16-JAN-1997.  
 PE 25-JUN-1996; G01523.  
 PR 28-JUN-1995; GB-013180.  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 PI Akopian AN, Wood JN;  
 DR WPI: 97-100165/09.  
 DR P-PSDB: W21737.  
 PT New isolated mammalian sensory neuron sodium channel protein - used  
 PT to identify modulators of the sodium channel, partic. for the  
 PT treatment of pain  
 PS Claim 9; Page 50-58; 128pp; English.  
 CC The sequences given in T77803-06 encode the wild type and three  
 CC variant forms of a rat sensory neuron sodium channel protein which  
 CC is insensitive to tetrodotoxin. The proteins can be used for  
 CC identifying modulators of the sodium channel. Blockers of the  
 CC sodium channel will block or prevent the transmission of impulses  
 CC along sensory neurons and thereby be useful in the treatment of acute,  
 CC chronic or neuropathic pain. The novel protein is found only in sensory  
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,  
 CC enteric or central nervous system. The protein is found preferably in  
 CC the neurons of the dorsal root ganglia or cranial ganglia.  
 SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T;

Query Match 2.0%; Score 145.6; DB 1; Length 6524;  
 Best Local Similarity 55.3%; Pred. No. 1.1e-21;  
 Matches 283; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 2248 atcatgctgcacatccctgctgcatatcatcctcagatgagcagatgagcagcagc 2307  
 DB 2214 ATCAACCTCTGCACTCGTGGAGAACCCGCTTCTATGCGCATGAGACCTACCGCTGAC 2273  
 QY 2308 gaggaagctcacaacgcccctggaatacagaacatcgtcttaccagcctctcgctt 2367  
 DB 2274 GATGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2333  
 QY 2368 gagaatgctgctgaacacgctgctgctgctgctgctgctgctgctgctgctgctg 2427  
 DB 2334 GAGATGCTTCAAGATCATATTCCTTGGACCTTACTATTTCTCCAGAGAGTGAAT 2393  
 QY 2428 atctttagtgatcatgtgcatcagatgtagtgagagatgtagtgagagagagag 2487  
 DB 2394 ATCTTCAGCTGTGTCATGCGACCGTGAAGCTTCTGAGCTGAGTGAATCCAAAGGCG 2453  
 QY 2488 ggcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 2547  
 DB 2434 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2513  
 QY 2548 ccgagccttgagagcagcagcgtcgtgctcattgaaagacattgacaagcgtgccaacctc 2607

|    |      |  |       |
|----|------|--|-------|
| Db | 2514 | CCCAACCTGAAACACCCGATCAACAGATCATGCGGAAATCAAGTGGGGCCCTGGGCAAACTGG      | 25173 |
| QY | 2608 | tgcatgtctccatcabyctgtcatctcatctcatctcaagcatccctgggcacatgcatctcttggat | 2607  |
|    |      |  |       |
| Db | 2514 | ACCTTTATCCGCGGCATCATCGTCTTCATCTTGGCCCTGGTGGAAAGCATGGCTTTCACA         | 26138 |
| QY | 2668 | tgcaagttgcacatctgaacgggattggggagacgtttgcacagacggagaagattgacatcc      | 2727  |
|    |      |  |       |
| Db | 2634 | GAGGACTACGGGGTCCGCAAGGAGGGGCTGTCGATGGAGACGGCGAAGCTCCGCTGG            | 2693  |
| QY | 2728 | ctgctctgggacatcgtgcactgctcttccagat                                   | 2759  |
|    |      |  |       |
| Db | 2694 | CACATGTGTGACTTCTTCATCTCCTTCTCTGT                                     | 2725  |

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RESULT      5
081328
AC          081328 standard; cDNA: 7555 BP.
ID          081328;
DR          05-AUG-1995 (first entry)
DE          Cardiac sodium channel protein coding sequence.
KW          Sodium channel protein; ds; therapeutic; diagnostic;
KN          antiarrhythmic; cadiant; cardioglycoside; PRH3-1; pRH4-23; pRH14-31..
OS          Rattus rattus.
FH          Key
FT          Location/Qualifiers
FT          cds
FT          196..6253
FT          /*tag= a
PN          U5538036-A.
PD          10-JAN-1995.
PF          13-FEB-1989; 331330.
PR          13-FEB-1989; US-331330.
PR          30-SEP-1991; US-768107.
PA          (ARCH-) ARCH DEV CORP.
PI          Rogart RB:
DR          WPI: 95-060381/08.
DR          P-PSDB: R67913.
PT          Purified DNA s encoding rat and human cardiac sodium channel
PT          protein - useful for recombinant expression to produce sodium
PT          channel proteins.
PS          Claim 8; Fig 1a-1n; 39pp; English.
CC          The cDNA is derived from 3 overlapping cDNA clones, designated
CC          plasmid pRH3-1 (ATCC 67885), plasmid pRH4-23 (ATCC 67886) and
CC          plasmid pRH14-31 (ATCC 67887). A virus/circular DNA plasmid vector
CC          comprising the cDNA may be transformed or transfected into a
CC          prokaryote/eukaryote host cell, and the resulting recombinant sodium
CC          channel protein has various therapeutic, diagnostic and prognostic
CC          uses. It may also be used to develop more effective antiarrhythmic,
CC          cardiac and cardioglycoside drugs.
SQ          Sequence 7555 BP: 1577 A: 2309 C: 2103 G: 1566 T;

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|                           |       |                   |          |             |
|---------------------------|-------|-------------------|----------|-------------|
| Query Match               | 2.0%  | Score 144.2       | DB 1     | Length 7555 |
| Best Local Similarity     | 52.0% | Pred. No. 2.4e-21 |          |             |
| Matches 354: Conservative | 0     | Mismatches 318    | Indels 9 | Gaps 11     |

|    |      |  |      |
|----|------|--|------|
| QY | 2248 | atataagatgcgcatctcgtgtgtaataaacctagaatcgtgacatgagtaacacagagagcgc | 2307 |
| QY | 2249 |  |      |
| Db | 2365 | ATACCACTATGTGATCGTCTCAATACGCTTTCATGCGCTGTGGAGATTACAACTATGAC      | 2424 |
| QY | 2308 | gaggaagctacccaacgcgcctcggaaatcagaacatcgtcttccaccagcctcttcgcttg   | 2367 |
| Db | 2425 | GCAGAGTTTGAAGAGATCTCTACAGTGGAAACCTGGTCTTCCGGGAATTTCCACCG         | 2484 |
| QY | 2368 | gagatcgtcgtaaactgcttgcctacgctcccttgcgtacataaagaatccctacaac       | 2427 |
| QY | 2369 |  |      |
| Db | 2485 | GAGATDACTTAAATATCATGCGCCTTGACCCCTACTACTACTTCCAGAGGGGTGAAAT       | 2544 |
| QY | 2428 | atccttgatgctgctcaattggtgtaacagtgctgtggagaatttctggccagaagggaggt   | 2487 |
| Db | 2545 | ATCTTGACAGAGCATATCGTATCCTCATGTCATGTGAGAGCTGGGGCTGTGCCGACATGGCC   | 2604 |
| QY | 2488 | ggcctgcggtctcgcggaacctccgcctgtagtgagggtcttgtaagcttggctgcctctg    | 2547 |

Db 2605 AACCTTCTCTGTCTAGCTTCCTCCGTCGTCGCGAGCTTCAACTGCGCAAGCTCG 2664  
 Qy 2548 ccgagccctcgaagcgcaagctcgtgtgtgtcattgaagaccatgaaagatggtccacctc 2607  
 Db 2665 CCCACCTTGAAACAGCTCATCAAGATCATCGGAACCTCGTGTGGCGCCCTGGGAAACTG 2724  
 Qy 2608 tgaatgtctcctaagctgcttcacatcttcacatccagacatccgtgagcatgactcttgt 2667  
 Db 2725 ACCCTGGGTGGCGCATCATGCTTCTTCACTTTCGCCGTGTGGCATCGAGCTTTGGCG 2784  
 Qy 2668 tgcagatcgcgcatcgaagcggaatgggagca-----cgtggcagaccggagaagt 2718  
 Db 2785 AAGAACTACTCAGAACTGAGGACCGCATCAGAGCATCCGGCGCTCTGCCCGCGCGCAC 2844  
 Qy 2719 ctgacatccctgtctctgggccatcgtcactgctcttcaagatctgacatcgaagaagctg 2778  
 Db 2845 ATGATGACCTTTTCCAGCGCTTCTCTATCATTTCCGATCCTCTGAGGAGATGATC 2904  
 Qy 2779 aataagtcctctcaacgagcagatgacctcacatcgctcttggagctgctcttactcatc 2838  
 Db 2905 GAGACATGTGGGACTGCATGAGAGGTGTGGGCACTGCTGTGCTGTGCTTCTCG 2964  
 Qy 2839 gccctcagatcttttggacaatagtgctctttaaactgcgtgtgtgcaatcttcttggaa 2894  
 Db 2965 CTCGTCATGTCATTTGGCAACCTGTGGTCTGCTAAATCTTCTTGGCTGTGCTCAGC 3024  
 Qy 2899 ggaatccagcagagaagaatc 2919  
 Db 3025 TCTTTACGCGCAGCAACTTC 3045

| Sequence | 7052 BP   | 1655 A              | 2009 C | 1795 G | 1593 T |
|----------|---|---------------------|--------|--------|--------|
| AC       | T77805 standard; cDNA; 7052 BP.   |                     |        |        |        |
| ID       | T77805  |                     |        |        |        |
| DT       | 09-Oct-1997 (first entry)   |                     |        |        |        |
| DE       | cDNA encoding variant rat DRG (SNS-B) #2.                               |                     |        |        |        |
| CC       | Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;  |                     |        |        |        |
| CC       | modulator; impulse; sensory neuron; acute pain; chronic pain;           |                     |        |        |        |
| CC       | neuropathic pain; glia; muscle; parasympathetic nervous system;         |                     |        |        |        |
| CC       | enteric nervous system; central nervous system; dorsal root ganglia;    |                     |        |        |        |
| OS       | Rattus rattus.  |                     |        |        |        |
| FT       | Key   | Location/Qualifiers |        |        |        |
| FT       | cds   | 204..6602           |        |        |        |
| FT       | /*tag= a  |                     |        |        |        |
| FT       | /product= Variant_Rat_DRG(SNS-B)  |                     |        |        |        |
| PN       | MO9701577-A1.   |                     |        |        |        |
| PD       | 16-JAN-1997   |                     |        |        |        |
| PI       | 25-JUN-1996; G01523.  |                     |        |        |        |
| PR       | 28-JUN-1995; GB-013180.   |                     |        |        |        |
| PA       | (UNLO ) UNITV COLLEGE LONDON.   |                     |        |        |        |
| PI       | AKopian AN, Wood JN.  |                     |        |        |        |
| DR       | WPI; 97-100165/09.  |                     |        |        |        |
| DR       | P-PSDB; W21739.   |                     |        |        |        |
| PT       | New isolated mammalian sensory neuron sodium channel protein - used     |                     |        |        |        |
| PT       | to identify modulators of the sodium channel, partic. for the           |                     |        |        |        |
| PT       | treatment of pain   |                     |        |        |        |
| PS       | Claim 9; Page 69-78; 128pp: English.                                    |                     |        |        |        |
| CC       | The sequences given in T77803-06 encode the wild type and three         |                     |        |        |        |
| CC       | variant forms of a rat sensory neuron sodium channel protein which      |                     |        |        |        |
| CC       | is insensitive to tetrodotoxin. The proteins can be used for            |                     |        |        |        |
| CC       | identifying modulators of the sodium channel. Blockers of the           |                     |        |        |        |
| CC       | sodium channel will block or prevent the transmission of impulses       |                     |        |        |        |
| CC       | along sensory neurons and thereby be useful in the treatment of acute,  |                     |        |        |        |
| CC       | chronic or neuropathic pain. The novel protein is found only in sensory |                     |        |        |        |
| CC       | neurons and not in glia, muscle or the neurons of the (para)sympathetic |                     |        |        |        |
| CC       | enteric or central nervous system. The protein is found preferably in   |                     |        |        |        |
| CC       | the neurons of the dorsal root ganglia or cranial ganglia. Thus         |                     |        |        |        |
| CC       | sequence encodes a 2132 amino acid protein that contains a 176 amino    |                     |        |        |        |
| CC       | acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)    |                     |        |        |        |
| CC       | (see also W21777).  |                     |        |        |        |

Query Match 2.0%; Score 144; DB 1; Length 7052;  
 Best Local Similarity 55.1%; Pred. No. 2.5e-21;  
 Matches 282; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 2248 atcatatgcgcacatcctgtgtcaatacactcagatggatgcagatgacagagagagcc 2307  
 DB 2739 ATCACCTCTGATCGTGTGAACACCGCTTCTATGAGCAGACACTACCCCATGACC 2798  
 QY 2308 gagagagtcacacagccctggaaatcagacacatgccttcacagcccttcgcttg 2367  
 DB 2799 GATGCGCTTCATGCCATGCTTCAAGCCGGCAACATGTCTTCAACCGTGTTCACAAATG 2858  
 QY 2368 gagatgtgtgaaactgtgtgtctacggtcccttggcacttaagatccctcaac 2427  
 DB 2859 GAGATGCCCTCAAGATCATTCCTTCGACCCCTACTATTCTTCCAGAAAGATGGAAT 2918  
 QY 2428 atctttgatgtgtcaltgtgtgtcacaagtgtgtggagatgtgtggcagagagagt 2487  
 DB 2919 ATCTTGACTGTGTCAATCGTCAACCGTGTGAGCTTCTGAGCTGATGATCAAGAAAGGGC 2978  
 QY 2488 ggccttgcgt 2547  
 DB 2979 AGCCTGTCTGT 3038  
 QY 2548 ccggccctgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2607  
 DB 3039 CCCACCTGAAACCTCAATCAAGATCATTCGGAATCACTAGTGGGGCCTTGCGCAACTG 3098  
 QY 2608 tgcattctctcattctgttcatcttcatcttcatcttcatcttcatcttcttctgt 2667  
 DB 3099 ACCTTATCTCTGCGCATCATTCGCTTCACTTCCGCTTGTGCGAAAGCAGCTTCTCTCA 3158  
 QY 2668 tgcagatgcagcatcgaagcagcagcagcagcagcagcagcagcagcagcagcagc 2727  
 DB 3159 GAGGACTAGGGGTCGCCGCAAGAGCGGCTCTCGTGTGAGAAAGCGAGAGCTCGCTGG 3218  
 QY 2728 ctgtctgtggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2799  
 DB 3219 CACATGTGTGACTTCTTCCATTCCTTCTCTGTGT 3250

RESULT 7  
 T77806  
 ID T77806 standard; cDNA; 6527 BP.  
 AC T77806;  
 DT 09-OCT-1997 (first entry)  
 DE cDNA encoding variant rat DRG (SNS-B) #3.  
 KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;  
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;  
 KW neuropathic pain; gila; muscle; parasympathetic nervous system;  
 KW enteric nervous system; central nervous system; dorsal root ganglia;  
 KW cranial ganglia; ss.  
 OS Rattus rattus.  
 FH Key  
 FT cds  
 FT location/Qualifiers  
 FT 204..6602  
 FT /tag- a  
 FT /product- Variant\_Rat\_DRG(SNS-B)  
 FT 299  
 FT /tag- b  
 FT /label- C>G  
 FT 1092  
 FT /tag- c  
 FT /label- G>A  
 FT /note- "Causes Val > Ile substitution"  
 FT 1096  
 FT /tag- d  
 FT /label- C>T  
 FT /note- "Causes Ser > Phe substitution"  
 FT 1964  
 FT /tag- e  
 FT /label- G>C

FT mutation  
 FT 1965  
 FT /tag- f  
 FT /label- C>G  
 FT /note- "Causes His > Asp substitution"  
 FT 2472  
 FT /tag- g  
 FT /label- A>T  
 FT /note- "Causes Thr > Ser substitution"  
 FT 2986  
 FT /tag- h  
 FT /label- G>T  
 FT /note- "Causes Ser > Ile substitution"  
 FT 3019  
 FT /tag- i  
 FT /label- A>G  
 FT /note- "Causes His > Arg substitution"  
 FT 3158  
 FT /tag- j  
 FT /label- C>T  
 FT 3525  
 FT /tag- k  
 FT /label- C>G  
 FT /note- "Causes His > Asp substitution"  
 FT 3556  
 FT /tag- l  
 FT /label- G>C  
 FT /note- "Causes Arg > Thr substitution"  
 FT 5893  
 FT /tag- m  
 FT /label- T>G  
 FT /note- "Causes Ile > Ser substitution"  
 FT 6525  
 FT /tag- n  
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 FT  
 FT W09701577-A1.  
 FT 16-JAN-1997.  
 FT 25-JUN-1996; G01523.  
 FT 28-JUN-1995; GB-013180.  
 FT (UNLO ) UNIV COLLEGE LONDON.  
 FT AKopian AN, Wood JN;  
 FT WPT; 97-100165/09.  
 FT P-P-SDB; W21740.  
 FT New isolated mammalian sensory neuron sodium channel protein - used  
 FT to identify modulators of the sodium channel, partic. for the  
 FT treatment of pain  
 FT  
 FT Claim 9: Page 85-93; 128pp; English.  
 FT The sequences given in T77803-06 encode the wild type and three  
 FT variant forms of a rat sensory neuron sodium channel protein which  
 FT is insensitive to tetrodotoxin. The proteins can be used for  
 FT identifying modulators of the sodium channel. Blockers of the  
 FT sodium channel will block or prevent the transmission of impulses  
 FT along sensory neurons and thereby be useful in the treatment of acute,  
 FT chronic or neuropathic pain. The novel protein is found only in sensory  
 FT neurons and not in gila, muscle or the neurons of the (para)sympathetic,  
 FT enteric or central nervous system. The protein is found preferably in  
 FT the neurons of the dorsal root ganglia or cranial ganglia. This  
 FT sequence contains 12 nucleotide differences to the wildtype rat  
 FT DRG(SNS-B) (see also T77803) causing nine amino acid changes.  
 FT Sequence 6527 BP; 1542 A; 1863 C; 1653 G; 1459 T;

Query Match 2.0%; Score 144; DB 1; Length 6527;  
 Best Local Similarity 55.1%; Pred. No. 2.5e-21;  
 Matches 282; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 2248 atcatatgcgcacatcctgtgtcaatacactcagatggatgcagatgacagagagagcc 2307  
 DB 2214 ATCACCTCTGATCGTGTGAACACCGCTTCTATGAGCAGACACTACCCCATGACC 2273  
 QY 2308 gagagagtcacacagccctggaaatcagacacatgccttcacagcccttcgcttg 2367  
 DB 2274 GATGCGCTTCATGCCATGCTTCAAGCCGGCAACATGTGTCTTCAACCGTGTTCACAAATG 2333









|    |      |  |      |
|----|------|--|------|
| Db | 2578 | TATTTGATATGACTCTACACTCTGCTTACAGTGGAGATGTGCTTCACATGACAAAC         | 2637 |
| Qy | 4000 | ctgggcctgggctttgggggacgggctacccgcgaagatgtgaatgctgtgaagcgc        | 4059 |
| Db | 2638 | TACGGCCCTTCCTGCACAAAGGCTCTTCTGCGCACTACTTCACAAATCCTGGACGTG        | 2697 |
| Qy | 4060 | tctgtgtgtcatalctccgcatcacgaatcctgtgtccatgtgtctccgaagcggcaac      | 4119 |
| Db | 2698 | CTGTGGTGGCGGTGTCTCATCTCATCTCCATGGGCTGTGATGCCAGCACCATCTCCGTGTA    | 2757 |
| Qy | 4120 | aagctccttgcaatgctgaaggggtgcggcgctgtgtcggaaacctgtccaaactaaggctc   | 4179 |
| Db | 2758 | AAGATCTGAGAGTGTCTAAAGGGTCTCCGGCCCTGTGAGC-----C                   | 2799 |
| Qy | 4180 | atcagccgggcccagggacggaactgtgtgtgtgaagacctgtatltcacctcaaaccc      | 4239 |
| Db | 2800 | ATCAACAGAGCCAAAGGTTGAGACACGTGGTCCATGTGGTGTGGATCCATCGGCAC         | 2859 |
| Qy | 4240 | atgtgaacattgtgtgcatctgtctgtctcttcatactatttggaaatctccggggtc       | 4299 |
| Db | 2860 | ATCGGAGACATCTCTCTGTGCACACGCTCTGTCACTTATGTTCCTGCATCGGTTC          | 2919 |
| Qy | 4300 | caagcttccaaaaggaaagtcttcctgtgtgtca-----gggttgaac                 | 4341 |
| Db | 2920 | CAGCTCTTCAAGGGCAGAGTCTTACGTGCAATGACCTTCCAGATGACAAAGAAAGAG        | 2979 |
| Qy | 4342 | acaggaagaaactaaactaaatccgcagctgctgtgaagcagcta-----               | 4386 |
| Db | 2980 | TGCAAGGCGCTACTCTTGTGTCTAAAGAGAGGGAGCCACCGAATGAGAGCTCGGCCCC       | 3039 |
| Qy | 4386 | --ccgatgtggtccggcaaaagtacaacttggacaacctgtggcaggctctgtatgtccctg   | 4443 |
| Db | 3040 | CGCCAGTGGATACACATGTACTTCCATTGCAACAGTGTCTCTCGGCATGATGTGCGCTC      | 3099 |
| Qy | 4444 | tctgtctgtgctctcaagagtgtgtgtgtgaatactgtatgaatgtgtgtgtgtgtgtg      | 4503 |
| Db | 3100 | TTCACGGTGTCACTTCTGAGAGGATGGCCCACTCTGTACAGGGCCATAGATCTCAAC        | 3159 |
| Qy | 4504 | gggtgtgatacgaagcccatcatgaacaacacccctgtgattgtcatlaactcacc         | 4563 |
| Db | 3160 | GAGAGGACATGGGCCCCGTTTACAAACACGAGTGAATGGCATCTTCTTCATCTATC         | 3219 |
| Qy | 4564 | tctccctccatcgtgtgacctctctgtccctaaagtgtgtgtgtgtgtgtgtgtgtgaagc    | 4623 |
| Db | 3220 | TACATCATCCCTCATGGCTTCTTTCATGATGAACATTTTGTGGCTTGTCTATCGTCAAC      | 3279 |
| Qy | 4624 | tctcataagtgcagacagcaaccaggaaggaaggcagggcggcgtgtgagaagaagcga      | 4683 |
| Db | 3280 | TTCACGAG-----CAGGGGGAGACGAGATCAACAACTGGAGGTGGACAGCAACG           | 3333 |
| Qy | 4684 | ctacggaaagctgggaaagaagaagaatctaagtgttgacgatgttaattgtcttcgggc     | 4743 |
| Db | 3334 | CGCCAGTGTGTGCAGTATGGCTGTGAAGGCCGCCCACTT--CGGTCTCTCATCCCAAGA      | 3391 |
| Qy | 4744 | agctcagccagcgtctgctgaagaagccagttgcaagccctaactactgtactactcaga     | 4803 |
| Db | 3392 | ACCCATACCACTACCAAGTGTGTGACTGTCT--CACCTCTCTACTTTGAAATACCTGTATG    | 3450 |
| Qy | 4804 | tctcgagctcctgtgcaaacacctgtgtacagcagctactactggaacctcttaactgtgt    | 4863 |
| Db | 3451 | TTGCGCTCATCATGCTCAAC---ACATGTGCTGTGGGATCGAGCATCAACCAAGTGC        | 3507 |
| Qy | 4864 | gtcatcgggtgtgaagctgtgactactatgtgcatagtgaacattaccagcagcccaagctctg | 4923 |
| Db | 3508 | GAGGAGATGAACCACTCTAGACATCTCTAAATGTGGCTTACCACTCATCTTTCACGCTG      | 3567 |
| Qy | 4924 | gaagaggtctgaagatctgcaattacatcttaccgtaactctgtcttgaagcagtt         | 4983 |
| Db | 3568 | GAGATGATTTCAAGCTCTTGGGCTTCAAGGCCAGGGGCTATTGTGGAAACCCCTGGAAT      | 3627 |
| Qy | 4984 | tccaacctgtggccttgtgcttccgcgcttcttccaggacaggtgtgaacagctgtgac      | 5043 |

|           |   |  |      |
|-----------|---|--|------|
| D0        | 3628  | GTGTTCACTTCCGATTCGATCGCATCGGCACAGATCATATGACGTATCCTCAGCGAATGCAC | 3687 |
| 01        | 5744  | ctggcatctgtctcgtccatccatcctcgtgagcatcacctgagagattgaattcaatgct  | 5103 |
| D0        | 3688  | ACTTCTCTGGCCTCCACCGGGGAGACTGTATGCTTGCGTGGCGGCTCGCGAAGCTTAC     | 3747 |
| CY        | 5104  | tcgctgtcccaatcaacccaccatcatccgatalcatgaggtgtctccgactgtcgaagt   | 5163 |
| D0        | 3748  | CCACACGAGAGCGCCGCCATCTCCAGTCCCTTCTCCGCCCTTTCGGGTTATGAGCGTG     | 3807 |
| OY        | 5154  | ctgaagctgtttgaagatgagctctgtcggcatgagggacactctgcaacggttgtagggc  | 5222 |
| D0        | 3808  | ATCAAGCTGCTGATCGGCGCCGAGGGCGTGCGACGCTGTGTGACGTTATCAAGTCC       | 3867 |
| OY        | 5224  | ctgcccacaagtgtaggaacctggaactctctcatgttatgttttcttccttgcagt      | 5283 |
| 1b        | 3868  | TTCCAGCGCCCTCCCTACGTCGCGCCCTGCTCATGTCATGTCATCTTCATCTACGCCCTC   | 3927 |
| CY        | 5284  | ctggagcttgagagctctcttggaagccctgg                               | 5311 |
| D0        | 3928  | ATCGCATGCAGATGTTGGAAAGATCG                                     | 3955 |
| RESULT 13 |   |  |      |
| 1D        | 087978  |  |      |
| AC        | 087978  | standard; cDNA; 5975 BP.                                       |      |
| DT        | 02-NOV-1995   | (first entry)  |      |
| DE        | Rabbit skeletal calcium channel (alpha)1-subunit.                     |  |      |
| KM        | Calcium channel; (alpha)1 subunit; ss.                                |  |      |
| OS        | Oryctolagus cuniculus.  |  |      |
| FA        | Key   | Location/Qualifiers  |      |
| FJ        | cds   | 79..5700   |      |
| FI        |   | /*tag= a   |      |
| ET        | polya_signal  | 5910..5915   |      |
| ET        |   | /*tag= b   |      |
| ET        | misc_difference   | 5501   |      |
| ET        |   | /*tag= C   |      |
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| ET        | misc_difference   | 5522   |      |
| ET        |   | /*tag= d   |      |
| ET        |   | /note= "different from Tanabe et al"                           |      |
| ET        | misc_difference   | 5582   |      |
| ET        |   | /*tag= e*  |      |
| ET        |   | /note= "different from Tanabe et al"                           |      |
| PA        | US5407020-A.  |  |      |
| PD        | 18-APR-1995.  |  |      |
| PF        | 04-APR-1988; 176899.  |  |      |
| PR        | 04-APR-1988; US-176899.   |  |      |
| PR        | 04-APR-1989; US-603751.   |  |      |
| PR        | 13-JUL-1992; US-914231.   |  |      |
| PA        | (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.                            |  |      |
| PI        | Brønner R., Ellis SB, Harpold MM, Schwartz A, Williams ME.            |  |      |
| PI        | WFL: 95-161088/21.  |  |      |
| DR        | P-PSDB: R73055.   |  |      |
| ET        | DNA encoding alpha-1 and alpha-2 calcium channel sub-unit(s) -        |  |      |
| ET        | for detecting calcium channel agonists/antagonists or                 |  |      |
| ET        | Lambert-Eaton syndrome.   |  |      |
| PS        | Claim 13: Fig 1; 32pp; English.                                       |  |      |
| CC        | The cDNA sequence 087978 is consistent with an approx 6,500 nt DHP    |  |      |
| CC        | receptor (alpha1) mRNA. It is 94% identical to the cDNA sequence      |  |      |
| CC        | encoding the DHP receptor reported by Tanabe et al., Nature, 328:313- |  |      |
| CC        | 318, 1987. No differences were identified at 33 posns. of which       |  |      |
| CC        | three (see FT) also result in AA changes (see R73055 FT). The         |  |      |
| CC        | deduced AA sequence yields a calculated Mr of 212,143, in contrast to |  |      |
| CC        | the observed Mr 155K-170K, previously reported by others using SDS    |  |      |
| CC        | polyacrylamide gel electrophoresis. The AA sequence is 99.8%          |  |      |
| CC        | identical to that described by Tanabe et al. It contains four         |  |      |
| CC        | internally repeated sequence regions. It has been proposed that the   |  |      |
| CC        | segments of the four internally repeated regions represent 24         |  |      |
| CC        | transmembrane segments. A eukaryotic cell expressing a chimeric       |  |      |
| CC        | cDNA is claimed, in which the first cDNA is selected from the gp.     |  |      |
| CC        | consisting of cDNA that encodes a protein that has the AA sequence    |  |      |

CC in R73055 but with the Tanabe et al substitutions indicated in FT  
SQ Sequence 5975 BP; 1291 A; 1834 C; 1693 G; 1157 T;

| Sequence | 5975 BP; | 1291 A; | 1834 C; | 1693 G; | 115 / 1 |
|----------|----------|---------|---------|---------|---------|
| SQ       |          |         |         |         |         |

| Query Match | Score  | DB 1; | Length |
|-------------|--------|-------|--------|
| 1.98;       | 136.4; | DB 1; | 5975;  |

Best Local Similarity 47.18; Pred. No. 9.8e-207

|         |      |              |    |            |      |        |     |      |    |
|---------|------|--------------|----|------------|------|--------|-----|------|----|
| Matches | 748; | Conservative | 0; | Mismatches | 771; | Indels | 69; | Gaps | 8. |
|---------|------|--------------|----|------------|------|--------|-----|------|----|

|    |      |   |      |
|----|------|---|------|
| Oy | 3760 | gattccgtggtcgccatatacttccctcccaagtcgaaggttgccttcgtgtccaaagg   | 3819 |
| Db | 2401 | GAACCCAGCTCTCTTTCATCTTCACTTCCACCACCAATTAAGTCCGTGTCTGTACACGC   | 2460 |
| Oy | 3820 | atcaaaccccaagaatgatttagcaccatggtgccttcgtatcatcttccctaactyratc | 3879 |
| Db | 2461 | ATCGTCAACGGCACTGGTTGTTACCAACTTCACTGCTGCTTCACTGCTGAGAGTCT      | 2520 |
| Oy | 3880 | accatcgctatgtagcgccccaataattgaaccccaagcgctgtagcattcttcagc     | 3939 |
| Db | 2521 | GGCTGGGCGCCGCGAGGAGCCCAATCCGGG---CGGAATCCGTGAGGAATCAGATCTTTGA | 2577 |
| Oy | 3940 | ctctccaaactaacatcttcacgagcagcttccttcagctcgaatgacagtgatgtgtgca | 3999 |
| Db | 2578 | TATTTTGATTTAGCTTTCACCTCTGTCTTCACTGTGGAGATTGTGCTCAATATCAAC     | 2637 |
| Oy | 4000 | ctgagctgtagtctttgtaggagcagcctaacctcygcaagctgtaatgtgtgagcgc    | 4059 |
| Db | 2638 | TACGGCGCTTTCGTGCAACAAGGGGCTCTTGCGCAACTTCAACATCTTGAGACTG       | 2697 |
| Oy | 4060 | ttgtctgtgtcctatctccgtcatcgaatccgtgtcttcattgtgtctccgaagsgaac   | 4119 |
| Db | 2698 | CTGGGTGGGGCGGTGTCTCATCTCCATGGGTCTCGAGTCCAGCAACATCTCCGTGTA     | 2757 |
| Oy | 4120 | aagatcccttgtagctgtaggagtggtcgtcggtctgtagaccctgtgcacatcaaggtc  | 4179 |
| Db | 2758 | AAGATCTCTCAAGAGTCTTAAGGGTCTCTGGGCCCTCGAGC-----C               | 2799 |
| Oy | 4180 | atcaagccgagcccaaggagctgaagctgtgtgtatgagaactctgtatccctcaaac    | 4239 |
| Db | 2800 | ATCAACACAGGCCAAAGGTTTAACACAGTGTCTCACTGGGTGTGTGTGGCATCCGAC     | 2859 |
| Oy | 4240 | attgccaacattgtgtcatcttgctgtcgcttccttcattcttggaaatctccggggt    | 4299 |
| Db | 2860 | ATCGGGAACATGCTCTGTGTACACAGCTCTCGAATTATGTTGACCTGCATCGGTCT      | 2919 |
| Oy | 4300 | caagctcttcaaggaggaattcttcgtgtgca-----gggtgagagc               | 4341 |
| Db | 2920 | CAGCTCTTCAAGGGAATTTCTTCACTGCAATGACCTATCCAAAGATGACAAAGAGAG     | 2979 |
| Oy | 4342 | accaggaacatctaatacaaatccgactgcgtgtgagccaagcta-----            | 4386 |
| Db | 2980 | TCGAGGGCTACTACTATGTGTAAACAAGAGGGGAGCCCCACGACATGAGCTCGGCC      | 3039 |
| Oy | 4386 | --cgatggtgtccgcacaaagttaaactttgaacaacttggccaaggtctgtatgcctg   | 4443 |
| Db | 3040 | CGGCAATGATATCAACAAGACTTCCACTTTGACACATGCTGTGCGCATGATGTGCTC     | 3099 |
| Oy | 4444 | tttgtgtcgtccccaagatgattgttggtttgacatcatgatgatgtgagctgtgtg     | 4503 |
| Db | 3100 | TTTACGGTGTCCACTTTGAGGAGATGGGCCAGTGTGTATACAGGGCCATATACATCAAC   | 3159 |
| Oy | 4504 | ggtgtgatacagagcccatcatgaacacaaacccctgtatgctgctatcatctcc       | 4563 |
| Db | 3160 | GAGGAGGACATGGGCGCGTTTACAAACACGAGTGGAGATGGCCATCTTCTTCAATTC     | 3219 |
| Oy | 4564 | ttctctcatatgttggtccttctgttccctgaacatgttttggtgcgtgtgtgtgagac   | 4622 |
| Db | 3220 | TACATATCTCTATTGCTCTTTCATATGATGAACATCTTTTGTGGCTTTGTATCTGCAC    | 3279 |
| Oy | 4624 | ttctcaaatgtcagaacagcaccagaagaagaagaagcgagcggtgtgagagaagca     | 4683 |
| Db | 3280 | TTTCCAGAGC-----CAGGGGGAAGACGAGATACAAAGAACTGCGAGGTGGCAAGAACCG  | 3333 |
| Oy | 4684 | ctacggaggtcgtgagaaaaagaagaagaatctaattgttgaacgatgtaatgtcttcggc | 4744 |

|           |   |   |      |
|-----------|---|---|------|
| Db        | 3334  | CGCCAGTGTGTGAGATGATGCGCTTGAAGGGCCGCCCACTT--CGGTGTACATCCCAAGA    | 3351 |
| Oy        | 4744  | agctcagcagcgctcgtctcagaagccagctgcaagccctactactctgactctcaga      | 4803 |
| Db        | 3352  | ACCCATACCCAGTACCAAGGTGTGTAGTGTGT--CACTCTCTCTACTTTGAATACCTGATG   | 3450 |
| Oy        | 4804  | ttccgcgtctcttgcacacacacctgtgtlaacagccactactcctggacctcttcactggt  | 4863 |
| Dc        | 3451  | TTGCGCCCTACATCATGCTCAAC--ACCATCTGCTGTGGGATCCACACATCACCAACATCG   | 3507 |
| Dc        | 3508  | GAGGAGATGAAACCACTCTCAGCATCTCTTAATATGCGCTTACCATATCTTCAAGCTG      | 3567 |
| Oy        | 4924  | gacgagctctcgaagactctcaatcatcttaccgtcatcttgccttcttgagtcagtt      | 4983 |
| Db        | 3568  | GAGATGATCTTCACAGCTCTTGGGTTCAAGGCGGCTATTTGGAGAACCCCTGGAAAT       | 3627 |
| Oy        | 4984  | ttcaactgttgaccttggcttcttcgcgcgtttcttcagagcaagtgtagccagctgac     | 5043 |
| Dc        | 3628  | GTTGTCGATCTTCATCGATCGATCGAGCATATTGAGCTATCTCTCAGCAGATCGAC        | 3688 |
| Oy        | 5044  | ctggtatgtgtctctcgtcatcatcgtgcatcacactgagagatltgagltcaatgct      | 5103 |
| Dc        | 3688  | ACTTCTTCGCGCTCCACGGGGGAGCTTATGCTCTGGTGGCGGCGGGAACGTGAC          | 3748 |
| Oy        | 5104  | tgcgtgccatcaaacccacatcatccgtatcatgagagtgctccgcatctcgtagtt       | 5165 |
| Dc        | 3748  | CCAGACGAGACCGCCGCCATCTCCAGTGCCTTCTCCGCTGTTCCGGGTATGAGCGTC       | 3807 |
| Oy        | 5164  | ctgaagctgttgaagatgagctgtgtgagtcagtcgggagctgcttgagcaggtgatgcagcc | 5223 |
| Dc        | 3808  | ATCAAGCTGCTGAGTCGAGCGGCGGAGGCGCTGCGACGCTGCTGTGAGCATTCATCAAGTGC  | 3867 |
| Oy        | 5224  | ctgcccacagtgaggagaaactctctcattcaatgtatgttttcaatcttgcagct        | 5283 |
| Dc        | 3868  | TTCCAGGCGCGTGCCTTACGTGCGCTCTCATGCTATGCTGTTTCATCTACGCGTGC        | 3927 |
| Oy        | 5284  | ctggagctgtgagctcttggagacctg                                     | 5311 |
| Dc        | 3928  | ATCGCATGCAGATGTTTGAAAGATCG                                      | 3955 |
| RESULT 14 |   |   |      |
| ID        | 005831  | standard: cDNA: 7555 BP.  |      |
| AC        | 005831;   |   |      |
| DT        | 10-JAN-1991   | (first entry)   |      |
| DE        | Cardiac sodium channel gene.  |   |      |
| KM        | Rat: arrhythmia; ss.  |   |      |
| OS        | Rattus rattus.  |   |      |
| PN        | W09009391-R.  |   |      |
| PD        | 23-AUG-1990.  |   |      |
| PF        | 09-FEB-1990; U00768.  |   |      |
| PR        | 13-FEB-1989; US-310330.   |   |      |
| PI        | (ARCH-) ARCH DEV CORP.  |   |      |
| RA        | Rogart RB:  |   |      |
| DR        | WPI, 90-275095/35.  |   |      |
| DR        | P-PSDB; R06584.   |   |      |
| PT        | New rat cardiac sodium channel proteins - and associated DNA        |   |      |
| PT        | sequences, polypeptides and peptides associated with                |   |      |
| PS        | proteins, useful as antiarrhythmic and cardiotoxic drugs.           |   |      |
| PS        | Claim 7; Fig.1; 65bp; English.                                      |   |      |
| CC        | The sequence is derived from 3 overlapping clones, PRH3-1, PRH4-23, |   |      |
| CC        | and PRH4-31. (deposited as ATCC 67885, 67886, and 67887 resp.)      |   |      |
| CC        | The clones were isolated from a cDNA library in the lambda Zap      |   |      |
| CC        | vector prepd. from mRNA obt'd. from newborn rat hearts using rat    |   |      |
| CC        | brain II cDNA probe. The isolated DNA can be used to screen a       |   |      |
| CC        | similar human derived cardiac cDNA library for the corresponding    |   |      |
| CC        | human gene. Proteins produced by expression of the DNA have         |   |      |
| CC        | diagnostic therapeutic and prognostic applications.                 |   |      |
| CC        | Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;                   |   |      |
| CC        | Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;                   |   |      |

PT New rat cardiac sodium channel/proteins - and associated DNA  
 PT sequences, polypeptides and peptides associated with  
 PT proteins, useful as antiarrhythmic and cardiotonic drugs.  
 PS Claim 7, Fig.1; 65pp; English.  
 CC The sequence is derived from 3 overlapping clones, pRH3-1, pRH4-23,  
 CC and pRH4-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)  
 CC The clones were isolated from a cDNA library in the lambda zap  
 CC vector prep'd. from mRNA obt'd. from newborn rat hearts using rat  
 CC brain II cDNA probe. The isolated DNA can be used to screen a  
 CC similar human derived cardiac cDNA library for the corresponding  
 CC human gene. Proteins produced by expression of the DNA have  
 CC diagnostic therapeutic, and prognostic applications.  
 SQ Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;





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OM nucleic - nucleic search, using sw model

Run on: January 15, 2000, 22:03:07 ; Search time 1834.3 Seconds

(without alignments)  
13322.638 Million cell updates/sec

Title: PCT-US99-19675-1  
Sequence: 1 atgacgagagagagagatgctg.....gtcccgacacacagagactg 7129

Scoring table: IDENTITY\_NUC

Searched: 4089388 seqs, 1713965092 residues

Database: EST:\*

Word size: 0

Number of hits that pass the threshold: 8178776

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2: em\_est2: \*  
3: em\_est3: \*  
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6: em\_est6: \*  
7: em\_est7: \*  
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23: gb\_est4: \*  
24: gb\_est5: \*  
25: gb\_est6: \*  
26: gb\_est7: \*  
27: gb\_est8: \*  
28: gb\_est9: \*  
29: gb\_est10: \*  
30: gb\_est11: \*  
31: gb\_est12: \*  
32: gb\_est13: \*  
33: gb\_est14: \*  
34: gb\_est15: \*  
35: gb\_est16: \*  
36: gb\_est17: \*  
37: gb\_est18: \*  
38: gb\_est19: \*  
39: gb\_est20: \*  
40: gb\_est21: \*  
41: gb\_est22: \*  
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45: gb\_est26: \*  
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47: gb\_est28: \*  
48: gb\_est29: \*  
49: gb\_est30: \*

50: gb\_est31: \*  
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53: em\_est21: \*  
54: em\_est22: \*  
55: em\_est23: \*  
56: em\_est24: \*  
57: em\_est25: \*  
58: em\_est26: \*  
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61: gb\_est35: \*  
62: gb\_est36: \*  
63: gb\_est37: \*  
64: gb\_est38: \*  
65: em\_est27: \*  
66: em\_est28: \*  
67: em\_est29: \*  
68: em\_est30: \*  
69: gb\_est31: \*  
70: gb\_est32: \*  
71: gb\_est33: \*  
72: gb\_est34: \*  
73: em\_est31: \*  
74: em\_est32: \*  
75: em\_est33: \*  
76: em\_est34: \*  
77: gb\_est35: \*  
78: gb\_est36: \*  
79: gb\_est37: \*  
80: gb\_est38: \*  
81: gb\_est39: \*  
82: em\_est35: \*  
83: em\_est36: \*  
84: em\_est37: \*  
85: em\_est38: \*  
86: em\_est39: \*  
87: em\_est40: \*  
88: em\_est41: \*  
89: gb\_est40: \*  
90: gb\_est41: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2             | 375.2 | 5.3             | 427 35 | AA537694 vk44907.r |
| 3             | 372.2 | 5.2             | 465 51 | A1712513 UI-R-AF1- |
| 4             | 365   | 5.1             | 450 46 | AA998239 UI-R-CO-1 |
| 5             | 349   | 4.9             | 540 42 | A1136718 UI-R-C2P- |
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| 7             | 333.4 | 4.7             | 425 33 | AA386626           |
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| 21            | 162   | 2.3             | 423 51 | A1705686 UI-R-AD1- |
| 22            | 149.6 | 2.1             | 365 22 | R75128 MDB1075 Mou |



REFERENCES  
AUTHORS

REFERENCE  
AUTHORS  
1 (bases 1 to 437)  
Marras,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubutun  
Eukaryota; Metazoa; Chordata; Crinata; Vertebrata; Mammalia  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
TITLE The MASTN-HMT Mouse EST Project  
JOURNAL  
COMMENT  
On Sep 12, 1996 this sequence version replaced gi:1328453.

Contact: Maira M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through ILNLT ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:546356  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 251.  
 Location/Qualifiers  
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| Matches 408; Conservative | 0;     | Mismatches 18;     | Indels 2; | Gaps 2      |

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|----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| QY | 6001 | 6002 | 6003 | 6004 | 6005 | 6006 | 6007 | 6008 | 6009 | 6010 | 6011 | 6012 | 6013 | 6014 | 6015 | 6016 | 6017 | 6018 | 6019 | 6020 | 6021 | 6022 | 6023 | 6024 | 6025 | 6026 | 6027 | 6028 | 6029 | 6030 | 6031 | 6032 | 6033 | 6034 | 6035 | 6036 | 6037 | 6038 | 6039 | 6040 | 6041 | 6042 | 6043 | 6044 | 6045 | 6046 | 6047 | 6048 | 6049 | 6050 | 6051 | 6052 | 6053 | 6054 | 6055 | 6056 | 6057 | 6058 | 6059 | 6060 | 6061 | 6062 | 6063 | 6064 | 6065 | 6066 | 6067 | 6068 | 6069 | 6070 | 6071 | 6072 | 6073 | 6074 | 6075 | 6076 | 6077 | 6078 | 6079 | 6080 | 6081 | 6082 | 6083 | 6084 | 6085 | 6086 | 6087 | 6088 | 6089 | 6090 | 6091 | 6092 | 6093 | 6094 | 6095 | 6096 | 6097 | 6098 | 6099 | 6100 | 6101 | 6102 | 6103 | 6104 | 6105 | 6106 | 6107 | 6108 | 6109 | 6110 | 6111 | 6112 | 6113 | 6114 | 6115 | 6116 | 6117 | 6118 | 6119 | 6120 | 6121 | 6122 | 6123 | 6124 | 6125 | 6126 | 6127 | 6128 | 6129 | 6130 | 6131 | 6132 | 6133 | 6134 | 6135 | 6136 | 6137 | 6138 | 6139 | 6140 | 6141 | 6142 | 6143 | 6144 | 6145 | 6146 | 6147 | 6148 | 6149 | 6150 | 6151</ |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |

| Db | 241  | TTCTGGGGGGGATGAGCATTCAGAGTGGACAG - GCTCTGGAGGACAGAGCAAGTCTCC         | 29   |
|----|------|--|------|
| QY | 6301 | aagcaacatcgcgcgtgcgaagcccttggccaggcgctggaaaccagcttggccaagagacct      | 6361 |
| Db | 300  | AACCAATCTCCGCTCCACGAGCCCTTGGCCAGGCGCTGGAACTCCAGTGGGCCAAGAACT         | 359  |
| QY | 6361 | ccagagaccgaagaagcagcttagagctctgagacagagagcttagcttga - ttccagagagacct | 6411 |
| Db | 360  | CAGGATCCGACAGCAAGCATTTGAGCTGGAAACGAGCTGAGCTGGATTTTAAAGAGACT          | 419  |
| QY | 6420 | ccctccca   | 6427 |
| Db | 420  | CTGTGCCA   | 427  |

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| LOCUS      |   |
| DEFINITION | A1712513 465 bp MRNA EST 08-JUN-1999                            |
| NID        | UI-R-Arl-aap-d-05-0-Ul-sI UI-R-Arl Rattus norvegicus cDNA clone |
| ACCESSION  | UI-R-Arl-aap-d-05-0-Ul 3, mRNA sequence.                        |
| VERSION    | A1712513  |
| KEYWORDS   | G5016313  |
| SOURCE     | A1712513.1 GI:5016313   |
| ORGANISM   | EST.  |
|            | Norway rat.   |
|            | Rattus norvegicus   |

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|-----------|---|
| REFERENCE | 1 (bases 1 to 465)  |
| AUTHORS   | Bonaldo, M.F., Lennon, G., and Soares, M.B.                                 |
| TITLE     | Normalization and subtraction: two approaches to facilitate gene discovery. |
| JOURNAL   | Genome Res. 6 (9), 791-806 (1996)   |
| MEDLINE   | 97044477  |
| COMMENT   | On Jun 22, 1998 this sequence version replaced gi:3246866.                  |

Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
441 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide POLY A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized AV canal at 15 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution. Clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-51,  
>AT\_rich#Low\_complexity  
Seq primer: M13 Forward  
POLYA=yes.

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                rat retroventricular (AV) canal. The tag is a string of 5
                nucleotides present between the Not I site and the
                oligo-dt track. The library was constructed as described
                by Bonaldo, Lennon and Soares. Genome Research 6:
                791-806, 1996. Tissue provided by Jim Lin, Department of
                Biology, University of Iowa."
    
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Db 90 AGCTG 86

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| DEFINITION | U1136718 540 bp mRNA EST 11-FEB-1999                             |  |
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| SOURCE     | EST.   |  |
| ORGANISM   | Norway rat.  |  |
| REFERENCE  | Rattus norvegicus  |  |
| AUTHORS    | Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;              |  |
| TITLE      | Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.               |  |
|            | 1 (bases 1 to 540)   |  |
|            | Bonaldi,M.F., Lennon,G. and Soares,M.B.                          |  |
|            | Normalization and subtraction: two approaches to facilitate gene |  |
|            | discovery  |  |
| JOURNAL    | genome Res. 6 (9), 791-806 (1996)                                |  |
| MEDLINE    | 97044477   |  |
| COMMENT    | on Jan 14, 1998 this sequence version replaced gi:1797529.       |  |

BASE COUNT  
ORIGIN

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|------|-------|-------|-------|

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| Matches 426; Conservative | 0;     | Mismatches 110;    | Indels 1; | Gaps 1      |

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QY 325 tggactcccaagcgcctgcggatcctcaagcgccttcgatactcatcttgcctcttc 384  
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LOCUS  
DEFINITION  
ACCESSION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

A1508640 435 bp mRNA EST 12-MAR-1999  
v554d08.v1 Ko mouse embryo 11 5dpf Mus musculus cDNA clone  
IMAGE:760815 5', mRNA sequence.  
A1508640  
94407545  
A1508640.1 GI:4407545  
EST.  
house mouse.  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (Bases 1 to 435)  
Marx,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,V.,  
Peterson,B., Swaller,T., Gibbons,M., Page,D., Harey,N., Schurky,  
Ritter,E., Korn,S., Shin,T., Jackson,Y., Gardens,W., McCann,  
Waterson,A. and Wilson,R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
On Jun 5, 1998 this sequence version replaced gi:3187437.

MGI:461735

This read is a RESSEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: Primer name ambiguous  
High quality sequence stop: 434.  
Location/Qualifiers

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Site:2: NotI; Total RNAs were extracted from 11.5 dpc  
embryos (excluding placenta and yolk sac). The  
double-stranded cDNA was synthesized with an oligo (dT)-1  
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3'. The cDNAs were ligated to LT-Sal13A: 5'  
GCTATTGACGTGACTATCC 3' and LT-Sal13B: 5'  
GGATAGTCGACGTCAT 3'. The cDNAs were size-selected and  
amplified by long-range PCR using Ex Taq polymerase for 18  
cycles. The PCR-amplifiable cDNA mixture went through  
one round of equalization and was digested with SalI/NotI  
and cloned into the SalI/NotI sites of the pSPORT1  
plasmid vector (Life Technologies). The library was  
constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong  
Wang."

BASE COUNT 92 a 162 c 95 g 86 t  
ORIGIN

Query Match 4.8%; Score 343.2; DB 47; Length 435;  
Best Local Similarity 96.4%; Pred. No. 1.5e-60;  
Matches 351; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 63 GATGTACTCTACACTGAGGAGAGAGCCAGTCCCTTAGACACAGACTCTGACTGTAG 122  
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DB 123 GAAGTGTGGTGTACGGCGGACACACTCTGCCCCATGACGCTACATGTGCCGCAATGG 182  
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DB 183 GACACACTGCGGAGAGATCCTTAGACACAGGGGCTGGGGCTCCCAAGCCAGTCAAG 242  
QY 5967 ctccatctgttcgttcaactcccaacagcagacacagctgcatctcctaagcttccaa 6026  
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QY 6027 agatgtgacatctgtctcagcctcaatggggcccccactgtgggcgcacatcctaact 6086  
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QY 6087 accccacccctggcgagtcctccctctggtcagagagcctctcagcgcacagcagaataag 6146  
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DB 423 GACT 426

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LOCUS

DEFINITION vb54d08.t1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone

IMAGE:760815 5', mRNA sequence.

ACCESSION AA386626

NID 92039612

VERSION AA386626.1 GI:2039612

KEYWORDS EST

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The Washington Mouse EST Project

Unpublished (1996)

On Apr 14, 1993 this sequence version replaced gi:693339.

Contact: Maria M/Mouse EST Project

WashU-HM Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:461735

High quality sequence stop: 396.

Location/Qualifiers

1. 425

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Site:2: NotI; Total RNAs were extracted from 11.5 dpc  
embryos (excluding placenta and yolk sac). The  
double-stranded cDNA was synthesized with an oligo (dT)-1  
primer GAGAGACACTACTCTAGATCGGCGCGCTTTT  
3'. The cDNAs were ligated to LT-Sal13A: 5'  
GCTATTGACGTGACTATCC 3' and LT-Sal13B: 5'  
GGATAGTCGACGTCAT 3'. The cDNAs were size-selected and  
amplified by long-range PCR using Ex Taq polymerase for 18  
cycles. The PCR-amplifiable cDNA mixture went through  
one round of equalization and was digested with SalI/NotI  
and cloned into the SalI/NotI sites of the pSPORT1  
plasmid vector (Life Technologies). The library was  
constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong  
Wang."

BASE COUNT 92 a 158 c 95 g 80 t

ORIGIN

Query Match 4.7%; Score 333.4; DB 33; Length 425;  
Best Local Similarity 96.7%; Pred. No. 1.6e-58;  
Matches 351; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 5787 gatgtaccaccccccagagaggtgtccagtcctcccttagaccagacactgtgactgtgag 5846  
|||||  
DB 63 GATGTACTCTACACTGAGGAGAGAGCCAGTCCCTTAGACACAGACTCTGACTGTAG 122  
QY 5847 gaagctgtgtcaagcagacactctctgcccatagtacactgtgacgaatg 5906  
|||||  
DB 123 GAAGTGTGGTGTACGGCGGACACACTCTGCCCCATGACGCTACATGTGCCGCAATGG 182



```

FEATURES
source      Location/Qualifiers
1. .476    "
/organism="Battus n

```

4.38; Score 306.4; DB 48; Length 476;

5

```

421 CCATGCTGGGAATGCTCCCTCCCTGCGCTTCGCTTCTTATCTTCAGCAT 476
RESULT 10
LOCUS Al167745
DEFINITION 0293f04.x1 Soares.parathyroid.tumor.NbHPA Homo sapiens cDNA clone
IMAGE1662911.3, similar to WP:CS4D2.5 CE02562 SKELETAL MUSCLE
CALCIUM CHANNEL ALPHA-1 SUBUNIT ;, mRNA sequence.
ACCESSION Al167745
VERSION 93700915
SOURCE Al167745.1 GI:3700915
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 427)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044050.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
CDNA library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 579 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 381.
Location/Qualifiers
1..427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1662911"
/clone_lib="Soares.parathyroid.tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pTV3D
(Pharmacia) with a modified polylinker; Site_1: Not I ;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dt) primer
5'-
TGTACCAATCTGACGAGCGAGCGCCGACCAATTTTTTTTTTTTTTTTTTTT
T-3', double-stranded cDNA was size selected, ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pTV3D
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."
BASIC COUNT 66 a 121 c 136 g 104 t
ORIGIN
Query Match 3 9%; Score 280.4; DB 43; Length 427;
Best Local Similarity 78.6%; Pred. No. 1.2e-47;
Matches 335; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
223 ctcgcagcagctcgtatcccggtgttcagagagatcagtatcgtgtcattcttccaac 282

```

```

/db_xref="GBD:416580"
/db_xref="taxon:9606"
/clone="IMAGE:44039"
/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: latmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I oligo(OT) primer [5' AACGGAAGAATCGCCGCCAGCAATTTTTTTTNNN 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the latmid BA vector library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT      76 a     137 c    107 g     84 t         3 others
ORIGIN

Query Match          3.6%   Score 257.4 : DB 22 ; Length 407 ;
Post Local Similarity 82.8% ; Pred. No. 6.1e+43 ;
Matches 328; Conservative 0 ; Mismatches 64 ; Indels 4 ; Gaps 3 ;

QY 3560 gcacagccagcgcgccggagctcgtgaccttgcagtgaacca-agaattgatgcgaactgcgt 3618
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 1 GCACGTCCAGTAGTGCCGAGGGGTCTCCTTCAGCACACAGAGACTGCAGAAAGCAATGCGGCT 60

QY 3619 tcaggcgcttgccccgccacccttcgagctgatgcaccccacaactgcgtatgggagtatgac 3678
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 61 TCAGGGCCCCCTTGCCCNMGCCCTGCGG-CGTATGACCCTCCCACCTGATTGGGGATGAGCC 119

QY 3679 aatgatgaggaaactctgacgaaaaggaggagcaatacaaacgctgggttagatcccgctt 3738
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 120 GATGACGAGGGCAACTGTAGCAAAGGGAGACGGTCCGCCGCTGATCCGAGCCCATC 179

QY 3739 ccctgcctttgcgcgagagcagagatctctgctgcgcatatatcttcctcctaagtaag 3798
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 180 CCTGCTCTCCTCCTTGACGAGACACTCCGTCGACGCTTCACTTCCTCCCTCAGCTCAGG 239

QY 3799 ttctgctcccgtytgcacggagatcataccaacaagaatggttacgactgtgctcgtc 3858
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 240 TTCGCGCTCTGTCGTGACCGGATATCAACCACAAGATGTGACACAGTGTCTCTTTC 299

QY 3859 atcaccttcctacaactgataccaatgctatgg -agcgcccaaaatlaccoccaca 3916
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 300 ATCAATCTCTTAATCATGCAATCCATGCCCATGGAGGCCCAAAAATTATACCCCCACA 359

QY 3917 gcgcctgagcgatcttcgtgacctcttcacaactca 3952
        ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 360 GCGTTGACAGCATCTCCTGGACCTTTTCCAATTNA 395

RESULT 12
LOCUS AA956477
DEFINITION UT-R-EI-Ik-e-01-0-UI-s1 UI-R-EI Rattus norvegicus cDNA clone
UT-R-EI-Ik-e-01-0-UI 3 similar to gi21921748|gb|AF027841|BNCA1G
Rattus norvegicus low voltage-activated, T-type calcium channel
alpha subunit (CACNA1G) mRNA, complete cds, mRNA sequence.
ACCESSION AA956477
VERSION 94238951
KEYWORDS AAS956477.1 GI:4238951
SOURCE EST.
ORGANISM Norway rat.
NOTES Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 377)
AUTHORS Bonaldi,M.F., Lemon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
```

| Query Match           | 3.6%         | Score 254.4  | DB 46         | Length 377 |
|-----------------------|--------------|--|---------------|------------|
| Best Local Similarity | 79.6%        | Pred No. 2.4e-42   |               |            |
| Matches 300           | Conservative | 0  | Mismatches 77 | Indels 0   |
|                       |              |  | Gaps          | 0          |
| QY                    | 205          | cgcgccgcgagctgctgctgcgcacgctcgtaacccgctgcttcgagcagctcatg         | 264           |            |
|                       |              |  |               |            |
| Db                    | 1            | CGGCCCGCAGCTGGGCGCTCGACAGGTTGTAAACCTGGTTCAGACACATCAGCAAG         | 60            |            |
| QY                    | 265          | cgtgctattcttcacactcgttgactcgttgatgttcgaagccgctgtgagacattgc       | 324           |            |
|                       |              |  |               |            |
| Db                    | 61           | CTGGCTATATGCTGAACCTCGGACACGGGGCATTTTAGGGCCCTGTAGAGATTGAG         | 120           |            |
| QY                    | 325          | tgtagctccagcgtcgtccgcgacatcctgaagccttcgatgaactcaatttcgtctctt     | 384           |            |
|                       |              |  |               |            |
| Db                    | 121          | TGCGGCTCCGGAAGCTTGCGACACATCTTTGAGGCGCTTGAGACATCTACTTGTGGCTTCTTC  | 180           |            |
| QY                    | 385          | gcctgtgaaatgctgttgaaagatgctgtgccttgagcatctcttggaagaatcttaactc    | 444           |            |
|                       |              |  |               |            |
| Db                    | 181          | GCCGTGAGATGTTGATCAAGATGCTTGTTGGGCTGTTTGGCAAAATGCTACCTG           | 240           |            |
| QY                    | 445          | ggaagacacttggaaccgcttgactcttcatcatgtcatcttgacaaggaatgctggaatttcg | 504           |            |

|            |      |       |       |      |          |
|------------|------|-------|-------|------|----------|
| BASE COUNT | 76 a | 129 c | 108 g | 57 t | 3 others |
| ORIGIN     | .    | .     | .     | .    | .        |





University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu

Oligo-dt track not found, Not I site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
Research Genetics (www.resgen.com)  
Seq primer: M13 Forward.

## FEATURES

## Source

## Location/Qualifiers

```
1..339
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-sd-e-12-0-UI"
/clone_1lb="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dt track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldi, Lennon and Soares, Genome Research 6:
791-806, 1996)"
791-806, 1996"
```

## BASE COUNT

61 a 91 c 103 g 84 t

## ORIGIN

Query Match 3.1%; Score 221.2; DB 47; Length 339;  
Best Local Similarity 78.4%; Pred. No. 1.5e-35;  
Matches 265; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
QY 205 cgcgcgcgagctggtgtcgcgaagctgaacccggtggtcagcagatg 264
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1 CGGCGCGGAGCTGCTCGCTCCACTGGGTGTAAACCGTGGTGCAGACATG 60

QY 265 ctggtcatcttcacactgtgtactctggtatgtcagccggtgagacattgcc 324
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 CTGGTCATCATGCTGAACGCTGACACATGGGCGATTTGATCCCTGTGAGATTTGAG 120

QY 325 tgtactccacgctgcgcgacatcctgcagccttcgatgaacttaactcttgcctctt 384
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 121 TGCCGCTCCGAAGCTTGCAGACATTTGAGGCTTCGACGACATCATCTTTCCTTC 180

QY 385 gctgtgaaatggtgtgaaatggtgtgacattgttggaagaatgttaactg 444
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 181 GCGGTGGCGGTGGTGAACAGATGTGGGCTTTGGGCGCAAAATGCTAACTG 240

QY 445 ggaagacacttggaaccgcttgacttttcattgtcattgcaggaatgctggaattcg 504
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 241 CGTGACACCTGGAACAGCGCTTGACTTCTTCATGTGATGCGGGCATATGAGTACTCT 300

QY 505 ctggaacctgcagaacgctcagctcccgcaagtcaagac 542
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 301 CTGGAAGACACAAAGTGAACCTCTCTGCATCCGAAC 338
```

Search completed: January 15, 2000, 23:06:36  
Job time: 3809 sec

Wed Jan 19 08:14:57 2000

pct-us99-15675-1.rst

Page 13



GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2000, 01:26:47 ; Search time 17.59 Seconds

(without alignments) 3196.749 Million cell updates/sec

Title: PCT-US99-19675-2

Sequence: 1 MDEEDGAGAEESGQPSRFT.....LKEEGKGSPVMPRLPTPGA 2374

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A\_Geneseq\_36.\*

Word size: 0

Number of hits that pass the threshold: 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 3958.5 | 31.7        | 1854   | 1     | W79161      |
| 2          | 1713   | 13.7        | 2337   | 1     | R33550      |
| 3          | 1711.5 | 13.7        | 2339   | 1     | R33549      |
| 4          | 1711   | 13.7        | 2337   | 1     | W37878      |
| 5          | 1708.5 | 13.7        | 2339   | 1     | R71005      |
| 6          | 1708.5 | 13.7        | 2339   | 1     | W63141      |
| 7          | 1703   | 13.7        | 2337   | 1     | R71006      |
| 8          | 1699   | 13.3        | 2270   | 1     | W63142      |
| 9          | 1653.5 | 13.3        | 2251   | 1     | R68604      |
| 10         | 1653.5 | 13.3        | 2251   | 1     | R71009      |
| 11         | 1608.5 | 12.9        | 1873   | 1     | R71010      |
| 12         | 1608.5 | 12.9        | 1873   | 1     | W18390      |
| 13         | 1602.5 | 12.8        | 1873   | 1     | R73055      |
| 14         | 1600.5 | 12.8        | 1873   | 1     | P95645      |
| 15         | 1600.5 | 12.8        | 1873   | 1     | R99639      |
| 16         | 1594.5 | 12.8        | 1873   | 1     | R92317      |
| 17         | 1591.5 | 12.8        | 1873   | 1     | R99641      |
| 18         | 1586.5 | 12.7        | 2016   | 1     | W23994      |
| 19         | 1586.5 | 12.7        | 2016   | 1     | W01875      |
| 20         | 1580.5 | 12.7        | 2516   | 1     | W01884      |
| 21         | 1580.5 | 12.7        | 2516   | 1     | R71002      |
| 22         | 1579   | 12.7        | 2161   | 1     | W63149      |
| 23         | 1579   | 12.7        | 2161   | 1     | W63149      |
| 24         | 1576.5 | 12.6        | 2104   | 1     | W57773      |
| 25         | 1576.5 | 12.6        | 2104   | 1     | W89578      |
| 26         | 1576   | 12.6        | 2161   | 1     | R71001      |
| 27         | 1576   | 12.6        | 2161   | 1     | W63137      |
| 28         | 1572.5 | 12.6        | 2105   | 1     | W57772      |
| 29         | 1572.5 | 12.6        | 2105   | 1     | W89578      |
| 30         | 1568   | 12.6        | 2161   | 1     | R33545      |
| 31         | 1567   | 12.6        | 2163   | 1     | R71003      |
| 32         | 1563.5 | 12.5        | 1957   | 1     | W21740      |
| 33         | 1557.5 | 12.5        | 1957   | 1     | W63139      |
| 34         | 1552   | 12.4        | 2020   | 1     | R06584      |
| 35         | 1549   | 12.4        | 2020   | 1     | R06584      |
| 36         | 1548   | 12.4        | 2100   | 1     | R89579      |
| 37         | 1547   | 12.4        | 2019   | 1     | R67913      |
| 38         | 1546.5 | 12.4        | 2138   | 1     | R72607      |
| 39         | 1541   | 12.4        | 2510   | 1     | R71007      |

40 1540 12.4 1967 1 R33547 Sequence of the al  
41 1530 12.3 1988 1 W69362 Tetrodotoxin-sensi  
42 1525 12.3 1978 1 W69361 Tetrodotoxin-sensi  
43 1522 12.2 2132 1 W21739 Variant rat DRG (S  
44 1504.5 12.1 2265 1 R71008 Human neuronal cal  
45 1494 12.0 2262 1 W56737 Calcium ion channel

## ALIGNMENTS

RESULT 1  
W79161  
ID W79161 standard; Protein; 1854 AA.  
AC W79161;  
DE 20-NOV-1998 (first entry)  
DE Human calcium channel subunit alpha-1 partial sequence.  
KW Human calcium subunit alpha-1; recombinant; alpha 2 delta;  
KW beta calcium channel; agonist; antagonist; alpha-11 calcium channel;  
KW histological assay; tissue distribution.  
OS Homo sapiens.  
PN W09R38301-A1.  
PD 03-SEP-1998.  
PE 27-FEB-1998: CA0173.  
PR 25-FEB-1998: US-030482.  
PR 26-FEB-1997: US-039204.  
PA (NEUR-) NEUROMED TECHNOLOGIES INC.  
PI Baillie DL, Snutch TP;  
DR N-PSDB: V57542.  
PT Newly identified calcium channel subunits alpha 11 and alpha 1H  
PT for development of cell lines which express the novel calcium  
PT channels; useful for screening channel (ant)agonists  
PS Claim 2; Pages 26-33; 45pp; English.  
CC This represents a partial sequence of a human calcium channel subunit  
CC alpha-1. The invention provides isolated DNA fragments coding for novel  
CC calcium channel subunits alpha-11 and alpha-1H. An eukaryotic cell  
CC transiently or stably transformed with an expression vector containing  
CC the calcium subunits encoding DNA fragments can be used for expressing  
CC the calcium channel. The cells are optionally further transformed to  
CC express alpha 2 delta or beta calcium channel or both the proteins. The  
CC transformed cells are useful for identifying compounds capable of acting  
CC as agonists or antagonists for the alpha-11 calcium channel. The nucleic  
CC acid sequences can be used in histological assay to determine the tissue  
CC distribution of the novel calcium channel subunits.  
SO Sequence 1854 AA.

Query Match 31.7%; Score 3958.5; DB 1; Length 1854;  
Best Local Similarity 47.0%; Pred. No. 1.2e-296;

Matches 913; Conservative 173; Mismatches 361; Indels 495; Gaps 48;

QY 27 GAGGRCG-----PSTERKPGSADSEAGLPYALAVVFFYLSQDSRPSWCRLRYC 79  
DB 77 GTGHTGTFOGCAEPSSQHPAEATYTAGCPAPGDPCCFVLD-----LYC 125  
QY 80 NPMFERSMKLVLLNCTVIGMFRPCEDACDSORCILOAFDDFTFAFVAVMYKVAL 139  
DB 126 T-WFECMSKLVLLNCTVIGMFRPCEDACDSORCILOAFDDFTFAFVAVMYKVAL 184  
QY 140 GFGKRCYLDGTVNRRLDFVIVAGMLEYSILDQNSFSAVTRVRLPRAINRPSMKI 199  
DB 185 GFGKRCYLDGTVNRRLDFVIVAGMLEYSILDQNSFSAVTRVRLPRAINRPSMKI 235  
QY 200 LVTLTLDTPMGLNVLCCPEVFFIGIVGLMAGLLNRCFLEPNTSLPLVDLEPY 259  
DB 236 LVNLIADTLPMLGNVLLCFEVEFFIGIIGVGLMAGLLNRCFLEPNTSLPLVDLEPY 295  
QY 260 QTNEDESPFGISQPRENMRSCRSVPLTRGEGGGPPCSL-----DYETINSSNTT 313  
DB 296 QPREDEDMFFICLSGSDNKGICHEIPLKEO---GRECLSKDVIYVFGAGRODLNMSG 352  
QY 313 -LVNMNQYITNCSAGEHNDFKCAINEDNIGVAMIAIFVITLEGWVDIMYFVMDAHSFYN 371





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Db 1645 LMLFRSATGEAMHEIMTSLCNOACDEQANATEGSDFAFYFVSFIFLCSFLMLNLFV 1704
Oy 1850 AVLMHLEESNKEAR-----EEALEAELE-----LEM-KTSLPQPSPL 1888
Db 1705 AVIMDNFELTWDSSILGPHILDEFIRWAELDPACACRISTYNDMEFLKAMSP-----PL 1760
Oy 1889 G-----SPELWPGVEGVNSDPSPKPGAPHTTAHGAAGSLE-----HPTWVP 1932
Db 1761 GGGKCPARNAVKRLVNMNMPISNEDMTVHFTSLMALIRALFIKIPAGTKHOCDAE 1820
Oy 1933 HPEEVPV-----PLGPDLLTVKSGVSPRTHSLPNDSYNGCRNGSAERSLG 1977
Db 1821 LRKEISVYWANLPORLTDLVLPKRPDEFTYKAYTAA--LMIFPT--KONKTTROMOQ 1875
Oy 1978 HRGWGLPKRAGSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPYGAIPKLPGRSP 2037
Db 1876 QAPGGL--SQMKPVSIFH-----PLKATL 1897
Oy 2038 AGRPLRQAIPTDLDVGLGREDLSEVSGSPCLTRSSFWGSSIQYQORSGIQS 2097
Db 1898 EQ--TOPAVLR-----GARVFLRQK-----SSTLSNGGAIQ--NOESGIRE 1935
Oy 2098 KYSKHTLRAPCGLESPMAKD-----PEPTRSLELDTLSMISGDLPSQEEPLSPR 2152
Db 1936 SY-----SMGTORTODAPHEARPLERG-----HSTELPVG-R 1967
Oy 2153 DLKCYVETOSGRRR-----PGSWLDEQRHRSIAVSCDLSGSGOPRLCSP--SSLG 2202
Db 1968 SGALAVDQMOGSTRRGPOGPEPOGLESGR--AASMPRLAETQVTDASPKRSISITLA 2026
Oy 2203 GQPLG-----GPGSRPKKLS-----PSISID--PES-- 2230
Db 2027 QGRRGTHLCTTPDRPPQASSHHHHRRRDRKQSLKSGSLADMGABSSAVG 2086
Oy 2230 QGRPRPCSPGVCLR-----RRAPASDKSPVSSPLDSTAAS-----PSPKD 2274
Db 2087 PGLPPEGPTGCRERERQERQERQERQERQERQERQERQERQERQERQERQERQERQER 2143
Oy 2275 SLGSLSDPTMDVPLPTLPHILSPGADSSASMAFLKSTPAASSHAPHL--PSSVAG 2333
Db 2143 --PSLSSHPTS-----PTAGOE--GPPHPOAGSAVG--PNTTCCRTPTASAWPLA- 2190
Oy 2334 GDEQNFRRDVKRQPM-----SPCLREEGKSGSPWP--RLPTPG 2373
Db 2190 -----LELALLTWGCVTVRPLSLPCLRTLSLST--LMPTRAPPG 2231

RESULT 3
R33549
ID R33549 standard; Protein: 2339 AA.
AC R33549;
DE 30-JUN-1993 (first entry)
DT Sequence of the alpha 1B-1 human calcium channel subunit.
KW Human calcium channel subunit; diagnosis; agonist; antagonist;
  Lambert Eaton syndrome.
OS Homo sapiens.
PN K09304083-A.
PD 04-MAR-1993.
PE 14-AUG-1992; U06903.
PR 15-AUG-1991; U5-745206.
PS 10-APR-1992; U5-868354.
PT (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
  Williams ME,
  WPI; 93-093936/11.
DR N-PSDB; Q37817.
PT DNA encoding specific human calcium channel sub-units - used for
  identifying calcium channel agonists and antagonists and
  diagnosing Lambert Eaton syndrome
PS Disclosure; Page 111-120; 150pp; English.
CC Human encoding the alpha 1B subunit was isolated by screening a
  cDNA basal ganglia cDNA library with fragments of the rabbit
  skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.

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CC A portion of one of the positive clones was used to screen an IMR32
CC cell cDNA library. Clones that hybridized to the basal ganglia
CC DNA probe were used to further screen an IMR32 cell cDNA library
CC to identify overlapping clones that in turn were used to screen a
CC human hippocampus cDNA library. In this way, a sufficient series of
CC clones to span nearly the entire length of the nucleotide sequence
CC encoding the human alpha 1B subunit was obtained. PCR amplification
CC of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC additional segments of the alpha 1B coding sequence. A full-length
CC alpha 1B DNA clone was constructed by ligating portions of the
CC partial cDNA clones (see Q37817, Q37818). Alpha 1B-1 and alpha
CC 1B-2 are derived by alternative splicing of the alpha 1B subunit
CC transcript. 2339 AA;
SQ Sequence 2339 AA;

```

```

Query Match 13.7%; Score 1711.5; DB 1; Length 2339;
Best Local Similarity, 24.2%; Pred. No. 7e-123;
Matches 645; Conservative 371; Mismatches 844; Indels 803; Gaps 91;

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Oy 27 GAGCGGPGSTKEDPSADSEAGLEPYPLAVF-----FYLSQDSRP 70
Db 25 GAGGAGGPGGGLQPGQRYLYKQSIAGRTMALNPLPVKONCTVNRSLFVSEDNV 84
Oy 71 RSMCLRTVCNPFERYSMLVILNCVTLGMPFRCEDIAOSORCHILQAFD--FIRAF 127
Db 85 RKAKRTTEPFENMILATINCVIAL-----EGHLPDGKTMSESLDTEPYFGI 140
Oy 128 FAYEMVKNVALG-IFGKCYGADTNRLDFPIVAGMEYS--LDLQNSFSAVRYR 183
Db 141 FCEGAGIKIILGTFVHKSGYLNGWNVDFVYVILGILATGTDFDLR--TLRAVR 195
Oy 184 VLPRRLINVPMSRLIYLLDTPMLGNVLLCFEVEFIGYVQVAGLIRNRCL 243
Db 196 VLRLKLVSSIPLOVYVLSIMKAVPILQIGLLEFALIMRAIIQLETFYMKFKAC- 255
Oy 244 PENISLPLSYLDEPYQOTENEDSPFICQPRENGRSCRSPVTLREGEGGPPCSLDYE 303
Db 255 -----PNSTDAEY-----GDFPGCKEAP 273
Oy 304 TYNSSVTTCVNNQOYTNCAGEHNPFKGAIFNDVIGVAMIAFOVITLEGVMDIMYV 363
Db 274 ARLECGDTEC--REYWP-----GPNFQITNEDILRLAIVLFOCTIMEGWTDLIYNT 323
Oy 364 MD-AHSFYNTFLYILLIVGSFPMINCLVVIATOFSETKORES-----QLMREGQRYVF 416
Db 324 NDAAGNTWNNWIFLPIITISFFMINIVLGVLSEFAKERERENRRALFKLRQOQIE- 383
Oy 417 LSNASTLASEFSEPGCYEELLYVILKRAARLQVSRALGVRAGLLSPVARSQGP 476
Db 383 -----RELNGYLEWIFKAEVYMLAEED-----RNAEER 410
Oy 477 QPSSCTRSRRLSVHLLVHHHHHHHLLGNGTLRVPRASPEIODRANGSRRLMPP 536
Db 411 SPLDYLKRAATKSRNDLIH-----AEEGDRRAD----- 441
Oy 537 PSTPTSGGPPRGAESVSEFYHADCHLEPVRCOAPPRPCPSAEGRTVSGKYVPTVHS 596
Db 441 -----LCAVGSPPFAR 450
Oy 657 ADSGACGDSQPCARTGAGBPESADHVMPDSDSEAYEFTQDAQSHDLDPHSRRORS 716
Db 451 AS-----IKSGTSESSYF-----RKREK 470
Oy 717 LGPDAPESVLAFWRLICDFRKIVDSKYFGRGIMAILVNTLSMGLTEYHDEPDELINAL 776
Db 470 -----MRFF-----IRRVKQASQFYWVYVLCVALNTICVAAVHNQRRRLITTL 514
Oy 777 EISNIVTSLFALEMLKLVLVGGFGITKPNYINFDGVIVYISWEIVGQ-----QGGL 831

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Db 515 YFAEFVFLGFTLMSLKMVGLGRSPYRSFSCFPGVYGVSEVVAATKPGSSFEI 574  
 Qy 832 SVATRTLMVAVLKLVFLPALQOLVYVLTQDNVATFCMLMLFFITSIIGMLFGCK 891  
 Db 575 SVTRALRLRFEFVYVWSLRNLVYSLNMSKSIISLFLFLFVYVALLGMOIFGGO 634  
 Qy 892 FASERDGLTPDRKNFDSLMAIVTVEFQILITODANKVLYNGM-----ASTSSMALYTI 946  
 Db 635 FNGODEPT-----TNEPTPAALITVFOILLTGEDMANVYHIGIESOGVSKMGSEFYFI 690  
 Qy 947 ALMTFENYVLFNLVAILVEGF-QAEI8K-----REDASGO-----LSCI 986  
 Db 691 VLLTFGNVYLLVFLAIVADNLANAQELTKDEEMEEAANOQLALOKAVEAVSPMSMA 750  
 Qy 987 QLPVNSOGDPAATSESEPPFSPVGDGDRKKRLVALVAGHAELRKSLLPPLIITRA 1046  
 Db 751 NISIAARQONSAAKARVME-----ORASQRLQNLASCEALYSEMDPEERLRA 800  
 Qy 1047 TPMSLPRSSSTGVE-----ALSGSRRTSSSGSAEPGA-----HH-----EMKS 1087  
 Db 801 TRHRLPDMKTHLRLVVELGDRGAPVVGKARPEAAEAEVDPRRHRHRHDKXT 860  
 Qy 1088 P-----PSARSS-----PHSPVSAASWTSSRSSNLSGRAPSLKRSPPS 1127  
 Db 861 PAGODRAEAAPKAESGEGERPRPRSHSKEMA--GPEARESERGRGP-----GPE 913  
 Qy 1128 GERRSLSGEGESODE-----ESSEDRASPAAGSHRRGSL-----REAKSSF 1174  
 Db 914 GGRHHRHRSPEEAEREPRHRHRHODPSCECAGKERRARHRGRAGPRAEAG- 973  
 Qy 1175 DLPTLQVPG-LHRTASGRSSASE--HODCNGKASGRLA-----RTLTDDPOLDG 1223  
 Db 973 -----EPPARRHRARHKAQPAHEAVEKETTEKATEKEAEIYEADKELRNHPRPH 1026  
 Qy 1224 DDNDENGLSKGERIQAWRSRLPACCRP-----DSM-----SAYIFPQSNFR 1268  
 Db 1027 CPLETSGVTVGP-----MHTLPSTCLOKVEOPEDADONRNTVMGSOOPDPNTYHI 1080  
 Qy 1257 -----SAYIFPQSNFR 1268  
 Db 1081 PVMLTGPLGEATVPVSGNVLDSEQAEGKEVEADVMRSGRPIVYVSMCLSPNLR 1140  
 Qy 1269 LICHRIITHKMDHYVLYIIFLNCITTIMERPKIDPHSAERITLTSYIETAVFLAEMT 1328  
 Db 1141 RECHIVITMRFEVYVILVIALSSIALAEDP-VRTDSPRNALKYLDYIFGVFTFEMV 1199  
 Qy 1329 VVVVALGWCFOAYLRSSMNVLDGLVLIVIDLIVSMV--SDSGTKILGMLRVLRLRT 1387  
 Db 1200 IKMIDGLLHGAFLRDLWNILD---FIYSGALVAFASFSGSKGKDINTIKSLRLVLR 1255  
 Qy 1388 LRLPLVISRAOGLKLVETLMSLSKPIGNIVYICAFPIIFIGILVOLFKGFVCOGE- 1447  
 Db 1256 LRLPLTKIRLRLKAVFCVYVNSLKNVNLILYVLMFIFAVIAYVOLFQKFFCYCDES 1315  
 Qy 1447 -----DTNN--ITNSDCAEASR-WVAHKYNFDNLGOALMSLVLAASKOGWDMTDL 1498  
 Db 1316 KELEFDCGQYLDYEKEVEAOPRQMKYDFHYDNVLMALTLTFTVSGEGMPVYLKHSV 1375  
 Qy 1499 DAVGVDOQPINMHNPMLLYFISFLIYAFVLMFVGVVVENHKKRQHEEAEARRE 1558  
 Db 1376 DATEEGQPSGYNRELSTFVYVYVFFVYVIFVALIITP-----QEOGDKYME 1429  
 Qy 1559 EKRLRLKRRNMLDDVVIASGSSASASEAQKPY--YSDYSR--FRLVHLHLSHY 1614  
 Db 1430 -----CSLEKNR-ACIDFAISA-----KPLTRVMPQNRQSPQYKTVFVVSPP 1472  
 Qy 1615 IDLFTVIGLVNVTMAMEHYQOPIIDEALKICNTYIFVYVFESEFKLVAGCFRRFPQ 1674  
 Db 1473 FEYITMAMIALNTVYLMKFTADAYEELMKCINIVTFSMFSMECVLKIIAEVGLVYFR 1532  
 Qy 1675 DRMNOLDLAVILSIMGITLEEIVNASLPINPTIIRIMRLVAVYVLLKLKMAVGRAL 1734

Db 1573 DAMVFDVYVYLGSTIDILVTEIETNNF-IN--ISFLRLFAARLILKILROGYTIRIL 1588  
 Qy 1735 LDTVQALPOVGNGLLFLMLFFLFFAALGVELDEDETHCEGLGRATRNFGMAF 1794  
 Db 1589 IYTFVOSKALPYCCLLIAMFLFFIYALIGVOYGNALDD---TSINRNNRRTLOAL 1645  
 Qy 1795 LTFEVSIGDNWNSIMKDTLRD--CDOE--STCVNTYISPIYVSEVYLAQVYLVNVVIA 1850  
 Db 1646 MLFRSATGEAMHEIMLSCLSNQACDEANATECGSDFAFYVSEFFLCSFLMLNLVFA 1705  
 Qy 1851 VIMKLEESNKEA-----EEALELELE-----LEM-KTLSQPSPLG 1889  
 Db 1706 VIMNFEYLRDSSLCPHHLDEFIRWAYEYDPAACGRISYNDMFELKHMSP-----HPTMVP 1761  
 Qy 1890 -----SPFLMPVEGVNSPDSPPKAPHTTAHIGAAGFSL-----HPTMVP 1933  
 Db 1762 LGKKCPARVAYKRLVRNMPISNEDMTVHTSTLMALIRALEIKIAPAGTKHOCDAEL 1821  
 Qy 1934 PEYVY-----PLGPDLLIVYKSGVSRTHSLPNDSTMCNRSSTAESLGH 1978  
 Db 1822 RKETSVYVWMLPOTKIDLVLPKHPDMTVGKYVAA--LMIFDY--KONKTTIDMOQ 1876  
 Qy 1979 RGWGLPKAAGSILSVH-----SOPADTSCILO-----LEKDVHILLOPGA----- 2021  
 Db 1877 APGL--SQMGVPSLPHPLKATLEOTPA-----VLNGARYFLKQKSTLSNGALQONDE 1930  
 Qy 2021 -----PTWGA--IPKLPGRSPL-----AORPLRQAAIRTD----- 2052  
 Db 1931 SGIKESVWGTORTODAPHEARPLERGHSTELPVGSGALAVDQMSITRRGDCERO 1990  
 Qy 2052 -SLDVOGLSREDLLEVSOPCLTRSSSFNGSSIQVQNSGICISKIIRLPAPCP 2110  
 Db 1991 PGLSQC--RAASMPRLAETOPTVDASPMKRSISTLAQPRG-----TLICSTTP-- 2040  
 Qy 2111 GLEPSWAKDPETRS-----SLMDTLEMSWISGLPLPSGDEPLSP-- 2152  
 Db 2040 -----DRPPSQASHHHHHRRRRDRKORSLEKGPBLS-ADMDGAPSSAVGGLPBG 2092  
 Qy 2152 -----RDLKCYIVETOSCRRRPQSWLDEQRHSIAVSCDSGQPLCPSPS----- 2200  
 Db 2093 EGPTRGRERERROERGRROEROPSSSSSEKORF--YSCDRFGREPPKPKSLSSHP 2149  
 Qy 2200 -----SIGGQPL-----GGPSSRRKKLSP-PSISIDPPES- 2230  
 Db 2150 TSPTAQOEPPHPOGSGSVNGSPBLTSCASTPGRGGRQOLPOTPLTPPSITLYTANSS 2209  
 Qy 2230 -----QGSRPCCSPG-----VCLRRAPASD-----SKPVSASPIDSTAA 2265  
 Db 2210 PIHFAAGQTSLPFSPGRSLRGLSEHMLLQRPDSQPLAPSPRGSDPYLQGRDSEAS 2269  
 Qy 2266 SPSPKKDTLSL-----SGLSS 2281  
 Db 2270 VHALPEDTLTFEEAVATNGRSS 2292

RESULT 4  
 W37878  
 ID W37878 standard; Protein: 2337 AA.  
 AC W37878;  
 DT 28-AUG-1998 (first entry)  
 DE Human calcium channel a1b subunit.  
 KW Calcium channel; human; central nervous system disorder;  
 KW Lambert-Eaton syndrome; diagnosis; therapy.  
 OS Homo sapiens.  
 PN W0981131-A2.  
 PD 19-MAR-1998.  
 PE 11-SEP-1997; U16146.  
 PP 16-SEP-1996; US-713118.  
 PA (AMHP) AMERICAN HOME PROD CORP.  
 PT Chen ARS, Franco R, Shuey DJ;  
 DR WPI: 98-207325/10.  
 DA N-PSDB: V29039.  
 PF DNA encoding human neuronal calcium channel subunit(s) - useful for

PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome

PS Disclosure: Fig 1: 89pp; English.  
 CC This polypeptide comprises the a1b subunit of the human neuronal  
 CC calcium channel. cDNA clones (see V28059-61) encoding the a1b  
 CC subunit, the a2d subunit (see W37879) and a b3 subunit (see W37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity,  
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
 CC calcium upstroke, indicating that the proteins expressed by the  
 CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.

Sequence 2337 AA:

Query Match 13.7%; Score 1711; DB 1; Length 2337;  
 Best Local Similarity 24.4%; Pred. No. 7, 6e-123; Mismatches 858; Indels 796; Gaps 93;  
 Matches 652; Conservative 367;

7 GAGAEESGGRSFTQLNDLSGAGRGPGSTKDPGASDSEAGLEPPALAPVF----- 62  
 16 GSGERANG-----GGAGAGGPGPGGLOPGORVLYKSIQARATMLPIPIV 64  
 62 -----FYLSDSRPRSMCLRTVCNPFERSMVLILNCTVTLGFRPCEDIAD 110  
 65 KQCFYVNRSLFVSEEDNVYKRYKRTIEMWPEYMILATIANCIYAL-----EHLDP 120  
 111 SQCRRIIADPD---FIAPFAVEMVYKVALG-IEGKKYLGDTWMRRDLFFIVIGMLE 166  
 121 GDKTPMSERLDDEPYTIGIFCFEAGIKITIALGFVFKGISTLRGNMVMDFVVLGIIA 180  
 167 YS---LDLQNVSFSAVRTVRLRLRAINRVPKRIITLLDLPMLGNVLLCEFEVF 223  
 181 TAGIDPDLR-----TLRAVRLRLPLKLVSGIPSLQVVLKSIKMAWVLLDGLLEFAL 225  
 224 IFGIYVQVLAAGLIRNCRFLPENFSLPLSVLEPYTOTENDESPPFQSPRENGRSCR 283  
 236 MFAITIGLEFYMGFKHACF-----PNSIDAEVY----- 264  
 284 SVPTLRGGGGGPPCSLDYETIYSSNNTGVNMNQYTNCSAGEHNPFGKAINFDNIGYA 343  
 264 -----GDFPCGKEAPRLCEGDTEC---REYWP-----GNPFGITNFDNLIFA 303  
 344 WIAIFOVITLEGWVIMYFVMD-AHSFYNYFITLLIIVGSEFMINCLVAVIATQSEIK 402  
 304 ILTYEQCTMGWMDILXNTNDAGNTMMMLYFIPLIISFFMLNVLVLSEEFKER 363  
 403 QRES-----OLMREQVRFLSNASTLASFSEPSQCYEELIKLVYLIRKARRLAQVSR 456  
 364 ERVENRRRAFLRLRQOOE-----RELNGYLEWIFKAEVMALED- 405  
 437 AIGVAGLLSPVARSQGPQSGCTSRHRLSVNHLVHHNNHHNNHNLGNGTLVPR 516  
 405 -----RNAEKSPDLVLRKAATKKSNDLIH----- 431  
 517 ASPEIODDANGSRRLMLPPSTPTPSGPRGAESVHSFYHADCHLEPRCAAPPRCP 576  
 431 -AEEGEDRFAD----- 441  
 577 SFAASRTVSGKVYPTVHTSPPELKKALVEVAPSPGPRTLSFNIPRPFSSMKLL 636  
 441 ----- 441  
 637 ETGTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHYMPDSDSEAVEEF 696

441 -----LCAVGSPPARAS-----LKGKTESSSYF----- 465  
 697 TODAQSHDLDPHSRRKRSRSLGDAEPSSVLAWRLICDTFRKIYDSKYFGKIMAILY 756  
 465 -----RRREK-----MFRFF-----IRRMVAQGFYVWLICVAL 494  
 757 NTLMSGIEIHOPEELTNALIEINITYFTSIFALEMLKLIVYPPFYINPNPIEGVIV 816  
 495 NTLCAVAVHNQPRRLITLTTFEAFVFLGLETEMLKMGLEPRSYFSSEFCDFPGVI 554  
 817 VIVSWEIVGQ-----QGGGLVTRTFEFLMRVLRVLEFLPALQRLVLYLKTMDNVATPCM 871  
 555 VGSFEEVYMAIKRGSSFGISVLRALRLIRFVITYWSSLRLVYLSNMSKSIISLLE 614  
 872 LLMDFIFITSLGNHLEFGCKFASERDGLPDRKNFDSLIMAVIYFQIITQDANKVLY 931  
 615 LLEFIYVFNALGMQLFGQFNODEPTPT---TNEDEFAAILTYFOIITGEDMNAVMY 670  
 932 NGM-----ASTSSMAALYFTALMTFGVYVFLNVLVATVEGF-QAEIIGK---REDASG 981  
 671 HGISQGVSKGMSSEYFVLTIFGNVTLNVLALANDLANAOELTKDEDEMEAN 730  
 982 QLSCTQ-----LPVNSQGG-----DATKSE 1001  
 731 QKLAQRAKEVAEYSPMSANISIAARQNSAKARSVQEQASQLRLQNLASCALYSY 790  
 1002 SEPD---FSPSPVDGDDRRKRL---ALVALG-----FHAEIKSLIPPLI 1041  
 791 MDPEERLEFATTRRRRDMKTHLDRLVLELGRDARGPYGKARPAEAAPGVPDPR 850  
 1042 IHTATQMSLKSSSTQGEALGSGSRRTSSGSAEPGAHH-----EMKSPPSA 1091  
 851 HHRHDKTKTAAGDQRAEA-----EKAESEGEAGAEERPRRHSKAEAGPEA 902  
 1092 RS-----SPH-----SPMSAASWTSR-RSSNSLGRAPSLKRSPPSGERSLS 1135  
 903 RSENGRGPGRGRRHNRGSPDEAEREPRHRAHRH---OPPSKECAGAKERRARHR 959  
 1136 GEGDSQDEESSSE-----DRASP-----AGSDHNRG 1164  
 960 GGRAGRPREASSGEPARHRRARHRAOPRAHEAVEKETTEKAEIYEDAKELRN 1019  
 1165 SLERAKSSFDPRLQVPGILHRTASGRSSASEHQ---DCNKSASGRIARTLRDTP--- 1220  
 1020 HOPRPHDPLETSGIYVYGRPHILPSTCLOKVEQRPEDADQNRVATMGSS---QPRDPNTI 1077  
 1220 ----OLDGD-----DDNDEG---NLKSGERIOAWYRSRLPACCRERDSMSA 1258  
 1078 VAIPLYMTGPLEAVVPSGNVLESQAEGKEVEADVDYMSGPRPIVPS-----SM 1130  
 1259 YIFPQSRFRLCHRIIHKMFEDHVLVIIFLNCITAMERKIDPDSAEIRIFLTSNYI 1318  
 1131 FCLSTFNILRRECHYIMRFEVYILVIALSIALAEDP-VRTSPRNNAIKYDIYI 1189  
 1319 FTAVALAETVYKVALGWCFCGEQAYLRSSANVLDGLLVLSIDVILVSMV-SDSGTKILG 1377  
 1190 FTGVTFEVYIKMIDGLLHNGAAYFRDLMWLD---FIYVSGALVAFASSGSKRDIN 1245  
 1378 MTRVRLRLTLRPLRVISRAQGLVYETLMSLKPIGNIYVICAPFIIFGILGIVOLK 1437  
 1246 IIKSLRVLRLVRLPLKTIKRLPLKAVFCVYNSLKNVILNIVYLEMFIYFAVAVOLFK 1305  
 1438 GKFFVQCGE-----DTRN---ITNKSQCAEASR-VWRHKNYFNPLGOALMSLFLVASKD 1488  
 1306 GKFFCTQDSKLEKDCQGVYIDYKEVEVAOPRMKYYDHYDNVLMALLTLTYSIGE 1365  
 1489 GWVINDVIGIDLVGVDOOPIMNHNPMMLLYISFLLIYAFVLNKNYGVVVENHKKRQH 1548  
 1366 GWPVYLKHSVDATYEQGSPPGYRMEISIFVYVYVVPFFVNFVALLIITE----- 1420  
 1549 QEEFEARRREEKRLRLEKRRNMLMDVIVASGSSASASAEKQCFY--YSDYSR--FRL 1604

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Db 1420 QEGGDKVMS-----CSLEKNER-ACIDFAISA-----KPLTRYPQNRSGFY 1462
QY 1605 LVHHLCTSHLDLFTGCVGLNVTYAMENHYOQPOLDEALKICNTIFVIVFESSVKL 1664
Db 1463 KTWTFVVSPEEFYIMAMIALNTVLMKRYDAPYEYELMKCLNTVFTSMESMCCVTKI 1522
QY 1665 VAFGRFRFODRMQDLAVLLSIMGITLEEIEVNASLPINFTIRIKRVIARVTL 1724
Db 1523 IAFVLYKFFDANWVFYVILGSIIDIVTEIANNF---IN---LSFRLFRARAKTL 1576
QY 1725 LKMAVGRALDLYMAQLPOVGNLGLFMLEFTFPAALVEFLGDECEDETHPCBGLRH 1784
Db 1577 LRQGYTRILMLTFVOSFKLPLFYCLLIMAFYIAIGMVGNTALDD---TSINRH 1633
QY 1785 ATRFNGMAFLTRFVSTGNNMGIMKDTLRD---CDOE---STGYNVISPIYFVSVTLA 1840
Db 1634 NNFETFLQALMLFRSATGEMHIMLSCLSNACDEQANATCGSDFAVYFVSIFLC 1693
QY 1841 QFVLNVAVIAVLMKHEESNKEAK-----BEALIEALEF-----LEM-KT 1879
Db 1694 SFLMLNLFVAVIMDNFEYILTRDSILGPHLDEFIRVMAEYDPAACGRISYNDMEMLKH 1753
QY 1880 LSPQHSPLG-----SPFLMPGEGVNSPDKPGAPHTAHIGAAGEFSE----- 1927
Db 1754 MSP-----PLIGKCKCPARVAKRLVRNMNISMEDMTVHTSTLMALITALEIKIAPAG 1809
QY 1927 ---HPTWPHDEEYV-----PLGPDLLTVKSGVSRTHSLPNDSTYCRN 1968
Db 1810 TKOQCDAELKEISVYVAMLPKTLDDLVPKHPDEMTGKYAA---LMIFDFY---KQ 1864
QY 1969 GSTERSIGHNGWLPKAGSGSILSVH-----SOPADTSCILQ---LPKDVHYL 2015
Db 1865 NKTTRDMQOAPGL---SQMGVSLFHPKATLEOTOPA---VLGARYFLKQKSTSL 1918
QY 2016 QPHGA-----PTWGA---IPKLPPGRSPL-----AQRPLRQAIFTD----- 2052
Db 1919 SNGGAIQNOESGIESVSWGTQRTODPHEARPLEKSHTEIPVSGALAVDQMSI 1978
QY 2052 -----SLDVGLSGREDLSVSGSPGLTRSSFFWGGSSIOYQGRSGIOSKYS 2100
Db 1979 TRRGDPGEPGLESQ---RAASMPRLAELQVVDASPMKKSITLAPRPG----- 2030
QY 2101 KHIRLPAPCPGLEPSMAKDPETRS-----SLEDDELTSWISGDLPS 2143
Db 2030 THLCSTP-----DRPPSQASHHHHRCHRRDRKQSLKGPISL---ADMGARS 2080
QY 2144 SQEPLSP-----RDLKCYSVETQSCRRRPGSMLEQRRHSIAYSCDLSGQPL 2194
Db 2081 SAVGGLPFGEGPTGCRERRERROERSRQERQPSSSSEKQF---YSCDRFGREPP 2137
QY 2195 CPSPS-----SLGQPL-----GGPGSRPKKLSL-P 2220
Db 2138 KPRKSLSHPTSTAGDEPHPGSGSVNGSPLSTSGASTPGRGRQLPQTLPIPRP 2197
QY 2221 SLSIDPPS-----QGRPPCSPG-----VCLRRAPAD-----SKDS 2255
Db 2198 SITTKTANSSPIHAGAOISLPAPSPGRLSRGISEHNALLQROPLAPGSRIGSDPY 2257
QY 2256 VSSPLDSTAASPKDLSL-----SGLSS 2281
Db 2258 LGRILDSASVHALPEDLTTFEEAVATNSGRSS 2290

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PD 16-FEB-1995.
FR 11-AUG-1994: 009230.
FR 11-AUG-1993: US-105536.
PR 05-NOV-1993: US-149097.
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
PT Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
DR NPI: 95-090900/12.
DR N-PSDB: 084657.
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT Octalizing agonists and antagonists
PS Disclosure; Page 138-149; 285pp; English.
CC DNA encoding the alpha 1B subunit was isolated by screening a
CC human basal ganglia cDNA library with fragments of the rabbit
CC skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
CC A portion of one of the positive clones was used to screen an
CC IMR32 cell cDNA library. Clones that hybridised to the basal
CC ganglia probe were used to further screen an IMR32 cell cDNA
CC library to identify overlapping clones that in turn were used
CC to screen a human hippocampus cDNA library. A series of clones
CC to span nearly the entire length of the nt. sequence encoding
CC the human alpha 1B subunit was obtd. Nucleic acid amplification
CC of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC additional segments of the alpha 1B coding sequence. A full-
CC length alpha 1B DNA clone was constructed by ligating portions
CC of the partial cDNA clones. Nucleic acid amplification analysis
CC of IMR32 cell RNA and genomic DNA using oligo primers corresp. to
CC sequences located 5' and 3' of the stop codon of the DNA encoding
CC the alpha 1B subunit revealed an alternatively spliced alpha
CC 1B-encoding mRNA in IMR32 cells. This second mRNA product is the
CC result of differential splicing of the alpha 1B subunit transcript
CC to include another exon that is not present in the mRNA corresp.
CC to the other 3' alpha 1B cDNA sequence that was initially isolated.
CC The alpha 1B subunit encoded by a DNA sequence contg. an additional
CC exon is referred to as alpha 1B-1 and given in Q84657/R11005,
CC whereas the other form is referred to as alpha 1B-2 and given in
CC Q84658/R11006. Following the sequence of the additional exon in
CC alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are identical.
SC Sequence 2339 AA.

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Query Match 13.7%; Score 1708.5; DB 1; Length 2339;  
 Best Local Similarity 24.2%; Pred. No. 1.2e-122;  
 Matches 645; Conservative 370; Mismatches 844; Indels 805; Gaps 91;

```

QY 27 GAGGROGPGSTENDGASDSEAGLEPYPALAVF-----FYLSQDSRP 70
Db 25 GAGGAGGPGGCGIOPGQRYLYKOSINORAKTALNIPVKNCTYVRSLEFVSEDNV 84
QY 71 RSMCLRTVCNPFWEERYSMVILNCTVLCMFPCEDDIACDSQCRRILOAFD---FIPAF 127
Db 85 RYKAKRITETPPRENNMILATIANCIVLAL---EQHLPDGDKTMSERLDTEPYFIGI 140
QY 128 FAYEMVYKMAIG-IFGKCYLQDTNKRDLDFIVTAGMLEYS---LDLQNSFSKVRVR 183
Db 141 FCFEAGIKITALLFVFKHSYLRKNGMNVDEVVVLGILATIGTDFDK-----TLRVR 195
QY 184 VLRLPRAINRPSMRILVTLTDLTLMGNVLLCFEVEFFIGIVQVDMAGLNNRFL 243
Db 196 VLRLPRLVSGPDLQVLAISKAMVPLQIGLLEFALIMAILGLEPYMKFKKACF- 255
QY 244 PENSLPLVDLDEPYVOTENEDSPFCQPRNMGRCRSVPITLRGSGGPGPSLYE 303
Db 255 -----PNSTDAEPV-----GDFPGKRAP 273
QY 304 TYNSSWTTCVNNQYTYNCAGEHNPFKGAINFDMIGYMAIFOVITLEGWYDMFV 363
Db 274 ARLCGGDTCC---REYWP-----GPNFGITNEDMILFALLTFQCITMEGMDILYNT 323
QY 364 MD-AHSRYNFTYLLILLYGSGFMVNLCLVIAIQPSSEKQES-----QLMRQRYRF 416
Db 324 NDAAGNTMNLVYIPIIIGSFMLNLVGLVSGEPAKEREVENRRRAFLKLROOQIE- 383

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417 LSNASTLASSEPGCYELLKYVILRKARRLAQVSRRAIGVRAGLLSPVANSQGP 476  
383 -----RELNGYLEMIFKAEBVMLAED-----RNAEEK 410  
477 QPSGCTRSHRLSVHLLVHHHHHHYHLNGTLKVPASPEIODRQANSRLMLP 536  
411 SPLDLKRAATKRSNDLH-----AEGEDRAD----- 441  
537 PSPTPSGCPRAESVHSFYHADCHLEPVRCQAPPPCPSEASGRTVSGKVPVTS 596  
441 ----- 441  
597 PPEELKOKALVEAPSPBPTLTFENIPPPSSMHKLLTOSTGASHCKISSPCK 656  
441 -----LCAVGSPPAR 450  
657 ADSGAGDSCPCYCARCAGEPESADHVMPDSDSEAVYFTQDAQSHDLRDPHSRRORS 716  
451 AS-----LKSGETSSSYF-----RKER- 470  
717 LGPDABSSVLAEMRLICDTEFRKIVDSKYFGRGIMAILVNTLSMGLIEHDEPBLTNA 776  
470 -----MRF-----IRRVAKQSFYVWVLCVVALNTLCVAMVHNOBRRLTTL 514  
777 EISNIVTSFPALEMLIKLLVYGPETIKNPYNIPDGVIVISVWEIYGO-----OGGL 831  
515 YFAEFVFLGLFTLEMSLKMYGLGPRSYRSSFNCDFGVIVGSFVFWMAIKPGSSFGI 574  
832 SVLTFRLMRVLYKRLVPLALOROLVLMKTMVATFCMLMFLIFESILGMHFGK 891  
575 SVLALRLIRLFKTKYKWSLRNLVSLMSKSIISLLEFLVIFVFLMOMQFQG 634  
892 FASERDQTLPRDRNFDLSMAIVYFOILLTOEDMKNVLYNGM-----ASTSMALYFI 946  
635 FNODETPT-----TNFDTPAAILTVFOILLGEDMNAVMYHGIESOGVSKGMSFTPL 690  
947 ALMFGNVYVNLVAILVEGF-QAEELG-----REDASQ-----LSCI 986  
691 VLTLEGTLLNLVLAIVDLANLNAQELTDEEMEDRANOKLAKAEVAYSPISA 750  
987 QLPVNSOGDATKSESEPDSPSVYDGDGRKRLALVALGEMALRSLPLIITHTAA 1046  
751 NISIAARQONAKARSWE-----QASQLRLONLRASCEALYSEMDPEERLFA 800  
1047 TPNLSPKSSSTGVGE-----ALGSGSRITSSSGSAEPGA-----HH-----EMKS 1087  
801 TTRHLRPMKTHLDRPLVVELGRDAGRPVGKARPEALAEPEGVDPRRHHRHRODKT 860  
1088 P-----PSARSS-----PHSPWASAASWTSRSSRSNLSRAPSLIKRSPS 1127  
861 PAAGQODAEAPKASGEPGARREPRHRSHSKMA--GPEKARSBRGRP-----GPE 913  
1128 GERSLSLGEQESODE-----ESSEEDRASPAGSDHRHRSLE---REAKSST 1174  
914 GGRHRHRRGSPPEAEERPRHRAHRHODPSKECAGAGERRARRHGGPRAGPREASG- 973  
1175 DLPTLOVPG-LHTASGRSSASE--HODCGKASAGRLA-----RLTRTDPPOLDG 1223  
973 -----EPPARRHRARHKAQOPHEAVENKETEKEKTEKALIVEADKEKELRNQPRPH 1026  
1224 DDDNDEGNLSKGERIQAWVRSLPACRER-----DSW----- 1257  
1027 CDLETSGLVTVGP-----MHTLPSTCLQKYVEQPEDADNRNTYBMGSOQPDPTIYHI 1080  
1257 -----SATIFPOSRFR 1268  
1081 PYMLTGPGEATVPSGNVDESQAEGKREVEADVMRSGPRPIVYSSMCLSPNTILR 1140  
1269 LICHLLIHKMDHVIVYIIFLNCITIAMERKIDPHSAERFLTSLVYITFAVLEMT 1328  
1141 RCHHIVTKRFEVVLVIALSTALAEEDP-VATDSFRNNALKYLDYITTGFTFEMV 1199  
1329 VVVALGMCFGBOAYLRSSMNVLDGLVILSVIILVSMV-SDSGTKILGMLRVLLRLT 1387

1200 IKMIDLILLHPAYFEDLNNLID-----FLVSGALVAPAFSSSKKODINTIKSLRVLR 1255  
1389 LRLPVRISRAQGLIVETLMSLKPDIGNIVICAFIIEGILGOLERKFEVCOGE- 1447  
1256 LRLPKTIKRLPKLAVDQVNSLKNVNLIIYMLFMFIFAIVAIQLEKGFEEYCTDES 1315  
1447 -----DTRN--ITNKSQCAASR-WVRKRYNDNIGQALMSLFVLAASDQWDIDYDL 1498  
1316 KRLERDRGOYLDYEKEEVAQOPOMKKYDFHYDNLVALLTLFTVSTGBGMVLYKSHV 1375  
1499 DAVGDOOPINNNPMLLFLISFLIAFVLMFVMEGVVENEHRCROHDEEARRRE 1558  
1376 DAYEEOGSPSGYMELSITFYVYFVFPFFFNIPALLIIF-----QEGGDVMS 1429  
1559 EKRRLREKKRRNMLDQVIASSASASEAOCRP--YSDYSR--FRLLVHLCTSH 1614  
1430 -----CSLEKNER-ACIDFAISA-----KPLIRYMPONROSFQYKVTTFVVSPP 1472  
1615 LDLPITGYIGINVTAMENHQOPQLDEALKICNTYFTVYFVESYFKLVAFGRFRFO 1674  
1473 FEYETMAMIALNTVLMKFEYDADYEYELMKLCNIVFTSMFMECYKLIAGVLYNR 1532  
1675 DRNOLDIAIVLISIMGITLEEI-EVNASLPINFTIIRKRVLIARVILKLMVAGMRA 1733  
1533 DAMNVEDPVYLGSIITDILVIEIETN-----NFINSFLRFRARILKILROGYTIRI 1587  
1734 LLDVYQALPOVNGILFLMFLFTFALVGLFGLDECEBTHPCBEGHAFRNGMA 1793  
1588 LMTFVOSFKALPYVCLLIMLFEIYALIGOVGNLTALDD--TSINHNNEFRFLQA 1644  
1794 FLTLFRSTGDNMNGIMKDLRD--CDOE--STCYNTVISIYFVSFLTAQVLYNVVI 1849  
1645 LMLFRSRTGEMNHIMISCSNACQDQANATECGSDPAFYVSTPIFCSLMNLV 1704  
1850 AVLMKHEESNKEAK-----EBALEABLE-----LEM-KTLPSPQSPPL 1888  
1705 AVIMNFEYLRDSSILGPHLDEFIRWAEYDPAACGRISYNDMFMLKHMSP---PL 1760  
1889 G-----SPFLMPGVEGVNSPDSKPGAPHTTAHIGASGSLF-----HPTMVP 1932  
1761 GLGKRCPARVAKRLVRNMPLISNEDMTVHTSTLMALIRALEIKLAPAGTNOQDAE 1820  
1933 HPEEVPV-----PLGPDLLTVRKSGVSRTHSLPDSYWCRCNGSTAESLIG 1977  
1821 LKELISVWMANLPQKTLDLVPRHPRDEMVTGKYAA--LMIDFY--KONKTRDOMQ 1875  
1978 HRGKGLPRAQSSILSVH-----SOPADTSCILQ-----LKVHYHLLQPRGA----- 2021  
1876 QAPGGL--SOMGPVSLFHLPLATLEOTQPA---VLRGARVFLKOKSSTLSNGALION 1929  
2021 -----PTWGA--IPKLPBPPGRSPPL-----AOPRLRQOALIRTD----- 2052  
1930 ESGIKESYWGQRTQODAPHEKAPPLERGHSTELPVGSGALANDVQOSTTRRGDPGE 1989  
2052 --SLDVQIGSREDDLSEVSGPCPLTRSSSFWGSSIOVQORSGIOSKXHLRLPAPC 2109  
1990 QPLESOG--RAASMPRLAETQPVTDASPMKRSISTLAORPRG-----THCSTTP- 2040  
2110 PGLFEPWADDPETRS-----SLEDTELTSWISGDLPLPSOEPELSP- 2152  
2040 -----DRPPSOASSHHHHHRRDRKORSLEKPPSIS-ADMDGAPBSANVGGLPP 2091  
2152 -----DLKKCYSVETQSCRRRPGSWLDEORHSHIAVSCUDSGSQRPLCPSPS--- 2200  
2092 GEGPTCRRERERROERGOSQORQPSSSSEKQF--YQDRRGGRPREPKPRPSLSH 2148  
2200 -----SLGGQPL-----GPGSRPPKKLSLSP-PSISIDPPES 2229  
2149 PPSPTAGCPGPHPOGSGSVNSPLISTSGASTPGRGRRQLPQPLPRPSIITYKTANS 2208  
2230 --QGSNPPGSPG-----VCLRRARASD-----SKDPSVSPLDSTA 2264

Db 2209 SPIHAGAGTSLPAPSPGRSLRGLSEHNALLQRPDLPSGLAPSGSRISGSDPYLQGRDSEA 2268

QY 2265 ASPSPKDDTSL-----SGLSS 2281

Db 2269 SVHALPEDTLTFEEAVATNSGRSS 2292

RESULT 6

W63141

ID W63141 standard. Protein; 2339 AA.

AC W63141;

DT 12-OCT-1998 (first entry)

DE Human calcium channel alpha-1B subunit.

KW Alpha-1B subunit; human; calcium channel; assay: detection;

OS Homo sapiens.

PN USS792846-A.

PD 11-AUG-1998.

PF 31-MAY-1995; 455543.

PR 04-APR-1994; US-223305.

PR 04-APR-1988; US-176899.

PR 04-APR-1989; US-603751.

PR 04-APR-1989; NC-U01408.

PR 20-FEB-1990; US-482384.

PR 30-NOV-1990; US-620250.

PR 15-AUG-1991; US-745206.

PR 31-MAY-1995; US-455543.

PA (SIBI-) SIBIA NEUROSCIENCES INC.

PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,

PI Williams ME; 98-456192/39.

DR WPI; 98-456192/39.

DR N-PSDB; V42685.

PT DNA encoding human calcium channel alpha 1B subunit protein -

PT useful for recombinant production of the channel for screening of

its modulators, and diagnosis of Lambert Eaton Syndrome

CS Claim 1: Columns 239-250; 166pp; English.

CC The present sequence represents the alpha-1B subunit of a human calcium

channel. Calcium channels are membrane-spanning, multi-subunit proteins

that allow controlled entry of calcium ions into cells. This leads

to depolarisation events required for muscle contraction. The recombinant

subunit, when expressed with nucleic acids encoding the complete calcium

channel, can be used in assays for the detection and characterisation of

compounds that modulate the channel. The DNA encoding the subunits can

be alternatively spliced when transcribed, giving more than one form of

the protein from the same transcript, each having slightly different

properties. In addition, the reactivity of the alpha 1 subunit with IgG

antibodies from the serum of an individual with Lambert Eaton Syndrome

CC (LES) can be used as a diagnostic for the disease.

SO Sequence 2339 AA.

Query Match 13.7%; Score 1708.5; DB 1; Length 2339;

Best Local Similarity 24.2%; Pred. No. 1.2e-122;

Matches 645; Conservative 370; Mismatches 844; Indels 805; Gaps 91;

QY 27 GAGGAGGPGSTKEDKDSADSEAGLEYPALAVF-----FYLSQDSRP 70

Db 25 GAGGAGGPGGGLQPGQRLYKQSIARATMALYPIPKONCFVNSLFVFEEDNV 84

QY 71 RSMCLRTVCNPFWEFERSMVLINLCVTGLMFRPCDIADCSORCLIAQFD--FIFAF 127

Db 85 RYKARKITMPFPEFNMIATITIANCIVAL-----EQLPDKGTMSERLDTPEYFIGI 140

QY 128 FAVENVKVALG-IFGKKCYLGDITWNLDFPIVIAGLMEYS---LDIONVSFAVTR 183

Db 141 FCFEAGIKIILAGFYFHGKSYLRNGMNWDFVVLTLGLATGTDFDLR-----TLRAVR 195

QY 184 VLRPLAIRNVRSMRLVTLTLDTPLMGNVLLCFEYFFITGIVGLWAGLNNRCEL 243

Db 196 VLRPLKLVSGISLVQVLSIKRAVPLLIQIGLLFFAILMFAIIGLEFYNGKFKKACF- 255

QY 244 PENFSLPLSVDELPEYTOTENEDSEPFICQPRENGMRCRSVPTLRGGGGGPPCSDIYE 303

Db 255 -----PNSTDAEPV-----GDFPCGKEAP 273

QY 304 IYNSSNTTCVMMNOYITNCAGSEHNPEKGAIFNDNIGYAMIAFOVTLTGWDIMFV 363

Db 274 ARLCGGDTFC---REYWP-----GRNFGITNDNIIIFALITYFOCTITMEGMDILNT 323

QY 364 MD-ANSEYNEFYILLIIVGSEFMINICLVYIAFOSETKQRES-----OLMREORYRF 416

Db 324 NDAAGNTWMLYFIPIILIIIGSEFMINLVGLVSGFEAKEREVRERRAFLRLRQOQIE- 383

QY 417 LSNASTLASFSPPGSCYDELLKLVYILIKRAARLAQVSRAGIAGLSSPVARSQGP 476

Db 383 -----RELNGYLEIFKAEVMAEED-----RNAEEK 410

QY 477 QPSGCTSRSHRLSVHNLVHHHHHHHHYHGLNGTLRVPRASPEIOPDRANGSRMLMP 536

Db 411 SPLDVLRKAATKRSNDLIH-----AEGEDRFAD----- 441

QY 537 PSTPTPSGPPRGAEVSASFYHACHLEPVACQAPPPRCPSSEASGRTVSGKVPVHTS 596

Db 441 ----- 441

QY 597 PPEILKDKALVEVAPSPGPTLTSFNIPGPFSSMKHLETOGTGACHSCKRISPCSK 656

Db 441 -----LCAYGSPFAR 450

QY 657 ADGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVEFTODAOHSDLRDPHSRRORS 716

Db 451 AS-----LKSGKTESSSYF-----RRREK- 470

QY 717 LGPDAPSSVLAFFRLICDTRFKYVDSKIFGRGIMAILVNTLSMGTEYIEQEPBLTNAL 776

Db 470 -----MRFF-----IRRWKASQSYWVYLCAVANTLCVAVAHNQPRLITTL 514

QY 777 EISNIFSTFALMLKLIVYGFGYIKNPYNIFDGVIVISWELVQG-----GGGGL 831

Db 515 YEAEFVFLGLELTMSLKMGLGPRSAFRRSFCFDGVIYGSEFYVMAAIRPGSGFI 574

QY 832 SVLTFRMLRKLKVRPLPALQRLVVLKMTQNVATFCLMLFTFISILGMHLFGCK 891

Db 575 SVLALRLRILFKTKYKWSIRNLVSLNSMKSIIILFLFLFVFFALMQLFQGG 654

QY 892 FASRFDGTLPRKRNPSLMAIVTFOILTOEDMKNVLYNGM-----ASTSSMALYFI 946

Db 635 FNFDEPPT-----TNFDFPALITVFOILTGEDMAVMHGISSGQVSKMFSSEFYFI 690

QY 947 ALMTFGYVLENLVAILVEGF-QAEIRGK---REDASQO-----LSCI 986

Db 691 VLTLEGNVTLINVEFLAIVADNLANAQLTKDEDEMEANOKLALOKAEVAEVSMSAA 750

QY 987 QLPVNSGGGATSESEPPDFSSVDGDRKKRLALVALGEHAEIRKSLPLIITHTAA 1046

Db 751 NJSTIAAQNSAKARSVWE-----ORASQILQNLIRASCALYSEMPDEERLRA 800

QY 1047 TPMSLSPSSSTGYGE---ALGSGSRRTSSGSAEAGAA-----HH---EMKS 1087

Db 801 TIRHLRDMTHIDRLPYVELGIDGARGPYGKARPAEADAPGCVDPRRHHNRDKDPT 860

QY 1088 P-----PSARSS---PSPMSAASWTSRRSSNSLSLKRASLKRSPS 1127

Db 861 PAAGDODRAAPRAEAGEGEPAREPRPRHSKKA---GPPEARESERGRP-----GPE 913

QY 1128 GERSSLSGEGESODE-----ESSEDRASPPGSDHRRHGSLE---REAKSEF 1174

Db 914 GGRHHRHRSPEEAAREPRRRAHRRHODPSKECACAKGERARRHGGPRAPRAESG- 973

QY 1175 DLPTLQVPG-LHRTASGRSSASE--HODCNGKSASGRLA-----RLRTDDPOLDG 1223

Db 973 -----EPPARRRRARHAKQPAHEAVEKETTEKAEKAEVLEADKEKELNHPREPH 1026

QY 1224 DDNDNGNSLKGERTIAQWYRSRLPACCRER-----DSW----- 1257

Db 1027 CDLETSGIYVGP-----MHFLPSTCLOKVEOPEDADNQNVTNRMGSPDPNTIVHI 1080

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OY 1257 -----SAYIEPOSRRR 1268
DB 1081 PVMLTGLGEATVPSGNVDLESQAEKKVEADVDWRSGRPPIVPPSSMFCISPTNLLR 1140
OY 1269 LLCRRITTHKMFHVAVIIFLNCITAMERPKIDPSAERITLNSNFTFVAVLAEMT 1328
DB 1141 RFCHYIYMRFEVAVIIVLIALSSIALAADP-VRTDSPNNMLKLYDIYFTGVTFEMV 1199
OY 1329 VKVVALGMCCEGOAYLRSSNMVLDGLLVLSVIDIIVSMV-SDSGTILMLRYLLRT 1387
DB 1200 IKMTDGLLHPGAYFRDMLNILD-----FIVSGALVAFAPSSGKGDMITISLARLY 1255
OY 1388 LRPLRVISRAOGLKYVETLMSLKPIGNIVICAFPIIFGLIGVLFKGFVCOGE- 1447
DB 1256 LRPLKTIKRLPKLKAFCVAVNSLKNVNLITLYMFMFIFAVIAYVOLFKGKFFYCIDES 1315
OY 1447 -----ITNKSQCAEASR-VWHRKYNPDNLGOALMSLFLVASKDQWDIMV DGL 1498
DB 1316 KELEDRCGOYLDYEKEVEEAQPRQMKYDFHYDNVLMALITLFTVSTGECMPVYLKHSV 1375
OY 1499 DAVGVDOQPINNHNPMLLVEISFLIYAFVLMFVGVVENHRCROHEEARE 1558
DB 1376 DATEEOPSPGSRMELSLFVYVVFVPPFFVNIYFALITITF-----QEGDKVMSE 1429
OY 1559 EKRLREKKRRNMLDVIYSGSSASASAEQCKPY--YSDYR--FLLVHNLCTSHY 1614
DB 1430 -----CSLEKNER-ACIDPAISA-----KPLTRYMPOROSFOYKWTVEVSP 1472
OY 1615 LDLFTGIVGNVYVMAHEHCOPIIDELKICNYIFTVFVESEFKIAVGFRRFP 1674
DB 1473 FEYFMAMIALNTVYLMKFDAPREYLMKCLNIVTSMFSMECVLKITAEBVLVYFR 1532
OY 1675 DWMNOLDIAYLLSITGITLEEI-EVNASLPINPTIIRIMVLIARVYLKLAACVMA 1733
DB 1533 DAMNVDEFVYVIGSTITLIVETIAETN-----NFINLSFLRFLPAARLIKLRGGYITRI 1587
OY 1734 LLDYVQALPOVGNIGLFLMLFFIFALGYELTGDLECDTHOEGGRATFRNGMA 1793
DB 1588 LMTVQSGFKALPYVCLLIAMLFYIATIGOVENALDDO---TSINRNNRRTLOA 1644
OY 1794 FTLFRVSTGDMWNGIMKDTLFD--CDOE--STCYNIYSPYSEVFLYAOVAVNVI 1849
DB 1645 LMLLRSATGEAMHEIMLSCSNQACQANTEGSEFAFEVFSFLLCSFLMLNLFV 1704
OY 1850 AVLMKHLESNKEAK-----EBAELFAELE-----LEM-KTLSQPHSPL 1888
DB 1705 AVIMDNFEYLTPDSSILGPHHIDEFIRVAEYDPAACGRISYNDMEFLMKHMSPL 1760
OY 1889 G-----SPELMPGVEGVNSPSPKPGAPHTAHIGAASGFLE-----HPTWVP 1932
DB 1761 GIGKCPRAVAYKRLVRNMPISNEDMVIHTSTIMALIRALEKLAPACTKHQCOAE 1820
OY 1933 HBEVAVY-----PLGPDLLTVKSCVSTHSLPNDSYNCRNGSTAEKSLG 1977
DB 1821 LRKEISVWANTPOKTLIDLVPKHPDDEMTGVYAA--LMIEPFY--KONKTRIDMOQ 1875
OY 1978 HGWGGLPKQSGSILSVH-----SOPADISCLQ-----LPDVAHYLLQPHGA 2021
DB 1876 QAPGGL--SOMGPVSLFHLKATLEOTOPA-----VLRGARVFLRKKSSTLSNGALIONQ 1929
OY 2021 -----PTWGA--IPKLPPEGSRPL-----AQRPLRQALRIKD----- 2052
DB 1930 ESGIKESVWGQRTQDADHARPLERHSTEIFVGRGALAVOVQOSTIRRGPDGP 1989
OY 2052 --SLDVOGLGSRBDLSEVSGPSCPLTRSSSWGSSIOVOQRSIQKSVKHTLPAPC 2109
DB 1990 QPGLESQG--RAASMPRLAETOPVTDASPMKRSISTLAQPRG-----THLCSTTP- 2040
OY 2110 PGLEPFWADDPETRS-----SLELDELMIWISGDLPLSSQOEPLSP- 2152
DB 2040 -----DRPPSQASSHHHHRCHRRRDKRQKRSLEKGSLS-ADMMDAPSSAVPGILP 2091

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OY 2152 -----RDLAKCYVETQSCRPRPGSNLDEORRHSAVSCLDGSPRLCPSPS----- 2200
DB 2092 GEGPLGCREREREROERGRSOERPOSSSEKORF---YSCDRFGREPKRPPLSLSH 2148
OY 2200 -----SLGQPL-----GGPSRPKKLSP-PSISIDPPES 2229
DB 2149 PPSPTAGEPPHPGQSSVYVSPPLSTSGASTPGRGRQLPOTPLTPRPSITLYKTANS 2208
OY 2230 -----QGSRPQCSRG-----VCLRRRAPAD-----SKDPSVSSPLIDSTA 2264
DB 2209 SPHFAGQSTSLPAPSPGRSLRGLSEHNALLORDPLSOPLAPGSRIGSDPYLGORDSEA 2268
OY 2265 ASPSPKDTLSL-----SGLSS 2281
DB 2269 SVHALPEDTLTFEEVAVATNSGRSS 2292

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## RESULT 7

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R71006
ID- R71006 standard; Protein; 2237 AA.
AC 01-DEC-1995 (first entry)
DT Human neuronal calcium channel subunit alpha 1B-2.
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
OS Homo sapiens.
PN M09504822-A.
PD 16-FEB-1995.
PF 11-AUG-1994; U09230.
PK 11-AUG-1993; US-105536.
PR 05-NOV-1993; US-149097.
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
PT Ellis SB, Gillespie A, Harpold MM, Mocue AF, Williams ME;
DR Wpt: 95-090900/12.
DR N-PeDB: Q84658.
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
PS Disclosure: Page 149-160; 285pp; English.
CC CC encoding the alpha 1B subunit was isolated by screening a
CC human basal ganglia cDNA library with fragments of the rabbit
CC skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
CC A portion of one of the positive clones was used to screen an
CC IMR32 cell cDNA library. Clones that hybridised to the basal
CC ganglia probe were used to further screen an IMR32 cell cDNA
CC library to identify overlapping clones that in turn were used
CC to screen a human hippocampus cDNA library. A series of clones
CC to span nearly the entire length of the nt. sequence encoding
CC the human alpha 1B subunit was obt'd. Nucleic acid amplification
CC of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC additional segments of the alpha 1B coding sequence. A full-
CC length alpha 1B DNA clone was constructed by ligating portions
CC of the partial cDNA clones. Nucleic acid amplification analysis
CC of IMR32 cell RNA and genomic DNA using oligo primers corresp. to
CC sequences located 5' and 3' of the stop codon of the DNA encoding
CC the alpha 1B subunit revealed an alternatively spliced alpha
CC 1B-encoding mRNA in IMR32 cells. This second mRNA product is the
CC result of differential splicing of the alpha 1B subunit transcript
CC to include another exon that is not present in the mRNA corresp.
CC to the other 3' alpha 1B cDNA sequence that was initially isolated.
CC The alpha 1B subunit encoded by a DNA sequence contg. an additional
CC exon is referred to as alpha 1B-1 and given in Q84657/R71005,
CC whereas the other form is referred to as alpha 1B-2 and is given in
CC Q84658/R71006. Following the sequence of the additional exon in
CC alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are identical.
SQ Sequence 2237 AA:

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Query Match 13.7%; Score 1703; DB 1; Length 2237;

Best Local Similarity 24.2%; Pred. No. 2.9e-122;

Matches 650; Conservative 364; Mismatched 850; Indels 826; Gaps 96;

OY 27 GAGGRGCGSTENDPQSAOSEMAGLPYPALAPYV-----FYLSQDSRP 70

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Db 25 GAGGAGGPGGLOPQGGORVLYKQSIQORAKTALMYNIPYKONCFYVNSLFEYSDNV 84
Qy 71 RSMCLRTVCNWEERBSVMLVLLNCVTLMGFRPCEDACDSORCLLOAFDD--FIFAF 127
Db 85 RYAKRITFEMPEPMLATIIANCIYIAL--EQHLPGDKTPMSERLDTEPFYIGI 140
Qy 128 FAVEMVYVWALG--IFGKKCYLSDTMNRDLDFEYIAGMLYS--LDLOVNSAATRA 183
Db 141 FCFEGITILGFVYFHKGSTLRNGMVMDFVYVITLITAGTDDLR-----TIRAYR 195
Qy 184 VLRLPRLNRVPSMRILYTLTLDLPMIGVNLCEFEYFIFGIVGYOLWAGLLNRNCL 243
Db 196 VLRLPLKTVSGIPSOVLVLSIMKAMVPLDGLLFFAILMFAIIGLEFYMGKFRHACF- 255
Qy 244 PENFSLPSTVDLEPYQOTENDESPFICSOBRNGMSCSVPTLNGEGGGPGCLDE 303
Db 255 -----FNSTDAEPV-----GDFPGCKEAP 273
Qy 304 TYNSSNTTCVNMNOYTYTNCAGEHNEFKGAINEDNIGYAMIAFOYITLLEGWVDIMYEV 363
Db 274 ARLCGDTFC--REYMP-----GNFGLTNDILFAILITVFOCITWEGTDLIYNT 323
Qy 364 MD-AHSFNFTYFILLITVGSFEMINCLVYIATQSETORES-----QLMREORVRF 416
Db 324 NDAAGNTNMNLYFPLITIGSFEMNLVGLVSGEFAKEREVENRRAFILKLRQOIE- 383
Qy 417 LSNASTLASEPSCYEELLYVYILRKARLAQVSAIGRAGILLSPARSGOEP 476
Db 383 -----RELNGYLEWIFKAEVWLAEED-----RNAEEX 410
Qy 477 QPSGCTSHRRLSVNHHVHHHHHHHNGTGLVPRASPELODRONGSRMLMLP 536
Db 411 SPLDLVLAARKKSRNDLIH-----AEGEDIRFAD----- 441
Qy 537 PSTPTSGGPRGAEVSASFHADCHLEPVRCQAPRPPCESEASGRTVSGKYPTVHTS 596
Db 441 ----- 441
Qy 597 PPPELRLKALVEVAPRSGPRTLSTFNIPROPPSSMKHLETOGTGCHSCCKIISPCSK 656
Db 441 -----LCAGVSPFAR 450
Qy 657 ADSGACGPDSCPYCARTGAGEPESADHYMPDSEAVEYFTODAHSDLRDPHSRRORS 716
Db 451 AS-----LKSCTESSYF-----RKREK 470
Qy 717 LGPDAEBSVLAFRLLICDTRKIVDSKYRGIMAILVNTLSMGIEYHGEDELTNAL 776
Db 470 -----MERFF-----IRRVYKASQFYVVLCVVANTLCVAMVHYNOFRRLTTL 514
Qy 777 EISNIVETSLALEMLKTLVYGFPGYIKNPYNIFDGVIVISWELVGO-----OGGGL 831
Db 515 YFAEYVGLITLTKSLKMYGLGRSFRSFCDFGVIVGSVEVYMAAIPGSSFGI 574
Qy 832 SVLRFRLMRVLKVLRLPALQRODVLVLMKTQVNAFCMLMFTIFSILGMHLFGCK 891
Db 575 SVLRALRLIRLFKYKYKWSLRNLVSLNSMKSIISLELLEFLFIVVALLMOQFQGG 634
Qy 892 FASEDGDGLDPRKPFDDLMAIVTFOILQEDMNKVLNGM-----ASTSSMALYFI 946
Db 635 FNFQDETFT-----INFDFPRAILITVFOILGEDMNAMVHGITSOGGVSKGMFSYFI 690
Qy 947 ALMTGNTVLENLVAILVEGF--QAEIGK--REDAQSG-----LSCT 986
Db 691 VLLTGNTVLLNVLAIVDMIANAOELITKBEEMEAANOGLALQKAEVAEVSMSAA 750
Qy 987 QPVRNSOGDATKSESEDFSPSVDDGDKRRLALVALGEHAEKLSLPLLIHTA 1046
Db 751 NISIAARONSKKASVY-----QASQLRLONLRASCALYSEMDPEERLRA 800
Qy 1047 TPMSLPKSSSTGVGE-----ALGSGSRTSSGSAEPGA-----HH-----EMKS 1087

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Db 801 TTRRLPRDKTHLDRPLVYELGHDGARGPVGKAREAAEAEGVDPRRHHRRHDXKT 860
Qy 1088 P-----PSARSS--PHSPWSAASWTSRRSSNSUGRABSLKRRSPS 1127
Db 861 PAACDQDRAAPRAESGEPQAREPRPRSHSKAA--GPPEASERGRGP-----GPE 913
Qy 1128 GERSLSGEGSEODEE-----ESSEDRASPAQSDHRRGSLD--REAKSSF 1174
Db 914 GGRHHRRGSPERAEERPRRHHRRHODPSKECAGAKGERARRRRGGRAPRAESEG- 973
Qy 1175 DLPTDLPVG--LHRTASGRSSASE--HODCNKSASGRLA-----RLTDDPOLDG 1223
Db 973 -----EPARRRHARKKQAPAEAAVEKETTEKEAEIIVEADKEELRNHOPREPH 1026
Qy 1224 DDNDDEGNLSKGERIQAMVRSRLPACCRER-----DSW----- 1257
Db 1027 CDLETSGTIVGP-----MHTLPSTCLOKEBQEPEDADNONVTRMGSQPPPTVYHI 1080
Qy 1257 -----SAYTFPQSRFR 1268
Db 1081 PVMLTGLGATVVPSSGNVDLESQAEKKVEADVMRSGPRPIVPSMFLSPNTDLR 1140
Qy 1259 LCHRIITHRMFDHYVLIIFLNCITIAMERPKIDPHSARIFILLNSYIFTAFLAEMT 1328
Db 1141 RCHYIVTMRFEYVILVIALSSIALAEDP--VRTDSRRNALKYLDITFGVETFEKV 1199
Qy 1329 VKVVALGMCGEQAYLRRSSMNVDGLVLISVDILSVKY--SDSGTKILGMRLVRLRT 1387
Db 1200 IKMIDLGLLHPAGYFDLWNID--FIVSGALVAFAGSGKGDINTIKSRLRV 1255
Qy 1388 LRLPRLVSRAGKIVYETLMSLKPIGNIVYCCAFFIIPDILVOLEFKGFEFCOE- 1447
Db 1256 LRLPKTKRLPKRAVFDVANSKLVNLILYIMLFMTFVIAVQLEKGFECTDES 1315
Qy 1447 -----DTRN--ITNKSDCAEASR--WVRHKYNEFDNLGALMSLFYASKDGVNDIMYDL 1498
Db 1316 KELBRDRCGYLDYKEBEVBAQROKKYDFHYDNLMTLLTFVSTGEGVPLKHSV 1375
Qy 1499 DAVGDDQPIIMNHPMLLYFISFLILVAFVILNMGVGVVENEFKRCHOEEERARRRE 1558
Db 1376 DAYEEOGSPSGYMEISTIVYVYFVFPFVNIIVALLITF-----OQOGKVNSE 1429
Qy 1559 EKRLRLRLEKKRRLMLDDVIVASGSSASAASEAOCBPY--YSDYSR--FRLVHNLCTSHY 1614
Db 1430 -----CSLEKNR--ACIDFALISA-----KLTLYMPONRQSGFOKYMTVVSPP 1472
Qy 1615 LDLEITGVIGLNVYTMAMEHYOQPOLDEALKICNTIFVIVFESVFKLVAFGRFRFP 1674
Db 1473 FEYFIMAMIALNTVLMKRYDAPYEYELMKCLNTVFTSMFMECVLIIAFGLANTFR 1532
Qy 1675 DRMQLDLAIVLISIMGITLEET--EVNASLPIPTIRIRMRVILRIARVILKLMAMVMA 1733
Db 1533 DAMVFPFVYVLSITDILVTEIAETN-----NFILSLRLFRARLKLKLROGYTIRI 1587
Qy 1734 LLDIVQALPOVGNLGLFNLFFITFALAGVELFGDLCEDETHPCEGLGRHATFPPGMA 1793
Db 1588 LLMTFVOSFKRLPYVCLLIMLFELFIYALIGMOYFGNIALDD--TSIRHNHNFPTLOA 1644
Qy 1794 FLTLFRVSTGDMNGIMKDLRLD--CDOE--STCYVTIVSPIYFVSFVLTAAQFVLANVI 1849
Db 1645 LMLFRSATGAMHEIMLSLSONACDEQANATEGSDRAYFYFISILGCFILMNLNV 1704
Qy 1850 AVLKMLHESNKEAK-----EAELEAELE-----JEM--KTLSPOPHSPL 1888
Db 1705 AVIMDNEEYLRDSSILGPHLDEFIYVMAEYDPAACGRISYNDMEMLKHMSP-----PL 1760
Qy 1889 G-----SPLMPGVEGVNSPDSPPGAPRTHYHIGAAGFSLE-----HPTWVP 1932
Db 1761 GLGKKCARAYAKVLVAMNPISNEDMTYHFTSTLMAILLRTALEIKLAPAGTKQOQCAE 1820
Qy 1933 HPEEVPV-----PLGDLTLVRKSGVSRTHSLPNDSYMCRNGSTAERSLG 1977
Db 1821 LRKEISYVAMNLPQKITDLILVPPHKPDEMVTGKYVAA--LMIFDY--KONKTRIDMO 1875

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CC transcript, each having slightly different properties. In addition, the  
 CC reactivity of the alpha 1 subunit with IgG molecules from the serum of  
 CC an individual with Lambert Eaton Syndrome (LES) can be used as a  
 CC diagnostic for the disease.  
 50 Sequence 2237 AA:

Query Match 13.7%; Score 1703; DB 1; Length 2237;  
 Pest Local Similarity 24.2%; Pred. No. 2.9e-122;  
 Matches 650; Conservative 364; Mismatches 850; Indels 826; Gaps 96;

1978 HRGWLKPKAOSGSLVSHSQPADTSCILQPKDVHYLLPHGAPTWGAIPKLPPEGSRPL 2037  
 1876 QAGGGL--SQMGVSVLFH-----PLKATL 1897

2038 AORPLRROAIFRDSLDVQSLGREDLLSEVSPSCPLRRSSSFQWGSSTIQVQGRGSLD 2097  
 1898 EQ---TQPAVLR-----GARVELRQK-----STSLNGALIQ-NQESGIRE 1935

2098 KYSHHILPAPCPGLESPMAKD-----PEPTRSSLELDTLSWISGDLPPSSQEPESLSPR 2152  
 1936 SV-----SWGTQRTQDAPHAPRPLENG-----HSEITVIG-R 1967

2153 DLKCYSEVETQSCRRR-----PGSMLEQORRHSTAVSCLDGSGQPLCPSP-----SSIG 2202  
 1968 SGALAVYVQMSITRRGPDGEPGLESGQR-AASMPRLAAETQPVYDASPMKRSISTLA 2026

2203 GQPLG-----GPGSRPKKILSP-----PSISID--PPPS--- 2230

2027 QRPKGTSLCTTPRPPPSQASSHHHHRRRRDRKQSLKPGSLADMDGAPSSAVG 2086  
 2230 QGSRPSPGVCLR-----RRAPASDKDPVSYSSPLDSTAASPSKCDTSL 2276

2087 PGLPPEGPPTCCRRERERORGRSGORQPSSESSSKQHFYSCDRFGREPKPK- 2143  
 2277 SGLSDPTMDPVLPTLPHLSPPGADPSSASMAFLKSPFAASSHAPHL-ESSVAGGD 2335

2143 PLSLSSHPTS-----PTAQOE---PGPHQOAGSAVG---PNTTCCRETPPSAPWPLA--- 2190

2336 DEQNRPRVDLKRQPM-----SPCLREEGKGESPVMP--RLPTPG 2373  
 2190 -----LELALITLWGSVMTVRPLSTPCLFTRLSLR-LMPPIRAPPG 2231

RESULT 8  
 W63142  
 W63142 standard: protein; 2237 AA.

12-OCT-1998 (first entry)  
 Human calcium channel alpha-1B-1 subunit, encoded by a splice variant.  
 Alpha-1B subunit; human; calcium channel; assay; detection;  
 Characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 Homo sapiens.  
 US5792846-A.  
 11-AUG-1998.  
 31-MAY-1995; 455543.  
 04-APR-1994; US-223305.  
 04-APR-1989; US-176899.  
 04-APR-1989; US-603751.  
 20-FEB-1990; WO-001408.  
 30-NOV-1990; US-482384.  
 15-AUG-1991; US-745206.  
 31-MAY-1995; US-455543.  
 (SIBI-) SIBIA NEUROSCIENCES INC.  
 Brenner R, Ellis SB, Feldman DH, Harpold KM, McCue AF,  
 Williams ME;  
 MPT: 98-456192/39.  
 N-PEDB: V42686.  
 DNA encoding human calcium channel alpha 1B subunit protein -  
 its modulators, and diagnosis of the channel for screening of  
 its modulators, and diagnosis of Lambert Eaton Syndrome  
 Claim 1: Columns 249-262; 166pp; English.  
 The present sequence represents the alpha-1B subunit of a human calcium  
 channel. The DNA sequence encoding this protein is derived from  
 alternative splicing of V42685. Calcium channels are membrane-spanning,  
 multi-subunit proteins that allow controlled entry of calcium ions into  
 cells. This leads to depolarisation events required for muscle  
 contraction. The recombinant subunit, when expressed with nucleic acids  
 encoding the complete calcium channel, can be used in assays for the  
 detection and characterisation of compounds that modulate the channel.  
 The DNA encoding the subunits can be alternatively spliced when  
 transcribed, giving more than one form of the protein from the same

transcript, each having slightly different properties. In addition, the  
 reactivity of the alpha 1 subunit with IgG molecules from the serum of  
 an individual with Lambert Eaton Syndrome (LES) can be used as a  
 diagnostic for the disease.  
 Sequence 2237 AA:

Query Match 13.7%; Score 1703; DB 1; Length 2237;  
 Pest Local Similarity 24.2%; Pred. No. 2.9e-122;  
 Matches 650; Conservative 364; Mismatches 850; Indels 826; Gaps 96;

27 GAGGROGPGSTKDPGSGADSEAGLPPALAPVFE-----FYLSDSRP 70  
 25 GAGGAGGPGGGLPGQGVLYLKOSIAORARMTALNIPYKONCTVNRSLFFVESDNV 84

71 RSWCLRTVYCNWFERVSKMLVLLNCVTLGMFRPCEDTACOSQCRILQARD---FFAF 127  
 85 RRYAKRITEMPFENMILATIANCIYAL---EQHLPGDKTPMSERLDDDEPTFGI 140

128 FAVENVVAVLQ--LEGKCYLGDWNRDLDFEIVIAGMLEYS---LDLQVSESAVTRV 183  
 141 FCFEAGITILGLGVYFHAGSYLRNGWVMDPVVLTGILMTAGTDPDR---TLRAVR 195

184 VLRPLRAINRVSMRILVTLTLLDTPMLGNVLLCFVFFIFGIVQVQMAGLRNCF 243  
 196 VLRPLKIVSGIPSLQVVLKSIKMAVPLDQIGLLFPAIMFALIGLEFYNGKFKACF- 255

244 PENFSLPLSVLEPYQYQENEDESPFCOSPRENGMNSCRVPTLRGEGGPGCSLDYE 303  
 255 -----PSTDAEPV-----GDFPCGKEAP 273

304 TYNSSNTTCVWNOYTYNCSAGEHNPFKGAINFDNIGYAMIAIFQVITLEGVNDYFV 363  
 274 ARLCGDTEC---REYWP-----GPNFGITNFDNIFALITVFOCITMGWTDILYNT 323

364 MD-AHSFNFYIFILLIIVSGFEMINCLVYIATQFSEFKRES-----QLMEQVRF 416  
 324 NDAAGNTWMLYFIPLIIGSFEMINLVGLVSGFAERERVENRRALFKLRQOIE- 383

417 LSNASTLASFSFGSCYEELKYVILKRAARLAQVSRAGILSSPVARSQOEP 476  
 383 -----RELNYLEMIKAEVMAED-----RNMEK 410

477 QPSGCTSRHRLSYHLLVHHHHHHHHYHLGNTLVRPASPETIORDAAGSRMLMP 536  
 411 SPLVDLKRATKRSNDLH-----AEEGEDRFAD- 441

537 PSTPTTSGGPRPGASVSHFYHADCHLEPVRCQAPPKPCSEASGRVGSKYPTVTS 596  
 441 ----- 441

597 PPEELIKRALVEVAPSPGPPLTTSFNIPGPFSMHKLETOGTGCHSSCKLSSPCK 656  
 441 -----LCAVGSRPFR 450

657 ADSGACGPDSCYCATGTAGPEBESADHWMPDSDSAVVEFTQDAHSDLRPHSRBRS 716  
 451 AS-----LKSQTESSSYF-----RRKEK- 470

717 LGPDAPSSVLAFWRLICTFRKIVDSKYFGRGIMAILVNTLSMGIEYHDEPELTAL 776  
 470 -----MERFF-----IRRMVKAOSFYVWVLCVVALNLTLCVAMVHYNOBRRLTTL 514

777 EISNIVTSLEALEMLKLKLVYGPFGYIKNPYNIFDGVIVISWEIYQ-----QGGGL 831  
 515 YFAEFVLGLFTEMLKRYGGLGPRSYFSSFNCFDFGVIVGVEVWMAALPKGSSFGI 574

832 SVATRTLRVAVLKVAFELALQRLQVLMKIMDNVATFCMLMLFTFISILGMLFCCK 891  
 575 SVTRALRLRLEFVTVWYSLRVLVSLNSKSIISLFLFLFTIVVFAIGMQLFGQ 634

892 FASEBDGDTLPDKRNDLSLMAIVVFOILQEDMNKVLVNGM-----ASTSSMALYFI 946



Db 635 FNFODEPT-----TNEFTFAAILTVFOILTGEDMNAVMTHGIESQGVSGKMFSSFFFI 690  
 QY 947 ALMTGNGVNLNLAIVLVEGF-QAEELGK-----REDAISO-----LSCI 966  
 Db 691 VLTGNTLLNLAIVLAVDNLANAQELTKDEEMEAOKLALOKAKVAEVSPPSA 750  
 QY 987 QLPVNSQGDATKSESEDFSPVSDGDDKRRKRLALVALGENAELKSLPLLIHTAA 1046  
 Db 751 NISIAARQONAKARSWME-----QASQLRLONLASEALYSMDDEERLRA 800  
 QY 1047 TPMSLPKSSSTGVGE-----ALGSSRTSSGSAEPGA-----HH-----EMKS 1087  
 Db 801 TTRHLRPMKTHLDRPLVVELGRDARGPVGKARPEAAEPEGDPDRHHHRKDKT 860  
 QY 1088 P-----PSARSS---PHSPMSAASMTSRSSSRNLGRAPSLKRSP 1127  
 Db 861 PAAGQDAAEAPKAESGPGARERPRHRSHKAA--GPPEAKSRGRGP-----GPE 913  
 QY 1128 GERNLSGEOESODEF-----ESSEDRASPAGSDHRHRSLE--REAKSSF 1174  
 Db 914 GGRHRHRGSEPEEAERPRHRRAHRQDPSEKACAGKGERRAHRGPRAGREAESG- 973  
 QY 1175 DLPTLOVPG-LHRTASGRSSASE--HODCNGKSAGRLA-----RLRTDDPOLDG 1223  
 Db 973 -----EPPARRHRARHKAQPAHAEVKEKTEKATEKEAEIYEADKEKLRHNRPREH 1026  
 QY 1224 DDDNDEGMLSKGERIOAWRSRLPACCRER-----DSW----- 1257  
 Db 1027 CDLETSGTIVGP-----MHTLPSTCLOKYEQEPEDADQNRNVTBMGSPPPPTIYH 1080  
 QY 1257 -----SAYIPPOSRRR 1268  
 Db 1081 PYMLTGPGEATVPSGVNDLESOAEKKEVEADVDVMSRPRTPVYSSMFCISPTNLR 1140  
 QY 1269 LICHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTSSNYFTAVLAEMT 1328  
 Db 1141 RCHYIVMRFEYVILVIALSSIALAEDP-VRTSPRNNAKLYDYIFTGVTEFEMV 1199  
 QY 1329 VKVVALGMCFOBAVYLRSSMNVLDGLVLISIDILVSMV-SOSGCTILQMLVRLKRT 1387  
 Db 1200 IKMIDGLLHPGATFRDMLNILD--FIVSGALVAFAPSGKGKDITITSLRLR 1255  
 QY 1388 LRLPRVISAAGLKLWVETLMSLRPIGNIVVICAFIIFGLVGLFKGFVCOGE- 1447  
 Db 1256 LRLPKTIKRLPKLAVCECVNSLKNVNLILVLMFMFIFAVIAVGLFKGFVCOGDES 1315  
 QY 1447 -----DTN--ITNKSQCAEASR-WVRHKNFNDLGOALMSLFLVASKGWDIMTDL 1498  
 Db 1316 KELEHDCRGYLDYEKEVEEAOPQMKKYDHYNDVLMALLTFTVSTGGMVPLKHSV 1375  
 QY 1499 DAVGVDOQPINNHNPMLLYEISFLIYAFVLMFVGVVVENHRCROHEEERARR 1558  
 Db 1376 DATEEQGSPSGYRMEISIFVYVYVFFVFIYFALLIITF-----QEOGDVMS 1429  
 QY 1559 EKRLRLKRRKRNMLDVLVASSSSASASAEAOCKPY--YSQSR--FRLLVHLLCTSHY 1614  
 Db 1430 -----CSLEKNR-ACIDFAISA-----KPLTRMPQNRQSFQYKTYTFVVSPP 1472  
 QY 1615 LDLFTGVIGLVVYVMAHEHQOPOILDEALKICNYIFTVYFVESYFKLVAGFRREFQ 1674  
 Db 1473 FEYFIMAMIALNTVYLMKFEADAYEYELMKCINIVFTSMFSHECLKIARGVLYNFR 1532  
 QY 1675 DRWNOJLAIVLISMGITLEET-EVNASLPIINFTIIRKRVLIARVYLKMAVGMRA 1733  
 Db 1533 DAMNVEDVYVLTGSTITDLVLEIETN-----NFINSFLRLEFRARLILLLQGYTIRI 1587  
 QY 1734 LLDYMAQLPOVGNLGLFMLELFIYFALGVELGDLCECETHCECGLGHAFNRNGMA 1793  
 Db 1588 LLMTVQSGFKALPYVCLLIAMLFYALITGIVGVGNIALDD--TSINHNHFRFLQA 1644  
 QY 1794 FLTFRVSTGDNMGIMKDTLRD--CDOE--STCYNTVISPFIYVSVLTAQFVLVNVYI 1849  
 Db 1645 LMLFRSATGEAMHEIMLSCLSNQACDEQANATCGSDFAVYFVSFIIFCLSLMLNLFV 1704

QY 1850 AVLMKHLSESKKAK-----EBALEAELE-----LEM-KTUSPQPHSL 1888  
 Db 1705 AVIDNEEYLTROSSIIGPHHLEFIRWAEYDPAACGRISYDMFEMLKHMSPP--PL 1760  
 QY 1889 G-----SPLMPVEGVNSPSPKPCAPPTTAHIGAAGFSLE-----HFTWVP 1932  
 Db 1761 GLGKKCFARVAYKLVMMNPISNEDMTVHTSTLMAILRTALEIKLAPAGTKOQCDAE 1820  
 QY 1933 HPEVPV-----PLGPDILTVKSGVSRHSLPNDYSKRNSTAEBSIG 1977  
 Db 1821 LRKEISYMANLPQKTLIDLVPKPKDEMVTGVYAA--LMTFDY--KONKTRDOQO 1875  
 QY 1978 HRGMLPRAQSGSILSVHOSADTSCILQPKVDHYLQPHGAPTGAIPKLPPEGRSP 2037  
 Db 1876 QAPGL--SQMGVPSLH-----PLKAL 1897  
 QY 2038 AORPLROAIRTDSLVOGLSREDILSVSGPCPLTRSSFWGSGSIYOQNSGIOS 2097  
 Db 1898 EQ--TOPAVLR-----GARVFLROK-----STSLNSGAIQ-NOESGIKE 1935  
 QY 2098 KYSKHRLPAPCPLEPSMAKD-----PPTRRSLDTLELWSIGDLLPSSQEEPLSPR 2152  
 Db 1936 SV-----SWGTQRTODAPHARPLERG-----HETLPVGR 1967  
 QY 2153 DLKCYVETOSCRNR-----PGSWLDEORRHSTAVSCLDSGQPLRCPSP-----SSIG 2202  
 Db 1968 SGALAYDQOMOSITRRQDPDEPQGLESOGR-AASMPRLAETQPTDASPMKRSISTLA 2026  
 QY 2203 GQPLG-----GPGSRPKKLTSP-----PSISID--PPES-- 2230  
 Db 2027 QRPGRHLCSTTPRPPRPPSQASSHHHRRRRDKKOSLEKGPLSDMNGAPBSAAG 2086  
 QY 2230 QGSRPSPGVCYLR-----RRAPASDKOPSVSSPLDSTAASPKKDTLSL 2276  
 Db 2087 PGLPPEGEPTGCRERERROERGRSQERQPPSSSSSEKOFYSCDFGGRPEPKY- 2143  
 QY 2277 SGLSDPDMQDVLPLPHLSPPGADPSSASMAALKSPSTAASHNEAHL-PSVAGSD 2335  
 Db 2143 PLSLSHPTS-----PLAGOE--PGRPHQGSAYGR--PNTYCCRETSASBPPLA- 2190  
 QY 2336 DEONFRVYDKRTQPM-----SPCLREKGESESPWP--RLPTPG 2373  
 Db 2190 -----LELALTLTWSVMTVRPLSTPLCRTSLRSR-LMPTTRAPPG 2231

RESULT 9  
 ID R69604  
 AC R69604 standard; protein; 2270 AA.  
 DT 30-AUG-1995 (first entry)  
 DE Calcium channel alpha-1E subunit.  
 KW Calcium channel alpha-1E; h-alpha-1E; neuron; NX-HL.  
 OS Homo sapiens.  
 FX Key Location/Qualifiers  
 FT misc\_difference 2106 /note="not known"  
 PN MO9504144-A.  
 PD 09-FEB-1995.  
 PP 29-JUL-1994; U08589.  
 BR 30-JUL-1993; U5100740.  
 PA (NEUR-) NEUREX CORP.  
 PI Jell JR, Cong R, Hashimoto C, Horne WA, Palma A;  
 PI Philp M, Zhou M;  
 DR WPI; 95-082228/11.  
 DR N-PSDB; 083735.  
 PT New DNA encoding new alpha-1E subunit of neuronal calcium channel  
 PT - and related vectors and transformed eukaryotic cells, useful  
 PT for screening cpts. for ability to block calcium uptake in  
 PT neurons  
 PS Claim 2; Fig.1; 43pp; English.  
 CC Overlapping partial cDNA clones H24, H6, H2 and 3-69A were isolated  
 CC from a human hippocampus library using probes based on rat calcium

CC channel sequences. These overlapping clones were ligated to generate  
 CC a full-length cDNA, designated NX-HE1 (given in 083735), encoding a  
 CC 5th neuronal calcium channel alpha subunit, termed 1E or h-alpha-1E  
 CC (R69604). 1E was expressed in Xenopus oocytes and human embryonic  
 CC kidney HEK 293 cells.  
 SO Sequence 2270 AA;

Query Match 13.3% Score 1659; DB 1: Length 2270;  
 Best Local Similarity 23.7%; Pred. No. 7 6e-119;  
 Matches 621; Conservative 405; Mismatches 848; Indels 750; Gaps 92;

41 PGASDSEA-----EGLPYALA-----PY-----VFY 63  
 12 PGSGDGGDGRNRGTPVPASGQAAYKQTKAORARTMALNYPVRCNCTVNSLFL 71  
 64 LSQDSRSMCLRTVCNPFVFRVSMVYLINCVTLMFR--PCEDIDCSGCRILQAFD 121  
 72 FGEDNIVAKKAKKLIDPPEFYMLATITANCIVALEQLPEDDKTPMSRR--LEKTE 128  
 122 DEFAFEAVEMVVMKVALG-IFGKKCYLGDTNRLDEFFIYAGMLSEYSLDLO--VSFSA 178  
 129 PFYFGIFGFEFGKIVAGLGFIFHKGSLRNGMNMVDFIVLSGITLAGTHFHTVDLRT 188  
 179 VRYVAVLRPLAIRNVPMSRMLVTLTDLTQPLMGNVLLCFYFFIFGIYGVQLMGLLR 238  
 189 LRAVAVLRPLKIVSGIPSLQIVLKSIMKAMVPLQIGLLFFALIMPAIIGLEYSGKLH 248  
 239 NRCFLPEFSLPLVDLEPYQTENEDSEPFICSGPRENGMRCRSVPLTREGSGGPPC 298  
 249 RACEFNN-----SGILEGF-----DPPHPC-----GVQGC 273  
 299 SLDTETYNSSNTTCVNNQYITNCISAGENPFKGAINEFDNIGYAMIALFOVITLESWD 338  
 274 PAGE-----CKDM-----IGPNDGITQFDNILEAVLVEFCITMEGWT 313  
 339 IMYFMDA-HSYNFYITVILIIYSGFMINCLVATQSEKREHOSQMLRQVRF 417  
 314 VLYNTNDLGATMWMVLYPIIIIGSFVLYLVGLVSGEFAKEFER-----ENRAF 368  
 418 SNASTIASFSEPGSCYEELIKLYILKRAARLAQVSRAI-GYRAGLLSPVARSQEP 476  
 369 K-----LRQOQIERELNGYRAVIDKAEVMALEN 399  
 477 QPSGCTSRHRLSVHLYVHHHHHHHHYHNGTLRPRASPQLQDQDAGSRMLMP 536  
 400 KNAGSTALEVLRAT-----IKRSTGMTDSS----- 429  
 537 PPTPPSGPRPGASVHSFYHADCHLEPVRQAPRCPSPBAGRTVSGKYPTVHTS 596  
 429 ----- 429  
 597 PPEILKDALVEVAPSPGPTLTSENIPPGFSSMKLELTOSTGACHSSCKISSPCK 656  
 429 -----SVOTPLAR 444  
 657 AMSGACGPSCYCARCTAGBPESADHWMPDSSEAVYEFTDQAQSDLRDPHSRRQRS 716  
 445 ASIKSAKYGVASY-----FHKKE----- 463  
 717 LGDAPSSVLAFAWRLICDTPFKIYDSKYFGGIMAILVNTLSMGIEYHEQPELTNAL 776  
 463 -----RLKRISIRHMKSVFYWIIVLSVLANACALYHNNRPOQLTHLL 508  
 777 EISNIVTSLFALEMLKLLVGPFGYIKNPYNIDGVIVISWEIYQ-----QGGL 831  
 509 YYAEFLFLGFLLEMLKMGKMPRLYFHSFNCFEGVTGVSIREVVAIRPSTSGI 568  
 832 SVYKTRRLKRVLYKIVRELALOROLVLMKTDNVAFCMLMDFEFSIIGMLPGCK 891  
 569 SVYKTRRLKRVLYKIVRELALOROLVLMKTDNVAFCMLMDFEFSIIGMLPGCK 891  
 892 FASERDGTLPDRKNFDSILMAIVTFOILTOEDMKNVLYNGM-----ASTSSMAALYFI 946

629 F-NRNDG---TPSANFTFPALATVTFQILTGEDNMEVAMNGIRSGGVSSGMSALYFI 684  
 947 ALMTGNYVLEFNILVALIVEGF-OAEIRG---REDASQLSCIDLPVNSGGDATKSE 1001  
 685 VLLFGNTLLNVLALAVDNLANAQELTKDEQEEBAFNOKHAL-----QRAKEVSPW 738  
 1002 SEPDEFSPVDGDKRRKRLAL-----VALGEH--AEUKRSI----- 1037  
 739 SAPNM--PSIRDRRRRHMSMWEPRSSHLRERRRHMSVWEQRTSQLKHKMQMSQEA 796  
 1037 -----LPLIHTAAMP-----SLPKSSSTGVALGSG-----SRTSS 1072  
 797 LNRFAPTMNPINPLNPLSLNPLNHPSLYRRRATLGLALALEKFEERISRGSL 856  
 1073 SGSAEPGAHHHMKSPSPASSPHSASASWTSSRSRSLGRASL-----KRR 1124  
 857 KGDGDRSSALDNORTPLSLGOREPWLARPCGNCPTQOEAAGGSVYTFEDRARHQ 916  
 1125 SPSSGRRLSLGEGQEQ-----DEESSEDRASPAGSDHRRHG-----SLERE 1169  
 917 SQRSRHRRVRETEGESSASRSASOERSLDEAMPTGKDELAGNCAKEPTIOE 976  
 1170 AKSSFDLPDLQVPLHRTASGRSSAS-----EHQDNGKSASGRLA 1211  
 977 RQDRLRTNSLWNSGSLAGLDEADTPVLPHPLEVGKHVYLTEQDEGSSSEQALLG 1036  
 1212 R-----TLRD-----DPLDGG----- 1224  
 1037 NVQLDMGRVISOSEPLDLCITANDKATTESTSVTAIPDVDPVLDSTVHISKTGGEA 1096  
 1224 -----DDNDEGNLSKGERLOAWVRSRLPACCRERDSWAIYFPPOSRELLCHR 1273  
 1097 SPLKAELEIREDEEVEKKKKKKRETEG-KAMVPHS-----SMFESTNPTRRACHY 1148  
 1274 ITHKMFEDHVLVLIIFLNCITIAMERPKIDPSAERIFLTNSITFAVAFLEMTVAYA 1333  
 1149 IYNLRYFEMCILLVIAASIALAEDPVLITNSERKV-LRFEYVFTGTFVFEVIMKID 1207  
 1334 LMCQGEQAYLSSNNVLDGLVILSVYDI-LVSVOSGSKILGMLRVLLRLTLPRL 1392  
 1208 QGLIIDGSIYFDNMTLDEVVYVGVALVAFALANLGNKGRDITKISLVAVLRLK 1267  
 1393 VISRAQGLVETIMSSLRKIGNIVICAFIIFGLIGVQLEKGFVC--QGEDTRN 1450  
 1268 TIKRLPKLKAAYDQVYTLKVENILIIYVLFMFIAVIAVOLFEGKFFYCTDSKDTK 1327  
 1451 -----ITKSDCAEASR-WVRHKYNDNLGOALMSLFVLASKRGWDIVDGLAVGV 1503  
 1328 ECIGNYVDHEKKMKMEYKGRHEHNDNIITALLTLFTVSTGGMPOVLOHSYDTEE 1387  
 1504 DOQPINHNPMLLPIISFLIYAFVLMFVGVVENEHCKROHEEBAARRREKRLR 1563  
 1388 DRGFSNNHMSIFVYVYVFFVFIYFALLIIF-----QGGKMKMECSLE 1440  
 1564 RLEKRRNMLMDVITASGSSASASEAQCKPYSDYSR--FLVYHHLCTSHYDLFTG 1621  
 1441 KNER-----ACIDFAISAOPLTRYMPQNRRTFQYRWVHEVVSPEYTIMA 1486  
 1622 VTGLNVTAMENHYQPOLDEMLKICNYITVIVFESEVFLVAFGFRFPODMNOLD 1681  
 1487 MIALNTVLMKKYSAPCYEALKTNLIAFWVSLECVLVIAFGFLNFRDWNIFD 1546  
 1682 LAIVLSTIMGITLEEIEVNASLPINPIIRIKRVLIARVLLKLMVAGMRALLDTVQA 1741  
 1547 FTYIGSITPIIILTDKLVNTSGFNNMSFLKFLRA--ALIKILRGQYIRILLWTPOVS 1603  
 1742 LPQVNGILFMFLFTIYALGVLEFGDLECD-ETHPCGGLGRHATFRFGAFLITFRV 1800  
 1604 FKALPYCLLIAMLEFTYALIGOVGNIKLDESH-----INKHNNFRSFFSMLLFRS 1659  
 1801 STGDNMNGIKMDL--RDCQESTC-----YNTVISPIFYFVSFVTLTAQVLANVY 1849

DB 1660 ATGEAMQEIIMLSCLGEKCEPDPTAPSGQENNERGCTDLAVVYFVSIFFCSLMLNLFV 1719  
 QY 1850 AVLMKHLESNKKEAK-----EEAELEALE-----LEMKTL-SPOPHSPL 1888  
 DB 1720 AVIMDNFEYLTRDSSILCPHILDEFVWMAEYDRAACGRHYTEMVMTLMSPL---PL 1775  
 QY 1889 G-----SPLFMPGVEGVNSP-----DSPKPGAPHTAHIGAAG-----FSL 1925  
 DB 1776 GLGRKCPKSVAVAKRLVLMNMPVADMTVHFTSLMALIRLADIKAKGAGDROQDSEL 1835  
 QY 1926 EHPITWV--PHPE-----VPPGLPDLITYRKSGVSTHSLPDSWMCNRSIAENSIG 1977  
 DB 1836 QKETAIWPHLSQKMLDLVMPKASD-LTVGKITYAA--WMINDYKOSKKORQOL- 1891  
 QY 1978 HNGMGLPRAQSGSILSVHSGPADTSCILQLPKV-----HYLLQPHGAPTWGALPKLP 2030  
 DB 1891 -----EQQKAPMPFQWMPDS-----SLPQELIANAKALPYLDQD---PVSGLSGRG 1934  
 QY 2031 PGRGSPLAORPLRQOAIKRTDSLVDYQIGSREDLSEYSGFSCPL-----TRSSSFV 2082  
 DB 1935 YPSMSPPLSPQDIFQIACM--DPTDGGQFQERQSLV--VTDSSMRKSFSTIRKRSNSW 1990  
 QY 2083 -----GGSSIOVOORSGIOS-KVSKHTRLPAPCPGLEPSPWAKDPETRSLENDTE 2132  
 DB 1991 LEFEMERSESEVTKSRRSYHSSLRLSAH-RL-----NSDSGHKSDTH 2033  
 QY 2133 LSWIGDILLPSQEEP--LSPDLKKCYSVETOSCRRRPGSWLDEQRHSHIANSCLDSGS 2190  
 DB 2034 RS--GGERGRKEREKHLSP-DVSRCNSE-----RGTQADWESPERRQS----- 2077  
 QY 2191 QRLCPSPSSLGQPLGPGSRPKKLLSPSIS--IDPPESQSGRPPCSPG-----VC 2241  
 DB 2077 -----RSPBEGRSQIPNNQGTGSLSESSIFSVSDKSTPRRRLDLPVPPKPRRLSYSS 2131  
 QY 2242 LRRRA-----PASDKDVSVPPLDSTAASPKKDLISGLSSDPTDMDPVLPLPHH 2296  
 DB 2132 LRRHAGSISPPADGSEE--GSPILTQAL-----ESNNACLTESSNSRH-----PQOSQH 2178  
 QY 2297 LSPPGADPSSASMAFLKSPFASGHEAPHLPSVAGGDQNF 2340  
 DB 2179 ASP-----QRYISEPYLA-LHEDSH--ASDQGEHEITLT 2209

RESULT 10  
 ID R71009 standard; Protein: 2251 AA.  
 AC R71009;  
 DT 01-DEC-1995 (first entry)  
 DE Human neuronal calcium channel subunit alpha 1E-1.  
 KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 OS Lambert Eaton Syndrome.  
 KW Homo sapiens.  
 PN WO9504822-A.  
 PD 16-FEB-1995.  
 PE 11-AUG-1994: U09230.  
 PR 11-AUG-1993: US-105536.  
 PR 05-NOV-1993: US-149097.  
 PA (SAK) SAK INST BIOTECHNOLOGY IND ASSOC.  
 PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME,  
 DR WPI: 95-090900/12.  
 DR N-PSDB: Q84662.  
 PT DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 PS Claim 34; Page 201-211: 283pp; English.  
 CC DNA encoding alpha 1E human calcium channel subunits have  
 CC been isolated from an oligo dT-primed human hippocampus  
 CC library. The resulting clones, which are splice variants,  
 CC were designated alpha 1E-1 and alpha 1E-3. These splice variants  
 CC differ by virtue of a 57 bp insert in 1E-3. Alpha 1E-1 has  
 CC a calculated mol. wt. of 254,836 and alpha 1E-3 has a calculated  
 CC mol. wt. of 227,348. Alpha 1E-3 has a 19 AA insert relative to  
 CC alpha 1E-1 in the region that appears to be the cytoplasmic loop

CC between transmembrane domains 11S6 and 11S1.  
 SO Sequence 2251 AA.

Query Match 13.3%; Score 1653.5; DB 1: Length 2251;  
 Best Local Similarity 24.0%; Pred. No. 2e-118;  
 Identities 625; Conservative 396; Mismatches 835; Indels 751; Gaps 94;

QY 41 PGSDSEK-----EGLPYPALA-----PV-----VFEY 63  
 DB 12 PGSDGSDSDSRNNGTTPVPSGQAAYKOTKQARATMALNPIRYRNCFTVNRSLFI 71  
 QY 64 LSQSRPSMCLRTVCNPFWEVSMVLINCVLTGFR--PCEDTADCSQCRILQAFD 121  
 DB 72 FGEDIYAKYKAKLIDMPPEYMIATIIANCIVLALEQHLPEDDKTPMSRR--LEKTE 128  
 QY 122 DFIFAFVENVVAVALG--IFGKKYLGDTMRRLDPEFIYAGMLEYSIDLQ--VSFGA 178  
 DB 129 PYFICIFEFEGIKIVALGTFHKGSTLRNGWVMDFIYVLSGLTAFGTHTHYDLRT 188  
 QY 179 VRTVRLRLPAIRVPSMRILVTLDDLPLMDGNVLLCFEVEFTFIVGQVMAGLLR 238  
 DB 189 LRAVAVRLPLVIGSIPSLQIVLKSKAMVPLQIGLILFEFALIMFAITIGLEFYSGKH 248  
 QY 239 NRCPLFENFSLPLSVLDLEPYVOTENEDSPFICQPRENMRCSRVPPLRREGGGGPC 298  
 DB 249 RACEFNN-----SGILEGF-----DPPHC-----GVQGC 273  
 QY 299 SLDEYTVSSNTTCVMMNOYTTNCSAGEHNPFGAINEFNIGYAIAYVITTEGVWD 358  
 DB 274 PAYGE-----CKDM-----IGPDGITQFDNLIIFAVLTFFOCITMGWT 313  
 QY 359 IMYFMDA-HSYNFIYFILLIIVGSEFMNLCLVIAIYVIAVFOSTKRESQLREQVRL 417  
 DB 314 VLVNTNDLGLTMMWLTIFPLIIGSFVLNVLVGLVSGFAERVR-----ENRRAM 368  
 QY 418 SNASTIASFSPGSCYBELLYVYLIRKARLAQVSRAT-GVRAGLLSPYARSQGP 476  
 DB 369 K-----LRQOQIERLNGYRAMWIDKAEVMAEEN 399  
 QY 477 QPSGCTSHRLSVHNLVHHHHHHHNGTLRVAPASIEDDRANGSRRLMLP 536  
 DB 400 KNAGTSALEVLRRAT-----IKRSITEAMTRDS----- 429  
 QY 537 PSTPSPGPPGAEVSHSEFYHADCHLEPVRCQAPPSPGSAGRVSGKYPTVHTS 596  
 DB 429 ----- 429  
 QY 597 PPPELTKALVEVAPSGPPTLTSENIPPGPPSMKLLLETOSTACHSSCKISSPCK 656  
 DB 429 -----DEHCVDIS-----SVGTPLAR 444  
 QY 657 ADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVEFTQAOQSDLRDPSRRQRS 716  
 DB 445 ASIKAKVDGVY-----FRKFE----- 463  
 QY 717 LGPDAEPSSVLAFWPLICDIFRKTVDSKYRGIMAILVNTLSKGIETHEDPELTNAL 776  
 DB 463 -----RLLRISIRHAKVQVFWYIVLSVALNATCAVAIVHNDPOWMLTHLL 508  
 QY 777 ELSNVEFSLFALEMLKLAVYGFYIKPNYNIPDGVIVIVVWEVYQG-----QGGGL 831  
 DB 509 YVAEFLFGLLLEMSLKMGMGRPLFHSFPCDFGCVGVSIFEVVAIFPGISFPI 568  
 QY 832 SVLRTFLMRVLKLVRELPAIQVLVLMKTMNVATFCMLMLFIFISILGMHLEGK 891  
 DB 569 SVLRALRLRLRFLTKYASLRNLVYVLSMSKSIISLLEFLTFVALLQMQLFGR 628  
 QY 892 FASEDGTDLDRKNPDSILMAIYTFQILTDPMNKNVLENGW-----ASTSSNALYPI 946  
 DB 629 F-NFMDG---TPSANFDTFPAINTVQIITGEDMNEVMYNGIRSGGVSSGMSMAIYI 684  
 QY 947 ALMTFGNVLENLVAILVEGF-QAEETIGK---REDASGQLSCIQLPVNSOGGATKSE 1001



Query Match 13.3%; Score 1653; DB 1; Length 2270;  
Best Local Similarity 23.8%; Pred. No. 2, 2e-118;  
Matches 626; Conservative 399; Mismatches 832; Indels 766; Gaps 95;

QY 41 PGASDSEA-----EGLPYALA-----PV-----VFY 63  
DB 12 PGSGDDGSDSRNRROGPPASGOAAAYKOTKQARATMALNPIVRNCFVNRSLFI 71  
QY 64 LSODSRPSRCLRTVCNPMFERVSMVLILNCTLMFR--PCEDJACDSQRRIQAD 121  
DB 72 FGEDNIVKRAKAKLIDMPPEYMITATIANCTIVLAEHQLPEDDTSPSR--LEKTE 128  
QY 122 DLFPAFVEMVYKVALG-IFGKCYLGDVTNRDLDFYIAGMLEYSIDLQ--VSFSA 178  
DB 129 PYIGIFCFEAGIKIYALGIFHKSYLRNGMVMDFIYVLSILATAGTHTHTDLFT 188  
QY 179 VRVVRVLRPLRAINRPSARILVTLTLLDPLMLGNVLLCFEYFIFGIYVQVLAAGLR 238  
DB 189 LRAVRVLRPLKLVSGIPSLQIYLSIKMAVPLQIGLLFFAILMFAITIGLEFYSGLH 248  
QY 239 NRCFLPENFSLPLVDLEPYOTENEDESPICSOPIRENGMSCRSVPLRGGGGPC 298  
DB 249 RACFMNN-----SGILBEF-----DPPHC-----GVQGC 273  
QY 299 SLDYETYNSSNTCVNMNQYITNCAGEHNPFGAINDNIGYMAIAFOYITLEGWD 358  
DB 274 PAYE-----CKDM-----IGPNDGITGDNLFLAVLYFOGITMEGWT 313  
QY 359 IMFYVMDA-HSFYNYFETLLIIVGSEFMINCLVIANQSETORESQMLREORVRL 417  
DB 314 VLTNNDALGATNMVLIPLIITIGSEFVNLVLGVLSEEFKABERY--ENRRFAM 368  
QY 418 SNASTLASESEPGSEYELLKYLVLIRKARLAQVSRAI-GVRAGLLSPVARSQEP 476  
DB 369 K-----LRQOQIEELNGYAMIDKAEVLAEN 399  
QY 477 QSGGSTRHRLSVHHLVHHHHHHHHYHLNGTLRVPASPEIODRANGSRRLMP 536  
DB 400 KAGISALEVLRAT-----IKSRTEAMTRDS-- 429  
QY 537 PSTPSPSGPPGASVHSFYHADCHLEPRVQARP RPSPASRTYSGSVYTVHTS 596  
DB 429 ----- 429  
QY 597 PPEELDKALVEVAPSPGPTLTSENIIPGPFSSMHKLLTOSTGACHSCKISSPCK 656  
DB 429 -----DEHCYDIS-----SVGTPLAR 444  
QY 657 ADSGAGPDSYCARGTAGBPESADHWMPDSSEAVIEFTODAOHSLDRPHSRORS 716  
DB 445 ASIKSAKVDGVS-----FRHKE----- 463  
QY 717 LGPDAPSSVLAFLRICDTFRKIVDSKYFGKIMATILVNTLSGICLYHEOPETMAL 776  
DB 463 -----RLNLSIRHMKSOYFVIYIVSLVALNACVAVIHHNOPOMLTHL 508  
QY 777 ELSNIVETSLFALEMLKLVYGPFGYIKNPYNIFDGIYIVISWEIYGO-----QGGL 831  
DB 509 YVAEFLFGLFLEMSLKMVGWGRPLYPHSSFNCFDVGISFEVYVMAIFRPGTSGI 568  
QY 832 SVLRTEFLRMVRLKIVRELPAJOROLVLMKTMDNATCMMLMFIFFSLGHMLGCK 891  
DB 569 SVLRRLRLRIFKIKTKYASLRNVLVSSMKSTISLLFLFIFVIFALGLQGLGGR 628  
QY 892 FASERDGTLPDRKNDLSLMAIVVFOILTQEDNKNVLYNGM-----ASTSSNAALYFI 946  
DB 629 F-FENDG---PSPANFOPPAIMIVFOILTGEDMNEVMYNGISOGGVSSGMSALYFI 684  
QY 947 ALMTGNVNLVNLVAILVEGF-QAEIEGK---REDASGOLSCITQLPVNSOGGDATKSE 1001  
DB 685 VLTGENTTLNLVLAIVDLNLANAQLTKEOEFEAFNOKHAL-----QKAKEVSPM 738  
QY 1002 SEPFFSVDGDDGRKRRLA-----VALGEH--AEIKRSL----- 1037

DB 739 SAPNM--PSIERDRRRRRHSMWEPSSHLRERRRRHHMSWEDRTISQLRKHMQSSQEA 796  
QY 1037 -----LPLLIHTATPM-----SLPKSSSTGVGALSG-----SRTSS 1072  
DB 797 LNREAPITMNLNLNPLSSLNPLNANPSLYRRPRALEGALGLAEKEFEERISRGSL 856  
QY 1073 SGSAEPGAHHEKSPSARSSPHSPWSA-----ASSWT 1106  
DB 857 KGDGDRSSALDNOPTLSIGOREPWLARPCGNCDPQOEAAGGEAVYTFEDRARHRQ 916  
QY 1107 SRSRNSLGR-----APSLKRSPSGERSL--LSGEOEOD-----EESSEED 1151  
DB 917 SQRSRHRVTEKESSSASRSASQERSLDEAMTEBEKHEIRGNHGAEPITQEE 976  
QY 1152 RASPADSHRHGSLEREANSF-----DLBDTLOVPLHRTASGRSSASEHOCNGK 1204  
DB 977 RA-----ODLRITNLAMVSRGSLAGLDEADTPLYLPHLE---VGNHYVLEQEPGS 1029  
QY 1205 SASGRLAR-----TLRTD-----DPOLDG----- 1224  
DB 1030 SEQALLGNVOLDMGRVISOSEPLDSCITANTDKATTESTSVTVAIPDVPLDVSIVHTS 1089  
QY 1224 -----DDNDEGNLSKGERIOAWRSRLPACCRERDSVAIFPPQR 1266  
DB 1090 NKTGEGASPLKEAIRDEDEVEKKKKKKRETG-KANVPHS-----SMFESTNP 1141  
QY 1267 FRLLCHRIITHKMDHVVLIIFLNCITIMERPKIDPHSAERIFLISYITAVFLAE 1326  
DB 1142 IRRACHYIVLRJFEMCILLVIAASSTIALAEDPVLNSERNV-LRYDYVTFGTFTTE 1200  
QY 1327 MTYVVALMGCFGQALRSRNVLDGLVLISYIDI-LYSWVSDSGTILGLMRYLRL 1385  
DB 1201 VTIKMDQGLIDGSEFRLMNLIDFVVVGVALVAFALAMALGTNKRDKIKISLRLV 1260  
QY 1386 RTRPLRIVISAAGLKLVLVETLMSLKPIGNIVICAFPIIGLIGVOLFNGKEPVC-- 1444  
DB 1261 RVLRPLKTIKRLPKIAVEFCVYTSIKVFNILIVKLMFIFAVIAYDLFGKFFCTD 1320  
QY 1444 QGEDTN-----ITNKSCEASYSR-WVRHKYFNDLQALMSLVLASKDWVIMYD 1496  
DB 1321 SSKTEKECIGNYVDHEKNMEYKGRMKRHEPHYDNIIMALLTFTVSTGGMQVLOH 1380  
QY 1497 GLDAVGYDOOPIMNHPMMLYFISFLIYAFVLYMFGVYVENHKKRODEEBEAR 1556  
DB 1381 SDVTEEDRGPSNRNEMSIFFVYFVVPFFVNIIFALLIITF-----OEGDKM 1433  
QY 1557 REBKRLRLKRRRNLMLDVLASGSASASEACKPY--YSYSR--FRLLVHHLTS 1612  
DB 1434 MECSL-----EKNERACIDPAISA-----KPLIRMPQNRHTFOYRWVHFWVS 1477  
QY 1613 HYIDLFTYIGLVNTVAMERTYQOPOLDEALKICNYITFVIFVESYFKLVAGFRFR 1672  
DB 1478 PSFEYTIMAIALNTVLMKKYSAFCYELALKYLNIAFTWFSLECVIYARGFLMY 1537  
QY 1673 FODRMNOLDLAIYLSIMGITLEEIVNASLPIINPIIRIMVLAIRAKTLKLAAGMR 1732  
DB 1538 FRTWNIIFPFIYIGSITEILITDSKLVTSFGRNMSFLERFA---ARIKLRGQYTR 1594  
QY 1733 ALLDVWQALPOYNGLLFMLEFFLFAALGVELFGDLECD-ETHPCBGLGHAFRRNG 1791  
DB 1595 ILLMTVQSEFKALPYCLLIAMLEFIYALIGNQVGNIRKLBESH---INHNHFRREF 1650  
QY 1792 MAFLEFRVSTGDNNGIKDYL--RDQOESTC-----YNTVISPIYVSFVLA 1840  
DB 1651 GSLMLFRSATBEAWOELMSCLGKCEPDTTAPSGONENERCOTDLAYVYFVSIFFC 1710  
QY 1841 QEVLVNVAVIYLMKHLSESNKAK-----EBAELEALE-----LEMKTL 1880  
DB 1711 SFLMLNLFAVAVIMDNFVYLTROSSILGPHHLEDEFYVVAEFDRAACGAIHTTEMETLTL 1770  
QY 1881 -SFQPHSLG-----SPLMPGEGVNSP-----DSKPGAPHTTAHGAASG-- 1923

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Db 1771 MSP-----PLGLGRCPSPKVAKKRLVLMNPFVADMTVHFTSLMALIRALDIKIAKGA 1826
QY 1923 -----FSLHPIMV--PHREE-----VPVPGPDLITVRKSGVSRTRSLPNDSYMGN 1968
Db 1827 DROOLSELCKETLAIWPHLSOKMDLLVMPKASD-LIVGKITYA---MMIMDYKQSK 1882
QY 1969 GSTAERSLGRHGMGLPKAQSGLSVHSQPADTSCILQPKDV-----HYLQPHGAP 2021
Db 1883 VKKORQOL-----EECKNAPVFORMEPS-----SLQEITIANAKALPYLOQD---P 1925
QY 2022 TWGAIPKLPPGSPPLAQRRLRQAARTSDSLDVGIGSREDLSIVSGPSCCL----- 2076
Db 1926 VSGISGSGYPSMSPLSPDIFQLACM--DPADGGQFERQSLV--VTDPSMKRRSFSTI 1981
QY 2076 --TRSSFFMGSSIOVQORSGIOSKVKHTRLPAPCGLEPSNAKDPPTETRSLELDT-E 2132
Db 1982 RDKRSNSM-----LEEFWMERS-----ENTYKSRRSYHSSLRLSAR 2021
QY 2133 LSWISG---DLIPSSQEP-----LSPRDLKICYETOSCRRRRPSWIDEQRHS 2180
Db 2022 LNSDGHKSDTHPSGGERRRKSKERKHLSP-DVSRCSNSEE---RGTQADWESPERRQS 2076
QY 2181 IAVSCLDSGSPRLCPSPSSIGGQPLGPGSRPKKTLSPSIS--IDPEESQGRPPCSP 2238
Db 2077 -----RSPSEGRSQTPNKRGTSISESITPSVSTSTPRKSRQLPPVP 2121
QY 2239 G-----VCLRRRA-----PASDKDPVSSPLDSTPAASPPKDTLSIGLSDPTDM 2286
Db 2122 KPRPLLSYSSLIHAGSISPPADGSEE---GSPLTSQL-----ESNNAMLTSSNSPH-- 2173
QY 2287 DPVLPITLPHLSPPGADPSSASMAFLKSPTAASHAPHLPSV 2331
Db 2173 ---PQOROHASP-----QRYISEPYLA-LHEDSHASDCV 2202

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FT modified_site 1854
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PN US618720-4
PD 08-APR-1997
PE 04-APR-1988; 176899
PR 04-APR-1988; US-176899
PR 04-APR-1989; WO-001408
PR 04-APR-1989; US-603751
PR 13-JUL-1992; US-914231
PR 28-SEP-1994; US-314083
PR 15-FEB-1995; US-404354
PA (SIBI-) SIBIA NEUROSCIENCES INC.
PI Brenner R, Ellis SB, Harpold NM, Sartor J, Schwartz A;
PI Williams ME;
DR MPI: 97-225431/20.
DR N-PSDB: T70228
PT Eukaryotic cell expressing heterologous calcium channel - comprising
PT alpha-1 and alpha-2 subunits; used in drug screening assays
PS Claim 3; Column 17-30; 50pp; English.
CC This sequence represents the rabbit skeletal muscle calcium channel
CC alpha-1 subunit. This protein comprises twenty-four potential
CC transmembrane regions and has a molecular weight of 212143. The
CC protein contains four internal repeated segments. Each repeat
CC comprises five hydrophobic segments and one segment with strong
CC positive charge. The alpha-1 protein lacks a hydrophobic amino
CC terminal sequence characteristic of a signal peptide and it is
CC thought that the four internal repeats represent the 24 transmembrane
CC segments and that the N- and C-terminal are extracellular. This
CC sequence may be used, in conjunction with the alpha-2 subunit coding
CC sequence (see also T70227) to transform a eukaryotic cell. The cell
CC may be used optionally with a reporter gene, in screening assays for

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CC Ca2+ channel agonists or antagonists.  
SQ Sequence 1873 AA;

Query Match 12.9%: Score 1608.5; DB 1; Length 1873;  
Best Local Similarity 23.6%: Pred. No. 4,5a-115;  
Matches 577: Conservative 356; Mismatches 692; Indels 823; Gaps 82;

QY 32 QGPSTKDPGADSEAGLPPALAPVFFYLSODSPRSMCLRTQCNPM--FEERYSM 89  
DB 7 QDEGLRKKQPKKPLPEV--LPRP--PALFCILQNPRLKACISY--EMKPEFTILL 59  
QY 90 VILLNCVTLGMFRPC-EDIADSORCRI-LQAPDFLPAFAVEMVVMVALG-IFGKKC 146  
DB 60 TIFANCVALAVLPMPEP---DNNSLNGLERLEFFELTFVSIAMAKITAYGFLFHODA 116  
QY 147 YLGDVWNRLDFFIVAGMLEYSLDQNY-----SFSVATRYVRLPRLAI 191  
DB 117 YLRSGMNVLDFTIVLGVFTALIEGVNYIQSNTAPMSKAGLDYKALRAFRVLRPLRV 176  
QY 192 NRPVSMRLVTLDDTLPMGLNVLLCFEVEFFIGVGVOLMAGLLRNRCFLPENESLPL 251  
DB 177 SGPVSLQVNLNIFKAMPLFHIALVLFVNYIYAIIGLELFKGMKTKCY----- 229  
QY 252 SYDLRPYQTEDESPRIGSOPRENGRSCRSVPILRGEGGGPCCSLDYEYNSST 311  
DB 229 -IGDIVATVENKPS--CART-----GSGRPC---TINGS-- 260  
QY 312 TCVMNQYTYNCSAGENHPKGAINEFNIGYAMIAFOVITLEGVMDIMFYMDA--HSFY 370  
DB 260 -----ECRGMPGNHGITHEFDMFGFMSLVYOCITMEGMDVLYWVDAIGNEM 309  
QY 371 NFITYELLIVGSEPMINCLVYIATQSEFTRKORESOQMRQRARFLSNSTLASFEPPG 430  
DB 310 PWITYVTLISGFILVNLVLSGF--TKERKAKSR-----GTQOKLEKO 357  
QY 431 SCYEELLVYILKRAARLAOYSRAIGVAGLISFVARSQEPQSPGSCSTRSHRLS 490  
DB 358 QLEEDLRGYSWITQ-----GEVMDVEDLRGKLS----- 388  
QY 491 VHHLVVHHHHHHHNLGTLRVPRASPELQDDANGSRRLMPPSTPRPSGPPRGA 550  
DB 388 -----LEEGG----- 393  
QY 551 ESHVSYHADCHLEPRCOAPRRPCSEASGRVYGKVPYVHTSPPEILKOKALVEY 610  
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DB 393 -----SDTESIVEIEGLNKIIQIFIR----- 414  
QY 725 SYLAWRLICDFFR---KIYDSKTFEGRGIMAILVNTLSGCIYHNOPELINALETISN 760  
DB 414 -----WROMNRYFRWKCHDLVKSRYFVWLVILIALNLTLSASHHNOPLMLTHLQDIAN 468  
QY 781 IYFTSLFALFEMLLKLLVYGPFGYIKNPYNIDGVIVAVISVEIYGOOGG-----GLSVLR 835  
DB 469 RVLTLFTIEMLLKMYGGLGKQYFMSIFNRDPDFCVYCGIIEILLVSGAMTPLGIGIVLR 528  
QY 836 TFLRLRVKLVRFPALORQOLVYLMKIMONVATFCMLMFIIFSLIGHLEKCFASE 895  
DB 529 CIRLRLRFRKIRKYMTSLNVLASLNSIRSIASLLLLFLFIIFALIGMOLFEGGRDFE 588  
QY 896 RDDDTLPKRNKNSLMAIVYFOILTOEDMNKVLVNMSTASS-----WAALYATLM 949  
DB 589 ---DIEVRSRNDNFPQALLISIVFOVLTGEDMNSVYKNGIMAYGSPSPGVLCYTFIILF 645  
QY 950 TFGNVLENLVALIVEGP-QAEIGKREDASGOLSCITQLPVNSQGDATKSESEPDFFS 1008

DB 646 VCGNVILLNVLALAVDNLAELAEGL-----TSQXKAKAE----- 680  
QY 1009 PSYDGDGRKKRLALVALGAEALRKSLLPPLLIHTRATMSLPKSSSTGVGEALGSGSR 1068  
DB 680 -----ERRKRRKMSRGIPDTEEEKSV----- 702  
QY 1069 RTSSSGSAEPGAHHEMKSPSARSSPHSPWSAASWTSRSSRNSLGRAPSLKRSPSG 1128  
DB 702 -----AKRIEOK-PRG 711  
QY 1129 ERSLLSGEGQODEEESSEEDRASPAGSDRRHRSGLERKASSFDLPDTLOVPELHRT 1188  
DB 712 EG---IPTTALKYDEEESNVNEVKDP-----YPSADFP----- 743  
QY 1189 ASGRSSASEHQQCKNGKASGRILARTDDPOLDGGDDNDNEGMLSGERGIOAWVRSLPA 1248  
DB 743 -----GDDEDEPEPIVSPRRPRLAEIQL-- 767  
QY 1249 CCRER---DSWSAYIFPPQSRFLCHRIITHKMFHVAVLIIFLNCITIAMERPKID 1303  
DB 767 --KERAVYIPASSFFIFSPNKRVYCHRIYVAVWFTNFIILFILLSAALAE-----D 820  
QY 1304 PHSARIFLTSNYI---TAVFLAEMTVKVVVALGMCFOGQALBSMNVYDGLVLLISV 1360  
DB 821 PIRASVANOILGFDIAFTISVFEVLYLKMITYGAFLHKGSCFRNYFNILLDLYVAAS- 880  
QY 1361 IDLVSNVSDSGTKILGMLRVLLRLTLRPLRVISRAOGLIVETLMSSLRKIGNIVI 1420  
DB 880 ---LISMLESST--ISVYKILRVLRPLRALINRAKGLKHVQCVFAIRIGIVLV 934  
QY 1421 CCARFIILGIVOLFPGKFPVOCGEDTNTITKSCAEASY-----RNV 1465  
DB 935 TTLDFMFACTGVDFEKGKFPSC--NLSKMT--EEBRGYIYYIKQGDPTOMELRRQMT 991  
QY 1466 RHKYNEFNLGALMSLFVLVASKDGVMDIMYDGLDAVQDQPLMNHNPWMLLYFISFLI 1525  
DB 992 HNDFFHDVNLASMSLFTVSFEQMPQLLYRAIDSNEDMGVYNNRVEMAKIFIIYIL 1051  
QY 1526 VAFVLMNFVGVVENHKKQHOEEEARREKRLRLERKRRMLMDVYVASSSSAS 1585  
DB 1052 IAFEMNIEFVGIATV--OEGETEYKNC-----LDKNOROCV-----OVAL 1093  
QY 1586 AASEACKPYYSYSRFLVYHNLCTSHYDLFTIGVIGLVNTYMAEHYQOPLIDEAL 1645  
DB 1094 KARPLRC---YIPKNPYQYVYVVISYFEYLMFALMINTICLOMHHQSEENHHS 1150  
QY 1646 KICNITFVIFVESYKLVAFGRREFQDRWQDLAIYLLSIMGITLDEIV----- 1700  
DB 1151 DILNVAFTIIFTEMLIKLAFKARGYFGDPWVVFELVIGSIIDVILSEIDTFLASSG 1210  
QY 1700 -----NASLIPNFIIRVRLARVYLKLLKMAVGNRALDITVM---OAL 1742  
DB 1211 GLYCGGGCGGVNDDESGARISSAFFRLFRVRL---IKLSRABGVRTLLIKSFQAL 1267  
QY 1743 POGVNLGLFMLLFTFPAALGVELGDLF-CDETHPCEGLGRATRFNGMAFLIFRVS 1801  
DB 1268 PYV---ALLIYMLFFIYAVIGMOMFGKIALVDGTO-----INRNNNQCTFOVALLEFRC 1320  
QY 1802 TGDMMNGIMKDTL--RODDOES-----TCYNTVISPISYFPLTQFOVYVNVAV 1851  
DB 1321 TGEAMOEILLACSGKICDPSDPAPEEYTC--GTNAYYIFISFIMLCAFLINIFAV 1379  
QY 1852 LM-----KHLESNKKEAEALAEAE--LELEMKTLSPQSPSLGSPFL 1893  
DB 1380 IMDNEDVLTDRMSLIGPHNIDEF-KAIIWAEYDEBAGRIKHLNVLVLLRIORPLGFGFK 1438  
QY 1894 WP-----GVEGVNSP-----DSPKPGAPHTAHIGAAGSFLEHP----- 1929  
DB 1439 CPHRACARLVGMMPPLNSDGTVFNATLFAVRLAKITBENEFQANDELRALITKKT 1498  
QY 1929 --TWVPHREVPVPLGDDLLTVKRSVSRTHSLPNDSYMCRNGNSTAERSLGHRCWGLPRA 1986

Db 1499 KRTSMKLLDQVIPPIDGDEVTVGKFATFLIOEHFRKFMKQ---EEYGYR---PRK 1550  
 QY 1987 QS---GSLISVHSQPA-----DTSCLDLPKDVHLLQPHGAPTWGAIPLKLPBG 2033  
 Db 1551 DYOIOAGLNTIEEAAPEIRRTISGDLTAEELERM-----V 1589  
 QY 2034 RSLPACRPLRROAAI-----RTDSTL-----DVQGLGSRDLISEVSGP----- 2072  
 Db 1590 EAAEENHIFRTGTGLFGQVDTFLERTNSLPPVANQRPLOFAEIEHEELESFVLEDFPQ 1649  
 QY 2072 ---SCLTRSSSWGSSSIQV---QQRGSIQSKYKHLRLPAPCGLEPSAKPPEPTRSS 2126  
 Db 1650 DARTNPPLARANTNANNAVYAGNSNHNQMFSSV-----CEREPGEAEIIPAAGRGA 1703  
 QY 2127 LELDTLSWISGDLTPSSOEPLSPRDLKCYSEVOTSCRRRPGSWLDEQRHSHIAVSCI 2186  
 Db 1704 L-----SHSHALGPHS-KPC-AGKLNGQLVOPGMPINQ----- 1736  
 QY 2187 DSGQPLCPSPSSLGQPLGPGSPKRLKS-PPSISTIPPE---SQSRPCSPGVCL 2242  
 Db 1736 ---APAPACQPPST-----DPERGQRTSLNGSLQDEAPORRSSEGSTP----- 1778  
 QY 2243 RRRAPASD--SKDPSVSPIDSTAASPKKDTLSGLSSDPDMDP 2288  
 Db 1778 RRPAPATLLIOEALVGRGLDTLAADAG---FVWATSOALVDACQMP 1822

## RESULT 13

W37711  
 ID W37711 standard; Protein; 1873 AA.  
 AC W37711;  
 DT 10-MAR-1998 (first entry)  
 DE Rabbit skeletal calcium channel alpha-1 subunit.  
 KW Rabbit; skeletal; calcium channel alpha-1 subunit; hybridisation;  
 OS Oryctolagus cuniculus.  
 PN US5686241-A.  
 PD 11-NOV-1997.  
 PF 28-SEP-1994; 314083.  
 PR 08-NOV-1990; US-603751.  
 PR 04-APR-1988; US-176899.  
 PR 13-JUL-1989; WO-001408.  
 PR 13-JUL-1982; US-914231.  
 PR 28-SEP-1994; US-314083.  
 PA (SIBI) SIBIA NEUROSCIENCES INC.  
 PI Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;  
 DR WPI; 97-558134/51.  
 DR N-PDB; T96811.  
 PT Oligonucleotide probes - for identifying calcium channel alpha-2  
 subunits.  
 PS Disclosure: fig 1A-J; 44pp. English.  
 CC This is a rabbit skeletal muscle calcium channel alpha-1 subunit.  
 CC The DNA sequences of the alpha-2 subunit (rabbit and human -  
 CC see T96812-13) are useful as hybridisation probes for identifying nucleic  
 CC acids encoding all or part of a calcium channel alpha-2 subunit. Certain  
 CC diseases, e.g. Lambert-Eaton Syndrome, involve autoimmune interactions  
 CC with calcium channels. The ready availability of calcium channel subunits  
 CC would make possible immunoassays for diagnosis of such diseases and an  
 CC understanding of them at the molecular level that could lead to effective  
 CC methods for treating them.  
 Sequence 1873 AA;

Query Match 12.9%; Score 1608.5; DB 1; Length 1873;  
 Best Local Similarity 23.6%; Pred. No. 4.3e-115;  
 Matches 577; Conservative 356; Mismatches 692; Indels 823; Gaps 82;

QY 32 QGGSTEXKPGSADSAEGLPYPALAVVFYLSQDSRPSRSCRTVCNFM--FEFVSM 89  
 Db 7 QDEGLKKQPKKPLPEV--LPRP---PRALFCLITLONPLRKACISIV--EMKPFETIILL 59  
 QY 90 VILLNCVTLGMRPC-EDIAQDSQRCRI-LQAFDFIFAFAVENYKVALG-IFGKKC 146

Db 60 TIFANCAVAVLMPED---DNNSLNLGLEKLEFELFVFSIEAAMKIIAYGLEFHODA 116  
 QY 147 YLGDWNRDLDFVIAQMLEYSTDLOV-----SFAVRVRYRLPLRAL 191  
 Db 117 YLRGMYVDFIIVLEFVFTALIEOVVIOSTNAPMSKAGLDVKAIRFRRLRLRV 176  
 QY 192 NRVPSMRLVTLTLDTPMLGNVLLCFEVEFFIGYGVOLMAGLLRNRCFLEPENS 251  
 Db 177 SGVPSLOWVLSIKRAMPLFHLVLLFVYIITAIIGLELFGKMKIKCY----- 229  
 QY 252 SVDLPEYVOTENEDSPFICSOPRENGMRSQSVYTLRGSGGPPCSLDYEYSSNT 311  
 Db 229 -IGDIYATVENEKSP--CART-----GSGRPC---TINOS--- 260  
 QY 312 TCVMNNOYTCSGAENHPFGALINPDNIGYAMIAIFOVITLEGVNDIMYFVDA-HSFY 370  
 Db 260 -----BGRGWPGPNHGIHFDFGSMITVQCITMBGMDVLYVWDAIGNEM 309  
 QY 371 NFYFILLIIVGSEFMILCLVATVATOFSETKORESOJMBEORYFLSNASTASFSEPG 430  
 Db 310 FWIYFVTLILGSPFIINLVGLVLSGER--TKEREKAKSR-----GTFQKLEKQ 357  
 QY 431 SCYEELLKYVLYLIRKAAIRLAQVSRALGVAGLLSPVARSQGPQPSGSCIRSHRLS 490  
 Db 358 QLEEDLRGMSWITQ-----GEWADVEDDLREGKLS----- 388  
 QY 491 VHHLYVHHHHHHHNLGNGTLRVPRASPEIQDDANGSRRLMPPSTPTPSGPPRGA 550  
 Db 388 -----LEEG----- 393  
 QY 551 ESVHSFYHADCHLEPRVQCAPRPPCPSPASGRVYSGKVYPTVHTSPPEILKDALVEY 610  
 Db 393 ----- 393  
 QY 611 APSGPPIITSNIPPGFPSSMHLKETQSTGACHSSCKISSPCSKADSGAGPDSGPCY 670  
 Db 393 ----- 393  
 QY 671 ARTGAGEPESADHVPDSSEAVE-----FTDQCHSDLRDPHSRRRSLGPDAPS 724  
 Db 393 -----SDTESLVEIENLKIQTIRH----- 414  
 QY 725 SYLAEWRLICDTR---KIYDSKYFGRCIMAILVNTLSGICIEHDEPELTNALEISN 780  
 Db 414 -----WRONNRYFRMKCHDLVRSRVFWYVILVIALNTLSIASEHNQPLWTLHQDIAN 468  
 QY 781 IVFTSLFALEMLKLIVGPFYIKNPYNIPDGVTIVSWEIVGOQGG-----GLSVLR 835  
 Db 469 RVLLSLFTEMLIKMIGLGRQYFMSIFNRFDCEYVCGILELLVBSGAMTPIGISVLR 528  
 QY 836 TFLRMVNLKLVLEFLPALQROLVVLKMTDNVATFCMLMLTFIFSLIGMLFGCKEASE 895  
 Db 529 CILLALLFKITFKWISLNLVSLNSIASLILLLEFLFIIPALIGMOLFGGRYDFE 588  
 QY 896 RQDGTPLPRKNDPSLMAIVYFOIITODMKVLYNGASIS-----MAATFELM 949  
 Db 589 ---DTEVRSNEDNFPQALISVFOYLTGEDMWSVYNGIMAYGPGSYGVLCITFILL 645  
 QY 950 TEGNYVLFNLVAVLVEGF--QAEIEKREDASGQSLQPLVNSOGGDAIKSESEPDFS 1008  
 Db 646 VCGNYTLNLFVLAIVDNIAEASL-----TSQKAKAE----- 680  
 QY 1009 PSYDGDGRRKRLALVALGEHELKRSLLPPLIHTAATPMSLPKSSSTGVEALGSGSR 1068  
 Db 680 -----ERRKRMKSGLDPKTTEEKSV----- 702  
 QY 1069 RTSSSGSAEPAHHEMKSPSPARSSPHSPWASASWTSSRNSLGRAPSLKRRSPSG 1128  
 Db 702 -----AKKLEOK-PKG 711  
 QY 1129 ERSILSGESESODEESESSEEDRASPDGHRHRSGLEREAKSSFDLPDITQVGLHRT 1188  
 Db 712 EG---IFTTKAKLVDEFESNVNEVKDP-----YPSADFP----- 743



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QY 1189 ASGRSSASEHODCNKASASRLARTLRDPOLDGDDNDGCLNKGERTQAWRSLPA 1248
Db 743 -----GDBDEDEPELTPSPRPPLAEIOL- 767
QY 1249 CCRER-----DSWATYFPPOSREPLLCRLITTHKMFDPVHVLITFNCTIATMERKID 1303
Db 767 --KKAAPDIPRASSFFIFSPNKRVRCHRIYNATWFTNFIITLLSSAALAE-----D 820
QY 1304 PHMERIFLITLNTI-----FTAVFLAEMTKVAVVAGMCFEGDQATYRSSWNVLDGLVLISV 1360
Db 821 PIRASVNRNQLGFIADIAFVSFTVEIVLTKMTYGAFLHNGSFERNYFNILDLIVAVS- 880
QY 1361 IDILVMSVDSGTKLKMLRVLRLTLRPLRVASRAQGLKLVETLMSLKPITGIVVI 1420
Db 880 ---LISNGLESTT--ISVKILRLVRLRPLRAINRAKGLKHVVQCVFVAIRITGIVLV 934
QY 1421 CCAFFITIGILVOLFGKFEVFCGEDTRITNKSCDAEASV-----RWV 1465
Db 935 TTLQFMFACIGVOLFGKFEFSC--NDLSKMT--EECRGYVYVKDGDPTQMLRPRQWI 991
QY 1466 RHKNFNPDLGALMSLFLVASKDQVMDYDGDVAVDQOPTMNNHNPMLLYFISPLI 1525
Db 992 HNDHFDPNVLASAMSLFTVSTFBSGMPOLYRAIDSNEDMGPVYNNVEMALIFITITIL 1051
QY 1526 VAEFLVNFVGVVVENFKCRQHOEEEARREKRLRLREKRRMLMDLVIASGSSAS 1585
Db 1052 IAFEMNIFVGFVIVTF-----QEOGETEYKNC-----LDKNQRCV-----QYAL 1093
QY 1586 AASAOCKPYYSDYSRRLVHNLCTSHYIDLITGYIGLVNTVAMERYQOPQIDELAL 1645
Db 1094 KARPLRC--YIPKNPYQYQVYVYVSSYFEYLMFALIMLNTICLQMOHQSEEMNHIS 1150
QY 1646 KICNYITVIFVESYFKLVAFGRFRFODRMNOLALYILSIMGITLEIIV----- 1700
Db 1151 DILNVAITIFTEMLIKLAFKARGFGDPNVFDELYIGITIDVILSEIDTFIASSG 1210
QY 1700 -----NASLPINPTIIRIMVRLIARVLLKMAVGNRALDVTM--QAL 1742
Db 1211 GLYCLGGCGGNVDPDESARISAFRLFVRML--IKLSRAEGVRLTLMTFKISQAL 1267
QY 1743 POYGNLGLFMLEFTFAALGVLEFGDLE--CDETHCEGGRATRNNGMAFLTFRVS 1801
Db 1268 PYV---ALIVYMLFTYAVIGMQMFGKIALVDGTO---INRNNNTQPTPQAVLLFRCA 1320
QY 1802 TGDNMNGIMKDTL--RDCQDES-----TCYNTVISPIYFVSFVLTAQFVLNVAVIV 1851
Db 1321 TGEAMOEIILACGYKLOPDESUYARGEYTC--CTNFAYYIFISFYMLCAFLIINLFVAV 1379
QY 1852 LM-----KHEESNKKEAEAELEAE--LELEMKTLSPQPHSPGLSPPL 1893
Db 1380 IMDNEDYLRDWSILGPHILDEF--KAIMEYDEPAKGRKIKHLDVYLLRRIQPILOFGKF 1438
QY 1894 WP-----GVEGVNSP-----DSPKGAFTTAHIGAASGFSLEHP----- 1929
Db 1439 CPHRVACKRLVGNMPLNSDGYTFNATILFALVRLALKTITBENFEQAAEELRAIITKIW 1498
QY 1929 --TMVPHPEEVVPLGPDLLTVARKSGVSRTHSLPNDSYNCRNGSTAESRIGRGMGLPKA 1986
Db 1499 KRYSMLLQOVIPPIIDDEVYTGKFAATFLIQEHFRKFKRQ---EEYGYR---PRK 1550
QY 1987 QS-----GSILSVHSPA-----DTSCILQPKDVTYLLQPHGAPWGAIPKLPPEG 2033
Db 1551 DTVQIQAAGLRTIEEAPRIRRTISGDLTAEBELEHAM-----V 1589
QY 2034 RSPPLAQRPLRQAAI-----RTDSL-----DVQIGSRREDLISEVSGP----- 2072
Db 1590 EAMERIRIFRRIGGLEGVDTFLERTNSLPPVMANORPLQFAIMEELIESPFLIEDPQ 1649
QY 2072 ---SCULTSSSFPWGGSSIQV--QORSGIQSVSKHIRLPADCPGLEPDMAMDPETRSS 2126
Db 1650 DARTNPLANANTNNANVANVAYGNSNHSNMQSSVH-----CEREFGAEETPAAGRGA 1703

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QY 2127 LEIDTFLSTISGDLIPSSOEPLSPRDLKCYSVTQSCRRRPGSWDEQRHSTAVSCL 2186
Db 1704 L-----SHSRALGPHS--KPC-AGKINQOLVQPGMPINO----- 1736
QY 2187 DSGSORPLCPSPSSIGGQGLGPGSRPKKLS--PSSIDPPE---SGSRRPSPGCVL 2242
Db 1736 ---APPAPQOQST-----DPERGQRRTISLGSLODEAPQRSSSGSTP----- 1778
QY 2243 RRRAPASD--SKDPSVSPDLSTAASPSPKKDTLSGLSSDPTMDP 2288
Db 1778 RRPAPATALLIOEALVIRGGLDTIADAG--FVWATSQALVDAQOMEP 1822

RESULT 14
R73055
AC R73055 standard; Protein; 1873 AA.
DI 02-NOV-1995 (first entry)
DE Rabbit skeletal calcium channel (alpha)1-subunit.
KW Calcium channel; (alpha)1 subunit.
OS Oryctolagus cuniculus.
FH Key Location/Qualifiers
FT region 950..1100
FT misc_difference 1808
FT /label= IIF7 monoclonal antibody epitope
FT /note= "In Tanabe et al"
FT misc_difference 1815
FT /label= Ala
FT /note= "In Tanabe et al"
FT misc_difference 1835
FT /label= Ala
FT /note= "In Tanabe et al"
FT misc_difference 1835
FT /label= Ala
FT /note= "In Tanabe et al"
FT modified_site 79
FT /label= Potential N-glycosylation site
FT modified_site 257
FT /label= see above
FT modified_site 797
FT /label= see above
FT modified_site 1464
FT /label= see above
FT modified_site 1674
FT /label= see above
FT modified_site 687
FT /label= see above
FT modified_site 1502
FT /label= potential CAMP-dependent phosphorylation
FT modified_site 1575
FT /label= see above
FT modified_site 1757
FT /label= see above
FT modified_site 1772
FT /label= see above
FT modified_site 1854
FT /label= see above
FT modified_site 1552
FT /label= see above
FT modified_site 52..70
FT /label= see above
FT protein 89..108
FT /label= transmembrane region
FT region 121..139
FT /label= see above
FT region 161..179
FT /label= see above
FT region 199..218
FT /label= see above
FT region 310..334
FT /label= see above
FT region 433..451
FT /label= see above
FT region 467..486
FT /label= see above

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QY 1189 ASGRSSASEHODCNKSGASRLARTLFTDQDGDNDNENGLSKGERIOAWVRSLPA 1248
DB 743 -----GDEDEBEELPVSPRRRLAEQL 767
QY 1249 CCRER-----DSWAVYIPPOSRRLCHRIITKMDHVYVYIPLNCTITIMERPXD 1303
DB 767 --KKAAPVPPASSEFFIIPNKVRLCHRIVNAWTFINFLILLSSALAE-----D 820
QY 1304 PHASERIFLTLSNYI---FTAVFLAEMTVKVALGCMFGCAQVRRSSMNVLDGLYLSY 1360
DB 821 PIRASVANOQLGFDIAFTSVFVEIYVKMTYGAFLHSGFCORNFENLIDLVAVS- 880
QY 1361 IDILYSWVSDSGTKILGMLRVLRILRLRPLRVISRAGOKLVETLMSSLPKGINVTI 1420
DB 880 ---LISMGLJESST--ISVVKILRLRVLRPLRAINRAKGVHVOCVFAIRITGINVIV 934
QY 1421 CCAFFIIFGILVOLFKKFEVCOGEDTRNTNKSDEASV-----RWV 1465
DB 935 TTLLOFMACIGVOLFKKFEVSC--NDLSKMT--EECRGTYIYKDDPTOMELRRQWI 991
QY 1466 RHKYNEDNLGOALMSLEVLASKDQVMDIDGDAVGVDQOPIMNHNPMLLYFISFLI 1525
DB 992 HNDHFEDVNLASMSLEFVSTSEEMPOLLYRAIDNEDMDGPNVNNHVEWAFIYIIL 1051
QY 1526 VAEFLNMFVGVYVNEFKHQHDEEFAREKRLRLKRRRNMLDDVIASSSSAS 1585
DB 1052 IAFEMNIFGVFIYTF---OEOGETEYKCE-----LDKOROCV-----QYAL 1093
QY 1586 AASEAOCPYYSYDSYRFLVHLCTSHYDLFTTGIVIGLVNVTAMERHQOQOILDEAL 1645
DB 1094 KARPLRC---YIPKPYOYQWYVYVTSSEYELMFALIMNTICLQGHQSEEMHIS 1150
QY 1646 KICNFIIVIVFEVEFLVAFGRFRFODRNODLAIYLSIMGTLEIEV----- 1700
DB 1151 DILNVAFTIIFLEMLTLKLFKASGIFGDPWNVDFLIYIGSLIDVLEIDTFLASSG 1210
QY 1700 -----NASLPINPTIIRIMRVLIARVLKLMAYGMRALLDTYV---QAL 1742
DB 1211 GLYLGCGGCGNVDPDESARISAFERLEFVRML---IKLSRACVATLMTFIKSQL 1267
QY 1743 PQYUGLGLMLLFFIFALGVELEFGDLE-CDENHPCBGJGRATFNFGMAELTFRVS 1801
DB 1268 PIV---ALLIYVLEFIYVIGMQMGKIALVDGTO---INRNNFOTFOQAVLLFRCA 1320
QY 1802 TGDMMNGIMKDTL--RDCDOES-----TCYNTVSIPIYFVSFVLTAFVLYNVAV 1851
DB 1321 TGEAQQEILLACSYGKLCDDPSDYAPGEYTC-GTNFAYYFISFYMLCAFLIINLVAV 1379
QY 1852 LM-----KHLESNKEAKEEELPAE---LELEKTLSPQPHSPGSPFL 1893
DB 1380 IMDNEDYLRWMSILGPHHLEDF-KAIWAEXDPKAKRIKILDVTLRLRIQPLGFGKF 1438
QY 1894 WF-----GVEGVNSP-----DSPKPGAPHTTAHIGASGFSLEHP----- 1929
DB 1439 CPHRAVCKRIVGMNPNLNSDGTVMFNALFLVLTALKITEGFEDANBELRAITIKTW 1498
QY 1929 ---TWPHPEEVPVPLGDLTLVRKSGVSRTHSLPNDISYMCNNGSTABRSGLHGWSGLPKA 1986
DB 1499 KRTSKMLLDQVPIPIGDDEVIVGKFYATFLIOEHFRKFMKQO---BEYGYR---PK 1550
QY 1987 OS-----GSLISVHSOPA-----DTSCLOLPRKDVHYLQPHGAPTMGALPKLP 2033
DB 1551 DTVOQAGRLTIEEAAFEIRRTISGDLTAEELERAN-----V 1589
QY 2034 RSLPLAORPLRQOAL-----RTDSL-----DVOGLSREDLLSEVSGP----- 2072
DB 1590 EAAEMERIFRRTGGLFGVDTFLERTNLSLPYMANORPLQAFATIEEMELSPVLEDPQ 1649
QY 2072 ---SCPLRRSSFMGSGSIQV---QORSGIQSKVSKHIRLAPCGGLSPMAKOPPEFRSS 2126
DB 1650 DARTPLPLARNANANAVAGNSHNSNMQFSSVH-----CREFPGGELETPAAGRGA 1703
QY 2127 LELDTLSMISGDLPSSEOEPLSPRLDKCYSVETOSCRRRPSPWLDQORRHISIAVSC 2186

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DB 1704 L-----SHSRALGPHS-KPC-AGKINGOLVOPGMPINO----- 1736
QY 2187 DSGQPRLCPSRSSLGQPLGCGSPKPKKLS-PPSISIDPPE---SOSRPPCSPGVL 2242
DB 1736 --APAPCQDPST-----DPPERQORTSLTGLSDPADPDRSSSEGSTP----- 1778
QY 2243 RRRAPASD--SKDPSVSSPLDSTAASPSPKKDTLSGLSSPDTMDP 2288
DB 1778 RRPAPVTTALLIQEALVVRGIDTLAADAG---FVMARISQALVYACQNEP 1822

RESULT 15
P95645 standard; protein; 1873 AA.
AC P95645;
DE 21-MAR-1990 (first entry)
DE Rabbit skeletal muscle alpha-1 sub-unit gene product.
OS Skeletal muscle (rabbit).
PN W68909834-A.
PE 19-OCT-1989.
PE 04-APR-1988; 001408.
PE 04-APR-1988; US-176899.
PE (SALK) Salk Inst for Biol Stud.
PE Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J;
PE WPI: 89-324236/44.
DR N-PSDB; N91778.
PT New DNA encoding alpha-2 subunit of animal calcium channel - also new
PT protein product and eukaryotic cells for testing cpds. for calcium
PT agonist or antagonist activity
PS Disclosure: page 16-1 to 18-3: 68pp; English.
CC Also used to diagnose Lambert-Eaton syndrome by reacting test serum
CC with alpha-1 and alpha-2 subunits. Labelled fragments can be used as
CC probes.
SQ Sequence 1873 AA:

Query Match 12.8%; Score 1600.5; DB 1; Length 1873;
Best Local Similarity 23.58; Pred. No. 1,9e-114;
Matches 576; Conservative 356; Mismatches 693; Indels 823; Gaps 82;

QY 32 QGPSTENDPGSADSEAGLTPALAPVFEYLSODSPRSMCLRTVCNPM--FERVSM 89
DB 7 QDEGRKKQPKPLPEV--LPRP---PRAFLCITLQNP LKACISIV--EMKPFETILL 59
QY 90 YILNCTYLGMRFC-EDDIACDSQCRH-LOAFDDPIFAFEAVEMVKKVVALG-IFGKRC 146
DB 60 TTFANCAVALAYLDPMD--DNNSLNLGLEKLEFFLVFVSTEAAMKIIAAGFLERHOG 116
QY 147 YLGDTWNLDFEYIYAGMLEYSLDQNV-----SFSAVTVVLRPLRAI 191
DB 117 YLRGWNVLDFIIVFLGVTALLLEQVNVVQSNTPAMSSKAGLDVAKALAPVRLRLRV 176
QY 192 NRVSMRLIVLLDLDTPLMGVNLILCFEYVFFIGYVQVQVQVQVQVQVQVQVQV 251
DB 177 SGVPSLOVJWSIKKMLPLFHALVLVLFVYIYAIIGLELFGKMKHCYV----- 229
QY 252 SVDLPEPYQTENEDSESPICOPRENMGRCRSVPYTLRGGGCGGPGCSIDYETNSSWT 311
DB 229 -IGIDIYATVNEKPS--CAKT-----GSGRC-----TINS--- 260
QY 312 TCVMNQYTYNCSAGEHNPFGALINFDNIGYAMIAFQVITTEGVWDIWFYMDA-HSFY 370
DB 260 -----ECRGGWGPVNHGITHFENFGFSMLTYQCITMGCTVDVLYWDAIGNEM 309
QY 371 NEFYILLIIVGSEFNLICVVIATOFSETKQRESQVMBEQVRLSNASRLASPSBG 430
DB 310 PWITFVILLIGSFITNLVGVLSGEF--TKREBAKRS-----GTFQKIREQ 357
QY 431 SCYEBELLYVYLIRKARLAQVRAIGVRAGLSSPVARSQEPQSGCTRSHRLS 490
DB 358 QLEEDLRGYMSWITO-----GEWMDVEDLREGLKS----- 388

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QY 491 VHHVHHHHHHHNGTGLVPRASPEIQORDANGSRLLMLPPSTPTSGGPRGA 550  
 Db 388 -----LEGG----- 393  
 QY 551 ESHVHYHADCHLEPVACQAPPPCPSEASGRTVSGKYPTVYHSPPPELLKOKALVY 610  
 Db 393 ----- 393  
 QY 611 APSPGPTLISFNIPRPFSSMKLLETOSTGACHSSCKISSPCSKADGAGCPDCPYC 670  
 Db 393 ----- 393  
 QY 671 ARTGAPESADHYMPDSEAYE-----FTQDAQHSDLRDPHSRRORSIGDPAES 724  
 Db 393 ----- 393  
 QY 725 SVLAFWRLICDTR-----KIVDSKYFGRGIMIALVNTLSMGIEYHPOBELTNALEISN 780  
 Db 414 -----KROQWNRVFMKCHDVKSRYFWLVLLVLTNTLSIASEHNOPLMLTHLODIAN 468  
 QY 781 IVFTSLALEMLKLVYGPFGYIKNPYNIEDGIVIVISWEIYGOOG-----GLSVLR 835  
 Db 469 RVLLSFTIEMLKMGGLGROYFMSIFNRFDCVYCSGILLELLVHSGAMPTLGISVLR 528  
 QY 836 TFRMLRVKLVRLPALOROLVLMKTMVNAIFCMLMLFIFIFSTLGHLEGCKFASE 895  
 Db 529 CIRLRLFKIKRYWTSLSNLVASLNSIRSIASLLLLFFIIFALLGQOLRAGRDFE 568  
 QY 896 RDGOTLPRKRDLLMAIVTFOILOEDMKNVLYNGMASTS-----MAALFYALM 949  
 Db 589 -----DVEARSRNFDPOLLSVFOVLGEDMNSVINGIMAYGSPSYVLYCIFYILF 645  
 QY 950 TFGNVLFENLVAILVEGF-CAEIEGRKEDASGOLSCIOLPVNSOGDATKSESEDPFES 1008  
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 QY 1069 RTSSGSAEPGAHHEKSPSARSSPWSAASWTSRRSSHNSIGRAPSLKRSPSG 1128  
 Db 702 -----AKKLEOK-PKG 711  
 QY 1129 ERRSLLSEGEODEEESSEEDRASPAQSDHHRGSLERAKSFDLPLOLVPGLHRT 1188  
 Db 712 EG-----IPTAKLVDEFESNVEKDP-----YPSADFP----- 743  
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 Db 992 HNFHFDNVLISAMMSLFTVSTEGWPOLLYRAIDSNEEDMGVYNNRYEMALFFIYIITL 1051

QY 1526 VAEFVLMPFYGVYENHKKROHOEEEARREKRLRLREKKRMILMDVYIASGSSAS 1585  
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 QY 1586 AASEAOCKPYSDSRFRLVHNLCTSHYDLFETGVIGLNVNTMAHEYOQDILDEAL 1645  
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 QY 1700 -----NASLPINPTIRRVLRJARVYLKILMAVGMALDIYV-----QAL 1742  
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 Db 1439 CPHRVACRLVGMNPLNSDGTVFENATLFLVRLTALKIKTEGNEFQANEBELRIIKKI 1498  
 QY 1929 --TWPBHEVVPRLGPDLTVRKSGVSRTHSLPNDYSMCRNGSTARSIGHRGMLPKA 1886  
 Db 1499 KRTSKLDDOYVPIGDDVYVGFATFLIOEHFRKFMKQO---BEYGYR---PKK 1550  
 QY 1987 OS-----GSILSVHSQA-----DTSCILQPKDVHYILOPHGAPYWCALPKLPFG 2033  
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 QY 2072 ---SCPLTRSSFMGGSIOV--QORSGIOKSVSKIRLPAPCPGLEFSWAKDPETRSS 2126  
 Db 1650 DARTNPANANNNANVANVAAGNSHNNQMFSSVH-----CEREPFGEAETPAAGRGA 1703  
 QY 2127 LETIDELWISGDLPLSSOEPLSRDLKCYSVETOSCRRRPGSWLDEQRHSHIIVSCL 2186  
 Db 1704 L-----SHSRALGPHS-KPC-AGKLINGOLVQPGMPIO----- 1736  
 QY 2187 DSGSORLCPSPSLGGQPLGGPGSRPKKILS-PSISIDPPE---SOGSRPPSPGVCL 2242  
 Db 1736 --APPAPQOPST-----DPPERGORRTLSLSDENAPQRSSSGSRP----- 1778  
 QY 2243 RRRAPASD--SKDPYSVSPDSTAASPSFKDTLSLGLSSDPTDMDP 2288  
 Db 1778 RRPAPATALLIOELAVRGDLDTLADAG---FVMATSOALYDACOMEP 1822

Search completed: January 19, 2000, 01:31:02  
 Job time: 255 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2000, 20:00:56 : Search time 13.64 Seconds  
(without alignments)

2073.407 Million cell updates/sec

Title: PCT-US99-19675-2

Perfect score: 12469

Sequence: 1 MDEEDGAGAEISGQPRFT.....LREDEKGEIPWPLPTPGA 2374

Scoring table: BLOSUM62

Searched: 122436 seqs, 11912922 residues

Database: Issued\_Patents\_AA:\*

Word size: 0

Number of hits that pass the threshold: 122436

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/PTUS9.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Match | Query Length | DB ID | Description       |
|------------|--------|-------|--------------|-------|-------------------|
| 1          | 1708.5 | 13.7  | 2339         | 2     | US-08-455-543A-47 |
| 2          | 1708.5 | 13.7  | 2339         | 2     | US-08-223-305C-47 |
| 3          | 1703   | 13.7  | 2237         | 2     | US-08-455-543A-48 |
| 4          | 1703   | 13.7  | 2237         | 2     | US-08-223-305C-48 |
| 5          | 1608.5 | 12.9  | 1873         | 1     | US-08-435-675B-4  |
| 6          | 1597.5 | 12.8  | 1873         | 1     | US-08-336-257A-7  |
| 7          | 1595   | 12.8  | 1872         | 4     | 5386025-6         |
| 8          | 1579   | 12.7  | 2161         | 2     | US-08-455-543A-51 |
| 9          | 1579   | 12.7  | 2161         | 2     | US-08-223-305C-51 |
| 10         | 1576.5 | 12.6  | 2104         | 2     | US-08-808-793-4   |
| 11         | 1576.5 | 12.6  | 2161         | 1     | US-07-745-206A-2  |
| 12         | 1576   | 12.6  | 2161         | 2     | US-08-455-543A-49 |
| 13         | 1576   | 12.6  | 2161         | 2     | US-08-223-305C-49 |
| 14         | 1576   | 12.6  | 2161         | 2     | US-08-311-363-2   |
| 15         | 1572.5 | 12.6  | 2105         | 2     | US-08-808-793-3   |
| 16         | 1552   | 12.4  | 1968         | 2     | US-08-455-543A-45 |
| 17         | 1552   | 12.4  | 1968         | 2     | US-08-223-305C-45 |
| 18         | 1548   | 12.4  | 2100         | 2     | US-08-808-793-23  |
| 19         | 1535   | 12.3  | 2509         | 2     | US-08-149-097D-35 |
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| 21         | 1498   | 12.0  | 1968         | 2     | US-08-311-363-7   |
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| 26         | 819.5  | 6.6   | 833          | 2     | US-08-311-363-15  |
| 27         | 808.5  | 4.7   | 433          | 2     | US-08-808-793-25  |
| 28         | 408.5  | 3.3   | 319          | 1     | US-07-745-206A-17 |
| 29         | 408.5  | 3.3   | 319          | 2     | US-08-311-363-17  |
| 30         | 188    | 1.5   | 1331         | 2     | US-08-317-110A-64 |
| 31         | 171.5  | 1.4   | 2843         | 1     | US-07-741-940-2   |
| 32         | 171.5  | 1.4   | 2843         | 1     | US-08-289-548A-2  |
| 33         | 171.5  | 1.4   | 2843         | 1     | US-08-289-548A-7  |
| 34         | 171.5  | 1.4   | 2843         | 1     | US-08-289-548A-7  |
| 35         | 171.5  | 1.4   | 2843         | 1     | US-08-452-654-2   |

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|----|-------|-----|------|---|------------------|------------------|
| 36 | 171.5 | 1.4 | 2842 | 1 | US-08-452-654-7  | Sequence 7, Appl |
| 37 | 171.5 | 1.4 | 2843 | 2 | US-08-452-655B-2 | Sequence 2, Appl |
| 38 | 171.5 | 1.4 | 2843 | 2 | US-08-452-655B-7 | Sequence 7, Appl |
| 39 | 171.5 | 1.4 | 2973 | 2 | US-08-821-355A-7 | Sequence 7, Appl |
| 40 | 171.5 | 1.4 | 2843 | 2 | US-08-370-235A-2 | Sequence 2, Appl |
| 41 | 164.5 | 1.3 | 732  | 1 | US-08-317-522A-5 | Sequence 5, Appl |
| 42 | 161.5 | 1.3 | 778  | 1 | US-08-439-818A-5 | Sequence 5, Appl |
| 43 | 161.5 | 1.3 | 778  | 2 | US-08-751-965-5  | Sequence 5, Appl |
| 44 | 161.5 | 1.3 | 778  | 2 | US-08-738-975-5  | Sequence 5, Appl |
| 45 | 161.5 | 1.3 | 778  | 2 | US-08-728-626-5  | Sequence 5, Appl |

#### ALIGNMENTS

RESULT 1  
US-08-455-543A-47  
Sequence 47, Application US/08455543A  
Patent No. 579,846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1983  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 238-0999  
 TELEFAX: (619) 238-0062  
 INFORMATION FOR SEQ ID NO: 47:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2339 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: Internal  
 US-08 455 343A-47

Query Match 13.7%; Score 1708.5; DB 2; Length 2339;  
 Best Local Similarity 24.2%; Pred. No. 5e-128;  
 Matches 645; Conservative 370; Mismatches 844; Indels 805; Gaps 91;

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 411 SPLDVLRKAATTKSRNDLH-----AEEGDRAD----- 441  
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832 SVLRTFRLMRVILKVLRELPALQROLVLMKTMNVATFCMLIMFIFPSTLGMHLFGCK 891  
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 691 VLTIFGVNTLLNVFLAIADVNLANAQELTKDEEEMEAANKLALOKAKEVAEVSPPMSAA 750  
 987 QLPVNSQGDARKESEDPFSPSVSDGODRKKRLALVALGEMHAEKRLPLIHTAA 1046  
 751 NISIAARQNSAKASVWE-----QRSQRLQNLNASCALYSEMDPEERLFA 800  
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 1088 P-----PSARS-----PASPMSAASMTSRSSNSUGRAPSLKRSPS 1127  
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 914 GGRHHRHRSPEBAERERRRARRHODPSKECAGACGERARRRGGPRAGPRRAESG- 973  
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 1224 DDNDGNSLKGRIQAWRSRLPACRR-----DSW----- 1257  
 1027 CDLETSGLTVVGP-----MHTLPSTCLOKVEQPEDADNQRNVTMGSQPPDPTIYHI 1080  
 1257 -----SAYTFPPQSRFR 1268  
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 1473 FEYIIMAMLTAVYLMKTYIDAPYEELMKCLNIVTSMFEMECVUKIAIAGVINTYR 1532  
 1675 DRWQOLDALVILASIMGITEEI--EVNASLPINPTIIRIRVRLIARVILKLKMAVGMA 1733  
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Db 1588 LMTFVQSFKALPYVCLLIMLFYIALIGMOVFNALDDO---TSINRHNFRFLQA 1644
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Qy 1850 AVLKMHLEESNKEA-----EEAELEAELE-----LEM-KTISPOPSPL 1888
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Db 1761 GLGKCKPARVAYKRLVRNMMPISNEDTVHFTSLMALIRTALEKILAPACTKHOCDAE 1820
Qy 1933 HPEEVPV-----PLGPDLLTVRKSGVSRTHSLPNDSTYCRNGSAEBSLG 1977
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Db 1930 ESGIKESVSWGTORTQDAPHEARPLERGHSTELPVGRSGALADVOMQSTRKRPDGP 1989
Qy 2052 --SLDVGLGSRREDLSEVSGSPCLTRSSSFWGSSIOVQORSGISKSHRLRPARC 2109
Db 1990 QPGLESQG--RAASMPRLAETOPTVDASPMKRSISTLAORPG-----THICSTTP- 2040
Qy 2110 PGLPSPNAKDPETRS-----SLEIDELSWISGDLPSOEEPLSP- 2152
Db 2040 -----DRPPSQASSHHHHRCHRRDRKORSLERKPSLS-ADMGDASSAVGPELPP 2091
Qy 2152 -----RDLKCYSVETQSCRRRPGSWLDEQRHSHVSCDSSGQPLCSPS----- 2200
Db 2092 GEGPTGCRREKROEGROERKOPSSSSSEKORF--YSCDRFGREPPKRPPLSSH 2148
Qy 2200 -----SLGQGPL-----GGPGSRPKKRLSP--PSISIPPEP 2229
Db 2149 PTPSPTAQEPGRPHPGSGSVNGSPLSTSGASTPGRGGRQLPOTPLTPRPSITTYTANS 2208
Qy 2230 -----QGRPPCSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTA 2264
Db 2209 SPIHFAQOTSPLAFSPGRLSRGLSEHNAALLQDRDPLQPLAPSGSDPYLQGRLDSEA 2268
Qy 2265 ASPSPKKDTLSL-----SGLSS 2281
Db 2269 SVHALPEDTILTFEBAVATNGRGS 2292

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RESULT 2
US-08-223-305C-47
; Sequence 47, Application US/082230305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCrene, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-47

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Query Match 13.7%; Score 1708.5; DB 2; Length 2339;
Best Local Similarity 24.2%; Pred. No. 5e-128;
Matches 645; Conservative 370; Mismatches 844; Indels 805; Gaps 91;
Qy 27 GAGGQGGSTGKDPGSDSABGLPYPALAPVY-----FYLSQDSRP 70
Db 25 GAGGAGGPGGLOPQGRVIXKQSIQARATMALYNPIPKONCFVNRSLFVFSSENNV 84
Qy 71 RSWCLRTVCNPMFERVSMVLLVILNCVTILGMRPCEDJACDSORCLIOARD--FFAF 127
Db 85 RYAKKRITEMPEFENMILATIANCIYAL-----EQLHPGDKTPMSERIDDEPEYFIG 140
Qy 128 FAVENVAKVALG--IFSKCYLGDWTNRLDFFVIAGMLEYS---IDLQNVSSAVRTVA 183
Db 141 FCFEAGIKIILGFVFKHSGYLRNGNMVMDVYVLTGILATAGIDPDLR-----TLRAVA 195
Qy 184 VLRLPRAINRVPSRRIIVTLLDITLPMLGAVLLCFVFIFGIVQVQIAGLNRNCEL 243
Db 196 VLRLPLVSGTSPSQVVLKSTIKRAMVPLDQIGLLEFAIIMFAIIGLEYMGKFKACF- 255
Qy 244 PENFSLPLVDLEPYTOTENEDSPFICOPRENGMRCSRVPFLRGEGGCGPCSLDYE 303
Db 255 -----PNSTDABPV-----GDFPCCKEAP 273
Qy 304 TYNSSWVTGVNNNOYVITNCSAGEHNPFKALFNDNIGVAMIAIFPVITLEGVNDIMFV 363

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Db 274 ARLEGDETC---REYWP-----GPNFGITNEDNIFALLIVFECITMEGTDLINYT 323  
Qy 364 MD-AHSEFNFIYFILLIVGSEFMINLCVVIATOFSETKORES-----OLMEQCFVRP 416  
Db 324 NDAAGNTWMLFYFILLIIGSFMLNLVGLVSEFPAKERRERVENRRAFLKLRNOQIE- 383  
Qy 417 LSNASTLASFSESPSCYELLKLVYIIRKARLAOVSAIGVAGLSSPAVRSQEP 476  
Db 383 -----RELNGYLEMIFKADEVMALED-----RNAEEK 410  
Qy 477 OPSGCTSHRRLSVNHLVHHHHHHHNLGNGFLVPRASPEIODRDANGSRMLLP 536  
Db 411 SPLDLKRAATKRSNDLIH-----AEGEDRFAD----- 441  
Qy 537 PSTPPSGPPGASVSFHADCHLEPVRCOAPPRPCPSASGRVSGKVPVHTS 596  
Db 441 ----- 441  
Qy 597 PPELTKALVAVASPGPPLISFNIPGPFSSMKLLETOSTGACHSSCKISSPSCK 656  
Db 441 -----LCAGSPPAR 450  
Qy 657 ADSGACGPDSCFYCARTGAGEPESADHYMPDSEAVYEFTODAQHSDLRDPHSRRORS 716  
Db 451 AS-----LKSGETESSYF-----RRREK- 470  
Qy 717 LGDPAEPSSVLAFWRLICDTEFRKIVDSYFEGNGIMAILVNTLSKGIYHQBEPILNAL 776  
Db 470 -----MERFF-----IRRWAKAOSFYWVWVLCVVALNTLCVAMVYHQPRLTTTL 514  
Qy 777 EISNIVETSLFEMLKLVYGPFGYIKNPINFDGIYVIVSWEIYGO-----OGGGL 831  
Db 515 YRAEFYELGFTESLKYGLGPRSYRSSNCFDGVIVSVEYVMAIKGSSSGI 574  
Qy 832 SVLRFRMLKVLKLVFALQRODLVIMKTNDVATCMIMLFIYFSLIGMHLGCK 891  
Db 575 SVLRALRLRIKRYKYSNLNVLVSLNSKSIISLFIYFVAFALGQLEFGQ 634  
Qy 892 FASERDGLTPRKKNFDSLMAIVYFOLLIOEDMNKVLVYNGM-----ASTSSMAALFEI 946  
Db 635 FNFODETPT---TNEFDTPAALIVFOLLIGEDMNAVWYHGISOGGVSGMFSYFYI 690  
Qy 947 ALMTFGNYVFLNVLVAILVEGF-QAEIIGK-----REDASGQ-----LSCI 986  
Db 691 VLTLEFNLTLLNVTLAIVDNLANQELTKDEEMEAANOKLAIQKAKEVAVSPMAA 750  
Qy 987 QLPVNSOGDATKSESEPDFFESPDGDRKKRLALVALGHAELKRSLLPILLIHTAA 1046  
Db 751 NISIAAROONSAAKARSVME-----QASOQLRLQMLRASCEALYSEMDPEERLRA 800  
Qy 1047 TMSLPLKSSSTGVGE---ALGSGSRRTSSGSAEPGAA-----HH-----EMKS 1087  
Db 801 TTHHLRPMKTHLDRPLVYELGDRGARGVYGKARPEALAEQVDPRRHHHRHDXKT 860  
Qy 1088 P-----PSARSS---PSPWSAASWTSSRSRNSJGRADSLKRSBS 1127  
Db 861 PAAGDDRAEPARKEGEGARERPRPHRSHEAA---GPEASESERGRP-----GPE 913  
Qy 1128 GERSLLSGGOSQDEE-----ESSEDRASPAAGSDHRRHGSLE-----REAKSF 1174  
Db 914 GGRHRHRGSPDEAAERPRHRARHODPSKECAGAKERRARHGGPRAGPRRESG- 973  
Qy 1175 DLDPDTLOVPG-LHRTASGRSSASE---HODCNKGSASGRLA-----RTLRTDDPOLDG 1223  
Db 973 -----EPPARRRRARHAKQAPAHAVKETEKEATEKEAEIYVADKEKELNHNQPREH 1026  
Qy 1224 DDDNDEGNLSKGERIQAWRSRLPACCRR-----DSW----- 1257  
Db 1027 CDLETSGTVVGP-----MHTLPSTCLQKVEQEPDADNORVNTMGSPDPPTIYHI 1080  
Qy 1257 -----SAYIFPPPOSRRP 1268  
Db 1081 PVMLTGPLGATVAVPSGNDLESQABGKKEVADDMVRSQPRPIYVYSSMFCISPTINLR 1140

Qy 1269 LICHRLTHKMDHVLVYIIFLNCITIAMERPKIDPHSAERIFLTSNYIFAVLAEMT 1328  
Db 1141 RECHYIVMRFEVEVILVIALISLALAEDEP-VRTDSPRNALKYIDYITFTGTFTEMV 1199  
Qy 1329 YKVVVALGMCFOAYLRSSWVNLGDLVLLISVIDLVSMV-SDSGTKILGMLRVLLRT 1387  
Db 1200 IKMIDGLLHFGAIFRDLMLND-----FIVVSGALVAFARSGSKGKDINTIKSLRLRV 1255  
Qy 1388 LRPRLVYSAQGLKLVETLMSLKPICGNIVYICAFIIFIGIGLOVFKRKEFVCGE- 1447  
Db 1256 LRPLKTIKRLPFLKAVFPCVYNLSKNVNLNLIYMLFMEFIVAVIAVOLKGFYGTDES 1315  
Qy 1447 -----DTRN---ITNKSDDAEASR-VWRHKNYFNLGALMSLVLASKDGMVIMTGL 1498  
Db 1316 KETERDCRGQYLDYKEEVEAOPOPKKTYDRHDVNLALLTLFTVSGEEMPVYLKHSV 1375  
Qy 1499 DAVGVDOOPINHNPMMLLYFISFLIYAFVLNNEVGVVNEFHCKQHODEEBARRRE 1558  
Db 1376 DAYEEQGPSPCYRMBELSFYVYFVFPFFEFVNIYFALIITF-----OEQDKVWE 1429  
Qy 1559 EKRRLKLEKRRNLMDVYIAGSSASASAESACKPY---YSOYSR---FRLVHNLCTSHY 1614  
Db 1430 -----CSLEKNER-ACIDFAISA-----KPLTRIMPONQOSQYKTWTFVSP 1472  
Qy 1615 LDLEFTVGICLVNVTMAMEHYOQOILDEALKICNYIFTVIFVESVFKLVAFGFRFEQ 1674  
Db 1473 FEYFIAMALNTVYLMKMFYDAPYEELMKCLMIVFTSMFSMBCVLIIFAGVLYNR 1532  
Qy 1675 DRWNOIDLAVILSTINGITLEEI-EVNASLPINPITIRIMRLRLARVYLKLLKAVGNRA 1733  
Db 1533 DAMNVDFVTYVIGSTIDILYETIAETN-----NFINLEFLTRFARLIKLRQYTTIRI 1587  
Qy 1734 LDTVMOALPOYNGILFMLEFTFIALGVELFGLDECDETHPECGIGRATERFNGMA 1793  
Db 1588 LMTFVYOSKALPYVCLLAMIPTIYAIIGMOYFNGINALDDO---TSINRHNFTFLQA 1644  
Qy 1794 FLTLFVSTGDMNNGIMKDTLRD---CDOE---STCYNTVISPILYFSEVYLAQVLYNVI 1849  
Db 1645 LMLFPSATGEAMHEIMLSCLSNQACDEQANATEGSDFAFYFVSFLFCFLMLNLFV 1704  
Qy 1850 AYLMKHLSESNKAK-----EEALEAELE-----LEM-KTISPQPHSL 1888  
Db 1705 AVIMDNFEXYLTROSSILGHHNDEFIRVAEYDPAACGISTNDMEMLKHSPP---PL 1760  
Qy 1889 G-----SPLMPGVEGVNSPDSPKPGADHTTAHGAAGFSLE-----HPTWVP 1932  
Db 1761 GLGKKCPARAYARLYVRMNPISNEDMTVHTSTLMALIRTALEIKIAPAGTKOQDAE 1820  
Qy 1933 HPEEVPV-----PLGPDLLTVRKSGVSRTHSLPNDSSYNKRNSTAFERSIG 1977  
Db 1821 LRKEISVYMANLPQKTLDLVPRHKEDEMTGVKYVAA---LMIFEFY---KONKTRIDMO 1875  
Qy 1978 HRWGGLPKAOGSILSVH-----SOPADTSCIQO---LPKDVHYLLOPHGA--- 2021  
Db 1876 QAPEGGL---SOMGVSLFHPYKATLEOTORA---VIRGARVFLRQKSSISLNGALIQO 1929  
Qy 2021 -----PTWGA---IBPLRPPGRSPL-----AQRLPRLROAIRTD----- 2052  
Db 1930 ESGIKESVSGTORQOAPHEARPLERGHSTEIPVGRGALAVADVOMOSITRRGPDCEP 1989  
Qy 2052 ---SIDVOJGDSREDLSEVSGPCLTRSSSFMGSSIOVOQSRSGISQVSHIRLAPAC 2109  
Db 1990 QPGLSEOG---RAASMRLLAETOPVTDASPMKRSISTIAQRRG-----TLGCTTP- 2040  
Qy 2110 PGLPESWAKDPPETRS-----SLELDELSWISGDLPPSSQDEPLSP- 2152  
Db 2040 -----DRPPPSOASHHHHHCHRRRDOKORSLEKGPBLS-ADMDGAPSSAVGGLRP 2091  
Qy 2152 -----RDLKCYSVETOSCHRRRPGSWIDQORRHISIAVSCIDSGQPLCBSPS- 2200  
Db 2092 GEGPTGCRERERERQOERGRQOERQPSSSSEKQRF---YSCDRFGGRPPKPKPLSSSH 2148

QY 2200 -----SLGQPL-----GGPGSRPKKLSL-PSISIDPPES 2229  
 Db 2149 PTPAGCEPBPBGSSGVNCSPLSTSGASTPGRGRRLQPPPLPRISITKTANS 2208  
 QY 2230 -----QGSPPRSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTA 2264  
 Db 2209 SPTHAGQTSPLAFSPGRSLRSLSEHNALLQRPDLSQPLAPGRIGSDPYLQGRDSEA 2268  
 QY 2265 ASPSPKDTLSL-----SGLS 2281  
 Db 2269 SVHALPEDITLTFEEAVATNSGRSS 2292

RESULT 3  
 US-08-455-543A-48  
 : Sequence 48, Application US/08455543A  
 : Patent No. 5792846  
 : GENERAL INFORMATION:  
 : APPLICANT: Harpold, Michael  
 : APPLICANT: Ellis, Steven  
 : APPLICANT: Williams, Mark  
 : APPLICANT: Feldman, Daniel  
 : APPLICANT: McCue, Ann  
 : APPLICANT: Brenner, Robert  
 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 : NUMBER OF SEQUENCES: 57  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Brown, Martin, Haller & McClain  
 : STREET: 1660 Union Street  
 : CITY: San Diego,  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 92101-2926  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ Version 1.5  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/455,543A  
 : FILING DATE: May 31, 1995  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/223,305  
 : FILING DATE: April 4, 1994  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/868,354  
 : FILING DATE: April 10, 1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/745,206  
 : FILING DATE: 15-AUG-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/620,250  
 : FILING DATE: 30-NOV-1990  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/482,384  
 : FILING DATE: 20-FEB-1990  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/603,751  
 : FILING DATE: 04-APR-1989  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: WO PCT/US89/01408  
 : FILING DATE: 04-APR-1989  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/176,899  
 : FILING DATE: 04-APR-1988  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seidman, Stephanie L.  
 : REGISTRATION NUMBER: 33,779  
 : TELECOMMUNICATION INFORMATION: 6362-52517  
 : TELEPHONE: (619)238-0999  
 : TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 48:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2237 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : FRAGMENT TYPE: Internal  
 : US-08-455-543A-48

Query Match 13.7% Score 1703; DB 2; Length 2237;  
 Best local similarity 24.2% Pred. No. 1.3e-127;  
 Matches 650; Conservative 364; Mismatches 850; Indels 826; Gaps 96;

QY 27 GAGGROGPSTERKPGSADSEAGLEPYPALAVF-----FYLGDSRP 70  
 Db 25 GAGGAGGPGPGGLPGQAVLYKQSIAGARATMALNPVKNCTVNRSLFVSEDNV 84  
 QY 71 RSWCLRTVCNPFERYSMLVILLNCVYLLGMFPCEDDACSQRCHLOAFDD--FIFAF 127  
 Db 85 RYAKRITLMPPEFNMIATIIANCIVIAL----EQLPDDGKTPMSRLDTEPYFIGI 140  
 QY 128 FAVENVKMAVAG-IFGKKCYLGTDMNRLDFEIVTAGLVEYS--LDLQNVSFSAVTR 183  
 Db 141 FCFEAGIKITIALGPFPHKGSYLRNGNVMADVYVLTGLATAGTDFDLR----TLRAVR 195  
 QY 184 VLRPLAIRVPSNARILVTLTDLPLMLGNVLLCFEVEFFIGVQVLMAGLNRCEL 243  
 Db 196 VLRPLKIVSGIPSLQVLYKSIKRAVPLIQIGLLFPAIMFAIIGLEFYNGKTHKACF- 255  
 QY 244 PENFSLPLSVLDLEPYQYQENEDESPFCQRENMRCSRVPTLRGGGGGPPCSLDYE 303  
 Db 255 -----PNSTDPEV-----GDFPGCKEAP 273  
 QY 304 TYNSSNITCVMMNOYTYNCSAGEHNPEKGAINFEDNIGYAMIAIPOVTLLEGWDIMFV 363  
 Db 274 ARLCGDTEC--REYWP-----GPNFGLTNPENITLIFALTYFQCITMGWTDIILNT 323  
 QY 364 MD-AHSFNFYIFILLIIVGSEFMINCLVIAVQFSTKQRES-----OLMREORYRF 416  
 Db 324 NDAAGNTNMWLYFIPLIIGSEFMNLVGLVSGFAKERERVENRRFAFLRQOQIE- 383  
 QY 417 LSNASTLASFSEPGSCYDELKLYLILKARLRAQVSRALGVRAGLISSPARVSCQEP 476  
 Db 383 -----RELNGYLEMIFKADEVMAED-----RNAEEK 410  
 QY 477 QPSSGCTSRHRLSYHNLVHHHHHHHHYHNGTLRVPRASPEIODRDANGSRRLMLP 536  
 Db 411 SPLDYLKRAATKKSNDLIH-----AEEGEDRFAD----- 441  
 QY 537 PSTPTPSGGPRGASVSFYNHACHLEPVNCOAPPPPCDSEASGRVGSQKYPVHTS 596  
 Db 441 ----- 441  
 QY 597 PPEELKDKALVEVAPSPGPTLTSFNIPGPFSMMKLELTOSTGACHSSCKTSSPCSK 656  
 Db 441 -----LCAAGSPFAR 450  
 QY 657 ADSGAGPDCPCYARTGAGEPESADHVMDSDSEAVEFTODAQHSDLDLPHSRRQRS 716  
 Db 451 AS-----LKSCTESSSYF-----RRREK- 470  
 QY 717 LGDAEPSSVLAFWRLICDTPRKIVDSKYGKRGIMAILVNTISMGIYEIOPELTLNAL 776  
 Db 470 -----MREF-----IRRVAKQASFTYVWLVCAVANTLCVAAVHYNQPRRLITTL 514  
 QY 777 EISNIVFTSLFALEMLKLYVGFYIKPNYNIFDGVIVISWELVYG-----GGGGL 831  
 Db 515 YFAEYVFLGLFTLMSLKMGLGPRSYFRSSPNCDFGCVIVGSVEYVAALPQSSFGI 574  
 QY 932 SVLRTFRMLRVLYKVRFLPALOROLVVLKMTMDNVATFECMLMLFFITSILGMHLFGCK 891

Db 575 SVLRALRLRIKFKVYKXWSSLRNIVSLNSMKSIIISLLELLFIVFVALLGMOLEFGGQ 634  
 QY 892 FASEBDGTLDPDRKNPSLLMAIVTFOILQEDMKNVLYNGM-----ASTSSMAALYFI 946  
 Db 635 FNFODEIPT-----INFDTFPAAILITVFOILGEDMNAVMHIGISQGVSKGMFSSHYFI 690  
 QY 947 ALMTFGNVYLENLLVAILVEGF--QAEELGK-----REDASGO-----LSCI 986  
 Db 691 VLLTFGNTLLNVFLAIVDMIANAOELTKDEEMEEANAOKLALQAKAEVAEVSMSAA 750  
 QY 987 QLPVNSOGDGTKSESEDFSPVSDGDDGRKKRLALVALGHEALFKSLPLIITAA 1046  
 Db 751 NISIAAROONSAKARSWE-----ORASOLRIQNLRASEBALXSEMDPERLIFA 800  
 QY 1047 TPMSLPKSSSTGVGE---ALGSGSRTSSSGSAEPGA-----HH-----EMKS 1087  
 Db 801 TTRHLRPMKTHLDBPLVVELRGDARGPVGKARPEAAEPEGVDPRRHRHRDKDT 860  
 QY 1088 P-----PSARSS---PHSPWASASMTSRSSRNSLGRAPSLKRRSPS 1127  
 Db 861 PAAGDQDAEAPKASGEPGARKEERPRPHRSKSEA--GPEAKSERGKP-----GPE 913  
 QY 1128 GERRELSGEGESQDEE-----ESSEEDRASPSGSDHRRGSLG---REAKSSF 1174  
 Db 914 GGRHHRGSGPEEAERPRHRRAHRHODPSKECAGAKGERARHRRGGPRAGPREASG- 973  
 QY 1175 DLPTLOVPG--LHRTASGRSSASE--HODCKGSASGRLA-----RLRTDPOLDG 1223  
 Db 973 -----EPPARHRAHRAOPAEHAEVEKETTEKEATEKEAIVEADKEKELRNHQPREPH 1026  
 QY 1224 DDDNDEGNSGERIQAWVRSLPACRER-----DSW----- 1257  
 Db 1027 CPLETSGVTVGP-----MHTLPSTCLOKVEDEPEDADNORANTRMGSOPEPDNTIYHI 1080  
 QY 1257 ----- 1257  
 Db 1081 PYMLTGLGEATVPSGNVDESQAEGKEVEADDMRSGRPPIYPYSMFLCSPTNLIR 1140  
 QY 1269 LCHRIITHKMDHVVYIIFINCTITAMERKIDPHSAERFIILSYITAVFLAEMT 1328  
 Db 1141 RCHYIVTMYREVEVLLVIALISTIALAEDF-VRTDSPRNALAYIDYITFGVTEBMV 1139  
 QY 1329 VAVVALGMCFGCAYLRRSSMNVLDELVLISYIDILVSANV--SDSGTKILGMLRYLRLRT 1387  
 Db 1200 IKMIDGLLLHGAIFRDLMNILD---FIVSAGALVAFARSGSKGXDNITIKSLRYLRY 1285  
 QY 1388 LRPRLVISAQGLKLVETLMSSLKPIGNIVVICAFIIFIGILGOVLFKGFYCGGE- 1447  
 Db 1256 LRPLKTIKRLPKLAVFDCVNSLNKVNILIVYMLFMEIFAVIYVOLFEGKFEYCTDES 1315  
 QY 1447 -----DTRN--ITNKSDCAEASVR--WVRHKYNFDNLGOALMSLFLVASDGVIMYDGL 1498  
 Db 1316 KELERCCROQYLDYEKEVEEAOPROMKATYDHYDNLVALLLFTVSGEGHPWLIKISV 1375  
 QY 1499 DAVGVDOQPIIMHNPMLLYFISFLIYAFVYLNMFVGVVNEFKRCHODEEBARRE 1558  
 Db 1376 DAYEEGSGSPGYRMLSLFYVYVYVPEPFVNFVALLITF-----QOQGSKVASE 1429  
 QY 1559 EKRLRLKKRRNLMDVYIAGSSASASEAQCKRY--YSYYSR--TRLLVHHCISHY 1614  
 Db 1430 -----CSLEKNER--ACIDFAISA-----KPLRYMDONQOSFOYKTWTFVVSPP 1472  
 QY 1615 LDFITGVGLNVYTMAMEHYOPOILDEALKICNYIIFIVFESVEFLVAFGERRFGQ 1674  
 Db 1473 FEYFIAMALNTVYTMAMEFYADPYEYELMKLNVFISMSMECVKIIIFVLIANFR 1532  
 QY 1675 DRWNQDLAIVLSINGITLEEI--EYNASLPINPITIIIRIVRLARLAKILMAVGMA 1733  
 Db 1533 DANNVDFVTVIGSIDIVYELAETN-----NFIMLSPLRFRARLIKRLROGTTIRI 1587  
 QY 1734 LDTVMOALPOVGNLGLIFMLLEFFITAAAGVELFGDLEDETHPGCGLORHATFNFGMA 1793  
 Db 1588 LMTFVQSFRALPYVCLLIAMLEFFIYAIIGMOVFGNIALDDD--TSINRHNHFRFLQA 1644

QY 1794 FLTLFRVSTGNGNIMKDLRD--CDOE--STCYNTVIPSIFYVSVFLTAQFVLVWVI 1849  
 Db 1645 LMLFRSATGEHWEHIMLSCISNOACDEQANATECGSDFAFYVSTIFLCSFLMLNLV 1704  
 QY 1850 AYLMKHEESNKEAK-----EEAELEAELE-----LEM-KTSLFQPHSPL 1888  
 Db 1705 AYIMNFEYLIRDSILGPHLDEFIRYMAEYDPAACGRISYNDMFMLKHMSP-----PL 1760  
 QY 1889 G-----SPFLMPGVEGVNSDPKPRGAPHTTAHGAASGSE-----HPTMVP 1932  
 Db 1761 GLGKCPARVAVKRLVYRNMNDSIMEDMTVHTSLMALTALITAIKILAPACTKOHQDAE 1820  
 QY 1933 HPEEVPV-----PLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSLG 1977  
 Db 1821 LKKEISYVWANIPOKTLDLLPAPHKPDDEMTYGYAA--LMIDFY--KONKTTRDQMO 1875  
 QY 1978 HRGWGLPKAOGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWCAIKPLPPGHSPL 2037  
 Db 1876 QAPGGL--SOMGPVSLFH-----PLKATL 1897  
 QY 2038 AQPLRROAATDSDLDVOGLSREDLSEVSGPSCPLTRSSSFWGSSIQVOQSGIOS 2097  
 Db 1898 EQ--TOPAVLR-----GARVFLROK-----SSTLSNGCATO--NDSGIKE 1935  
 QY 2098 KYSKHRLPAPCPGLEPSWAKD-----PPEYRSSLELDTLSTWISGDLPLPSGOEPLSPR 2152  
 Db 1936 SV-----SNGTROTQDAPHEARPLERG-----HSTEIPVG-R 1967  
 QY 2153 DLKCYSVETQSCRRR-----PGSWLDRQRHSTAVSCUDSGSQPLCSP-SSLG 2202  
 Db 1968 SGALAVDVQMOGITRGPDEGEPOLIESGR--AASMPRIAEOTQPYTDASPMKRSISTLA 2036  
 QY 2203 GQPLG-----GPGSRPKKLSP-----PSISID--PPES- 2230  
 Db 2027 QRPGRTHLCSTTPDRPPPSQASHHHHRCHRRDRKORSLKEGSLDADMDGAPSSAVG 2086  
 QY 2230 QGSRPPSPGVCLR-----RRAPASDKDPSSVSLDSTAASSPKKDTLSL 2276  
 Db 2087 PGLPPEGPTGCRKERERQERGRSGOERQOPSSSSSEKQRFYSCDRFGREPPKRX- 2143  
 QY 2277 SGLSOPTMDPVLPLPHLSPPGADPSSASMAFLKSPTAASHAEAPHL-PSVAGCD 2335  
 Db 2143 PSLSSHPTS-----PTAAGE--PGHPQAGSAVG--PNTTPCCRETPSAPWLA- 2190  
 QY 2336 DPQNFRRVDLKTQPV-----SPCLREGEKGESEVPW--RLPPTPG 2373  
 Db 2190 -----LELALITMGVSWTVRPLSTPOLRTRISRR-LWPPTRAADPG 2231

RESULT 4  
 US-08-223-305C-48  
 ; Sequence 48, Application US/08223305C  
 ; Patent No. 5851824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael  
 ; APPLICANT: Ellis, Steven  
 ; APPLICANT: Williams, Mark  
 ; APPLICANT: Feldman, Daniel  
 ; APPLICANT: McCue, Ann  
 ; APPLICANT: Brenner, Robert  
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brown, Martin, Haller & Mcclain  
 ; STREET: 1660 Union Street  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92101-2926  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223.305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-48

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Query Match 13.7%; Score 1703; DB 2; Length 2237;
Best Local Similarity 24.2%; Pred. No. 1.3e-127;
Matches 650; Conservative 364; Mismatches 850; Indels 826; Gaps 96;

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QY 27 GAGGAGGPGSTKDPGSDSEAEGLPYALAPVVF-----FYLSQDSRP 70
DB 25 GAGGAGGPGGPGGLQGGQVLYKQSIQARFATMALYNPIPVKQNGFTVNRSLFVSESDNV 84
QY 71 RSMCRJTCNPFERFVSMVLINCVLTGMFPCEDDIACDSORCRILQAFDD--FTFAF 127
DB 85 RYARIRIEMPFEMMILATIANCIYAL-----EQHLPGDGKIPMERLDDTPYITGI 140
QY 128 FAVENVKVALG-IFGKKCYIGDTNRLDFEVIAGLXES---LDLQNVSESAVTR 163
DB 141 FCFEAGIKIALGFVFGHGSYLRNGMVMDFVVVLGTILATAGTDFDLR-----TLRAVR 195
QY 184 VCRPAIRIRVPSMRILVTLTDLTPMLGNVLLCFVFFIFGIVGVQIANGLLRNCF 243
DB 196 VLRPLKLVSGISLOVLYKSIKAMVPLIQTGLLFIILFAITGLFEYIGKHKACF- 255
QY 244 PENFSLPLSVLDLEPYQYQENEDSEPFICSQPRENGMRSRCSVPTLRGEGGPGCSLDYE 303
DB 255 -----PNSTDAEPV-----GDFPCGKEAP 273
QY 304 TYNSSNTTCVMMNQYITNCAGHNPFKGAIPNDNTGYAMIAITFOYITLEGVWDIMYFV 363
DB 274 ARLCGSDTCC--REYVP-----GNFGITNEDNLLFALITVFQCLTMGMDLILXNT 323

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QY 364 MD-ASHFYNYFTYILLIVSGFENINICLVIAITQSEIKORES-----QLMREQRYAF 416
DB 324 NDAAGNTWMLYFTIPLIGSFMLNIVLGVLSGEFAKEREVENRRAPFKLRQOOIE- 383
QY 417 LSMNSTLASFSPGSCYEELIKYLVYILRKARRLQVSAIVRRGLSLSPARSGQSP 476
DB 383 -----RELNGYLEWLFKAEEVMALED-----RNAEEK 410
QY 477 QPSGCTSRHRLSVHHLVHHHHHHHHHGLNGTLEKVPASPEIODRDANGSRRLMLPP 536
DB 411 SPLDYLRKAATKSKSRNDLIH-----AEQGDREFAD----- 441
QY 537 PSTPTSGGPPRGAEVSASFYHADCHLEPVRCQAPPPRCSEASGRTVSGKYPTVHTS 596
DB 441 ----- 441
QY 597 PPEELIKQALVEVAPSPPTLTSFNIPGPFSMHKLETOGTACHSKICKSSPCSK 656
DB 441 -----LCAVGSPFAR 450
QY 657 ADSGACGDPSCPYCARTGAGEPESADHVMPDSDSEAVEYFTQAOHSDLRDPHSRRORS 716
DB 451 AS-----LKSQTESSSYF-----RKREK- 470
QY 717 LCPDAEPSSVLAFWRLICDIFRKIVDSKYFGRGIMAILVNTLSMGIEYHEOPELTNL 776
DB 470 -----MFRF-----IRRVAKQSFYVYVLCVALNTLCVAMVHYNDPRRLITTL 514
QY 777 EISNIVFTSLFALEMLKLKLVYGPFGYIKNPYNI PDGVIVISWEIVQO-----OGGL 831
DB 515 YFAEVEFGLFTLMSLKMVGLGRSYFSSFCDFGVIGSVFVMAAIKPGSSFGI 574
QY 832 SVLRFRRLMRVLKIVRFLPALOROLVLMKTMNVATFCMLLFIETISGMHFGK 891
DB 575 SVLRALRLRLRFKVKTKWSSLRNLVSLNSKSTISLFLFLFYRLVRLSMQLGQ 634
QY 892 FASERDGTLPDRKNSFDLSLMAIVTVFQILTDWKNVLYNGM-----ASTSSMAALYFI 946
DB 635 FNFODETPT-----TNDFPAILITVFQILGEDMNAVMVHGIESGGVSKGMSFYFI 690
QY 947 ALMTFGNVLEFLNLVAILVEGF-QAEIIGK-----REBASQ-----LSCI 986
DB 691 VLTTFGNTLTLLNVLPAIVDNLANAQELTDEEBEMEANAQKIALOKANEVAEVSMSA 750
QY 987 QLPVNSQGDATKSESEDFSPVSDGDRKKRLALVALGEAEELKSLPLILHTPA 1046
DB 751 NTSIARQONSAAKRSYWE-----QASQLRLQNLRASCALYSMDDEELRFA 800
QY 1047 TPMSLPKSSSTGVGB-----ALGSGSRRTSSGSAEPGA-----HH-----EMKS 1087
DB 801 TTRHLRPMKTHLRPLVLVELGRDARGPVGKARPEAAEAPGVDPPRRHHRDRDKRT 860
QY 1088 P-----PSARSS-----PHSPMSASAMTSRRSRNSLGRAPLKRSPS 1127
DB 861 PAAGQODAAEAPKAESGEPGARERPRPHSHSKTEA--GPPARSRGRGP-----GPE 913
QY 1128 GERRSLLSGEOESODEE-----ESSEDRASPAQSDHHRGSLF-----REAKSSF 1174
DB 914 GGRFHRHRGSPPEAEERPRHRRAHRHODPSKCECAGKGRRAHRHGGPRAGPREAESG- 973
QY 1175 DLPTLQVPG-LHRTASGRSSASE--HODONGKSASGRLA-----RLTRDDDDQLDG 1223
DB 973 -----EPPARRHRRAKAPRAEVAVEKETTKEKATEKELEYEADKEKELRNHOREPH 1026
QY 1224 DDDNDEGNLSKGERIQAMVRSRLPACCRER-----DSW----- 1257
DB 1027 CDLETSGTIVGP-----MHTLSTCLQKVEQPEDADNQNRVTRMGSGOPDPDNTIVHI 1080
QY 1257 -----SAYIFPQSRFR 1268
DB 1081 PYMLTGLGEATVYVSGNVDSQAEFKKVEYADVDWRSGPRPIVYSSMFCISPTNLIR 1140
QY 1269 ILCHRITTHKMDHVAVIIFLNCITIAMERPKIDPSAERIFLTLSNYITFAVLAEMT 1328

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1141 RCHIVIMRFEVIVILVIALSSIALAEDP-VRTDSPRNNAKLYDLYFTGFFEMV 1199
1339 VKVVALGMCFOEOAYLRSSBNDGLLVILSVIDLVSVM-SDSGTKILMLRLRLRT 1387
1200 IKMIDGLLHPGAFRDLNILD-----FIYSGALVAFASGSKGDIINTKSLRLRV 1255
1388 LRPLRVISRAOGLKLVETLMSLKIPGIVNICCAFFIIGLVOLFGEKFEVCGE- 1447
1286 LRPLKTRKRLKRAVDCVNSLKNVNLILVYLMFIFPAVAVOLFNGKFEYCTDES 1315
1447 -----DTN--ITNKSDEASR-WVRHKYNPNLGOALMSLVASXGQWVIMDGL 1498
1316 KLEERDCGOYLDYEKEVEAOPQWKKYDFHYDVMALTLFTVSTGESMPVILHNV 1375
1499 DAVGDOOPIMNHPMLLFIYFLLIYAFVLMFVNVENHCKROHDEEABRE 1558
1376 DATEEGSPSGYRMLSLIFVYVFPVFPFFVNFVLIITF-----QEGDKVME 1429
1559 EKRLRLEKRRNMLDVLVIGSGASASEROCKPY--YSDYSR--PRLVHLCTSHY 1614
1430 -----CSLEKNER-ACIDPAISA-----KPLRYPONQSFQYKWTFTVSP 1472
1615 IDLFTGVIGLVNVMAMENHQQOILDEALKICYFTVIFVESYKLVAFGRFRFQ 1674
1473 FEFTMAMALTVVLMKFDIAPYEELMLKLNIVFTSMFMCVAKIIFGVLANFR 1532
1675 DRMNOLDLAVLLSIMGITLEEI-EVNASLPIPTIRIMVRLIARVLKILKAVGNRA 1733
1533 DAMNVDFEYTVGSITDLIVTEIAETN-----NFYINLSEFLRFAARLIKILROGYTTRI 1587
1734 LLDTVQALPOVGNIGLFLMLFFIFALVGLVFDLDECHPEGGRHATRNFGMA 1793
1588 LMTFVQSFRAKPYVCLLILMFLIYALIGVFGNIALDDO--TSINRNNRTFLOA 1644
1794 FTLFVSTGDMNGIMKDLTD--CDOE--STCYNTVISPITYSEVLYAOVLYNVI 1849
1645 LMLTFPSAIGEMHEIMSLCSNOACDQANATEGSDPAFYFVSFELCSLMLNFV 1704
1850 AVLKHLSESKNEAK-----EERLEPAELE-----LEM-KLSPQPHSPL 1888
1705 AVIMDNFEYLTGDSILGPHHDEFLRVAEYDPAACGRISYDNFEMLKHSNPL 1760
1889 G-----SPLMPGVEGVNSPSPKGAHTAHIGAAGFSL-----HPTWVP 1932
1761 GLCKKCPARAVAKRIVRAMPISNEMIVHTSTLMALRTMLKILAPAGTKOQCAE 1820
1933 HPEEVPV-----PLGPDILTVRKSGVSRTHSLPNDSTYCRNGSTABESLG 1977
1821 LRKEISVVMANLPKTLIDLVPKPKDEMTGVKYAA--LMIFDFY--KOKKTRDQMO 1875
1978 HRWGLPKAKOSGILSVHQPADTSCILDLPRDVNLLQPHAPWGAIPKLRPPGRSPL 2037
1876 QABGGI--SOMGEVSLFH-----PLKATL 1897
2038 AQRPLRROAIRTSLDVOGLSREDILSEVSGPSCPLTRSSFWGSSIOYQOBSIGQS 2097
1898 EQ---IQPVLNR-----GARVFLRQK-----SSTSLSNGAIDQ-NQESGIKE 1935
2098 KVSKNIRLPAPCGLEPSWAKD-----PPTNSSLDELDELWISGDLPLSSQOEPLSPR 2152
1936 SV-----SWGTORTODAPHEARPLERG-----HSTELIPVG-R 1967
2153 DLKCYSVETOSGRRR-----PGSWLDEORRHIAVSCDLSGSRPLCSP-----SLIG 2202
1968 SGALADVQMOSTTRKRODGPGLSOGCR-AASMPRLAETQPTDASPKKRISITLA 2026
2203 GCPUG-----GPGSRPKKLSP-----PSISID--PPES--- 2230
2027 QRRGRTGLCSTPDPRPPQASSHNNHRCRRDRKORSLEKPSLSADMGAAPSAAVG 2086
2230 QGSRPPCSPEVCIR-----RRAPRADSNDPSVSSPLDSTAAPSCKDTLSL 2276

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Db 2087 PELPBGPGTCRRRERERGRSGRQERRQPSSSSSSEKORFYSCDRGGRPEPKK 2143
Qy 2277 SGLSSDPTDMDVPLETLPHLHSPGADPSSASNAFLKSPFAASHAPH-PEVSGD 2335
Db 2143 PSLSSHPTS-----PTAQOE--PQHPQASAVGF--PNTTPCCRTFPSASPPPLA 2190
Qy 2336 DQGNFRVYLKRTCPW-----SPCLREKKGESPVMP--RLPTPG 2373
Db 2190 -----LELATLWGSWVYVRPLSTPCLTRLSRR-LMPPTRAAPG 2231

RESULT
US-08-435-675B-4
Sequence 4, Application US/08435675B
Patent No. 5710250
GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Brenner, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435, 675B
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314, 083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914, 231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603, 751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53193
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-435-675B-4

Query Match 12.9%; Score 1608.5; DB 1; Length 1873;
Best Local Similarity 23.6%; Pred. No. 3,9e-120;
Matches 577; Conservative 356; Mismatches 692; Indels 823; Gaps 82;
Qy 32 QGPGSTKDPGASASEAGLEYPALAVVFFYLSODSRPSWCLRTVCNW-FEVSM 89
Db 7 QDEGLRKKOPKPLPEV-LPRP---PRAFLCILTIONPLKAKISIV-EWKFFETIILL 59

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Db 1650 DARTNPLARANTNANAVNGSNNSNNQMFSSVH-----CERFFPCEAEETPAAGRGA 1703  
 Qy 2127 LEIDTELSTWISGDLPSQEEPLSPDLKCYSEVETQSCRRRPGSWLDEQRHSHAVSCL 2186  
 Db 1704 L-----SHSRALGPHS-KPC-AGKINGOLVQGMGMINO----- 1736  
 Qy 2187 DSGSOPRLCPSPSLGQOLPGSPGSRPKKLS-PPSISIDPPE---SOGSRPPCSGVCVL 2242  
 Db 1736 ---APAPCOQPSY-----DPPERQORTSTLGSLODEAPORRSSEGSTP----- 1778  
 Qy 2243 RRRAPASD--SKDPSVSSPLDSTAASPSPKKDLISGLSDPTDMDP 2288  
 Db 1778 RRRAPATALLQELALVNGGIDTLAADAG---FWAITSQALVDACQMDP 1822

RESULT 6  
 US-08-336-257A-7  
 : Sequence 7, Application US/08336257A  
 : Patent No. 5726035  
 : GENERAL INFORMATION:  
 : APPLICANT: Jay, Scott D  
 : APPLICANT: Ellis, Steven B.  
 : APPLICANT: Harpold, Michael M.  
 : APPLICANT: Campbell, Kevin P.  
 : TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 : NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Brown, Martin, Haller & McClain  
 : STREET: 1660 Union Street  
 : CITY: San Diego  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 92101-2926  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ version 1.5  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/336, 257A  
 : FILING DATE: 07-NOV-1994  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seigman, Stephanie L.  
 : REGISTRATION NUMBER: 33,779  
 : REFERENCE/DOCKET NUMBER: 54898  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (619) 238-0062  
 : TELEFAX: (619) 238-0062  
 : INFORMATION FOR SEQ ID NO: 7:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1873 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : FRAGMENT TYPE: internal  
 : ORIGINAL SOURCE:  
 : US-08-336-257A-7

Query Match 12.8%; Score 1597.5; DB 1; Length 1873;  
 Best Local Similarity 23.4%; Pred. No. 3e-119;  
 Matches 574; Conservative 356; Mismatches 666; Indels 841; Gaps 82;

Qy 32 QCPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRRPSKCLTYCNPW--FERVSM 89  
 Db 7 QDEGLRKKQPKRPDPEV--LPRP---PRALFCLTLQNPRLKACISIV--EWMKPEITILL 59  
 Qy 90 VILLNCVLTIGMRPC-EDIACDSQRCRT-LQAFDFTFAFVAVVAVMALG-IFGKKC 146  
 Db 60 TIFANCVALLAVLPMPEP---DNNSLNLGLEKLEFFFLVESIEAMKIIAYGFLFHODA 116

Qy 147 YLSDTNRLDPEFIYIAGMLEYSLDIONV-----SFSAVTVRLRLRAI 191  
 Db 117 YLRSGMKNVDEITVELEFFAILLEOVNAVIOSTNAPMSKSGAGIDVAKALAEFVRLRLRLV 176  
 Qy 192 NRPVSMRLVTLIDTLPMLGNVLLCFEVEFFETGIVQVQVLMAGLLRNRCFLDENFSLP 251  
 Db 177 SGVPSLOVAVNSIFKAPMLPFHIALVLFWIITAIIGLELFGKHNKICY----- 229  
 Qy 232 SYDLEFYQIENDESPFISQPRENEMRSCRSVPTLRGGGGGPPCSUDYEYSSNT 311  
 Db 229 -IGDIYAATVENEKPS-CART-----GSGRPC-----TINS- 260  
 Qy 312 TCVMNNGYITNCASGEHNPEKAINFDNIGYAWIAIFOVITTEGWDIMYVMDA-HSEY 370  
 Db 260 -----ECRGWPGPNHGITHFDNPGFSMLTYQCLTMGMWDVLVWVNDALIGNEW 309  
 Qy 371 NEIFYILLIIVGSEFPMINCLVITATOFSETKQRESQLMREORYRFLSNASTLASSEFG 430  
 Db 310 PWIYFVTLILGSEFILLVLGLVSGEF--TKEREKAKSR-----GTQKLEKQ 357  
 Qy 431 SCYEELLKYLVIILKARLAQVSRALGVRAGLLSPVARSGEQEPQSGGCTSRHRLS 490  
 Db 358 QLEEDLRGKMSWITQ-----GEVMDVEDLREGKLS----- 388  
 Qy 491 VHLVHHHHHHHHYHLNGTLFVPRASPEIQRDANGSRMLPPTPTPGGPPRGA 550  
 Db 368 -----LEEG----- 393  
 Qy 551 ESWHSEFYADCHLEFVRQCAPPPCPSPASGRIVGSKVPTVHTSPPELIDKALVEY 610  
 Db 393 ----- 393  
 Qy 611 APSPPPLTSLNIPPGPFSSMHKLETOSTGACHSSCKISSPCSKADSGACGDCPYC 670  
 Db 393 ----- 393  
 Qy 671 ARTGAGEPESADHVDPDSSEAYE-----FTQDAQSHLDHPHSRRRQSLGPDAPS 724  
 Db 393 -----SDTESIVEIEGLNKIIQFIRH----- 414  
 Qy 725 SYLAFWRLICDTER---KIYDSKYFGGIMAILVNTLSGITYHHPPELTALAEISN 780  
 Db 414 -----WROMNRVFERKCHDLVKSRYFVWLVILVALNTLSIASHHNPDWLTHLODTAN 468  
 Qy 781 IYETSLEFLEMILKLLVGPREGYIKNPINIFDGVIVISWEIYGOOG-----GLSVLR 835  
 Db 469 RYLLSFTIEMLLKRYGGLGRYFMSITFNRPDCFYVCGIIEILLVSEGANTPIGISVLR 528  
 Qy 836 TRLMRVLELVLPALOROLVLTMDNVATFCMLMLFTIFISILGHLFGCKASE 895  
 Db 529 CIRLRLFKITRYKWTSLSNLVASLNSIRSIASILLLLEFIIFALGLOFGGRVDFE 588  
 Qy 896 RQGDITPDKKNFDSLLMALVYFOLITQEDMKVLYXNMASTSS-----MAALYFALM 949  
 Db 589 ---DTEVRRSNFDPQALISVFOVLTEBDMNSVNTGIMAYGGEYSYGVLYCIYIFILE 645  
 Qy 950 TEGNVYLFMLVAIIVEGF-QAEIIGKREDASGQLSCIQLPVNSOGGATKSESEDPFFS 1008  
 Db 646 VCGNITLLVFLAVNDNAEASL-----TSAQAKAE----- 680  
 Qy 1009 PSYDGDGDKRRKLALVALGEHAELKSLPLIITHTAATPMSLPSKSSSTGVGEALGSSR 1068  
 Db 680 -----ERRKRRMSKGLPDKTEEKSVV----- 702  
 Qy 1069 KTSSSGSAEPGAHHHMKPPPARSSPHSPWASASWTSRRSRSNLSGRAPSLKRSPSG 1128  
 Db 702 -----AKKLEK-PKG 711  
 Qy 1129 ERRSLISGEOSEODEEESSEEDRASPAQSDHRHSGSLEREAKSSFDLPDLQVYGLHRT 1188  
 Db 712 EG---IPTAKLKVDFEENAVNEVKDP-----YPADPP----- 743  
 Qy 1189 ASGRSSASEHOCNGKSSASGRILARILRTDDPOLDGDNDNDBGNLSKGERIQAWVNSRLPA 1248



[illegible]

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Db 1695 ETPLAGSAL-----SHSRALGPHS-KPC-AGKINGOLVQMPMPINO-- 1736
QY 2175 RSLAVSCLDSGSPRLCPSPSSIGCGPLGPGSRPKKLS-PPSISIDPE---SOGSR 2233
DY 1736 -----APPACQGPST-----DPERGQRRLSLIGSLQDEAPQSRSEGST 1776
QY 2234 PRCSPGCLRRRAPAS--SKDPSVSPDLDAASPSPKKDLTSLGSLSDPTMDP 2288
Db 1777 P-----RRPAZATALLIOEALVNRGDLDTLADAG---FVATSOALVDAQMER 1822

RESULT 7
5386025-6
Patent No. 5386025
APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
M.; CAMPBELL, KEVIN P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,384
FILING DATE: 20-FEB-1990
SEQ ID NO: 6
LENGTH: 1872
5386025-6

Query Match 12.8%; Score 1595; DB 4; Length 1872;
Best Local Similarity 24.7%; Pred. No. 4,7e-119;
Matches 492; Conservative 300; Mismatches 535; Indels 666; Gaps 58;

QY 32 QCGSTKDPGSDSAEGLPYALAPAYVEFLSDQSRPSMCLTYCPW--FERVSKL 89
Db 7 QDGLAKKQPKRPLEV--LPRP--PRALFCLTLQNPRLKACISIV--EMRPFETILL 59
QY 90 VILLNCVYLGMFRPC-EDIACDSQRCRI-LQAFDDFEAFVAVENVYKVALG-IFGKK 146
Db 60 TIFANCVAAVLYLPMED--DNNSLNLGELKELEYFLLVFTEAMAMKIIANGFLHODA 116
QY 147 YLGDTRNLDFEFLVLAGMLESLDQNV-----SFSAVRYAVLRPLRAI 191
Db 117 YLRSGNNVLDFTIVLGVFTALILEOVNVIQSTAPMSKAGLDVAKRARVRRLRY 176
QY 192 NRVPSMRILVTLDLTLPMLGNVLLCEFEVFIFGIVQVLMAGLRRRCFLPENFSLPL 251
Db 177 SGVPSLQVVLNSIFRAMPLPHIALVLFMVIIYIILGELFKGMHKTYY----- 229
QY 252 SVDLLEYVYTEHEDESPFLCSQPRENGMRSCRSVPTLRGEGGCGPCLDYETYNSSNT 311
Db 229 -IGTDIVATVENEKSP-CART-----GSGRPC-----TINGS--- 260
QY 312 TCVNNQVYTTNSAGEHNPFKGAINEFDNIGYAMIAIFOVITLEGVDMIVYMDA-HSFY 370
Db 260 -----ECRGTPGNGHITHEDFNGFMSMLTYVCTIMEGTDVLYVDNAILGEMW 309
QY 371 NITVITLLIIVSFMVINCVLVIATQFSETKQRESQIMREQVRFLSNASTLASFSFPG 430
Db 310 PVIYVITLLISFPLINDLVGVLSGEF--TKEREKASR-----CTPQKLEKQ 357
QY 431 SCYEETKLVLYTLKKAARLAAOVSRAIGVANAULLSSVVAASGDEPQPSGCTSHRRLS 490
Db 358 QLEEDLRGYMSITQ-----GEVNDVJDLREGKLS----- 388
QY 491 VHHLVHHHHHHHHYHLNGTLRVPRASPEIODRDANGSRRLMDPPSTPPSGPPRGA 550
Db 388 -----LEEG----- 393
QY 551 ESVSHFYHADCHLEPYRCQAPRRPCPSASRTYVSGSKVYPTVHTSPPELTAKDLAVEY 610
Db 393 ----- 393
QY 611 APSGPPLTISFNIPGPFSSMHKLELTQSTGACHSSCKLSSPCSKADSGACGPDSCPYC 670
Db 393 ----- 393

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QY 671 ARTGAGEPEADHWPDSDSEAYE-----FTQDAQSHDLRDPHSRRORSIGPDAPS 724
DB 393 -----SDTESLEYIEGLNKIIQFIRH-----414
QY 725 SYLAFWRLICOTFR-----KIYDSKIFGRCIMAILVNTLSMGIEYHQPPELTALNISN 780
DB 414 -----WRCMNVRFRWKCHDLVSRYFWLVILVAILVANTLSASEHHNQPLMLTLQDIAN 468
QY 781 IYFTSLFALMLLKLIVYGPFGYIKNPYNIDGVIVIVISWEIYGOOG-----GLSVLR 835
DB 469 RYLLSLFTIEMLLKMYGGLRGYEFMSINRFDCEYVCSGIELLELLVEEGANTPGISVLR 528
QY 836 TFRLMRVKLVEFLPALOROLVYLMKTMQNVATFCMLMFIYFISILGMLFEGCKRASE 895
DB 529 CIRLLRLEKITKYWTSLSLNVLASLINSIRIASLILLFLFIIFALGMOLFGRYDFE 588
QY 896 RQGDLLPRKKNFDSLMLIVYFOILTOEDMNVKVLNGMASTSS-----WAALYFIAM 949
DB 589 -----DTEVRSRNPDNPQALISVQLYTGEDMNSVYNGIMAYGSPVLCVITIFILE 645
QY 950 TEGNYVLFNLVAILVEGF-QAEIIGKREDASGOLSCIQLPVNSQGDATKSESEPDFS 1008
DB 646 VCGNILLNVFLAIVDNLAESAEST-----TSAQKAKAE-----680
QY 1009 PSYDGDGDKRKLALVALGEHAEHLKSLPLIHTATPMSLPKSSSTGVGALGSGSR 1068
DB 680 -----ERRRRMSRGLPDKTEERSVM-----702
QY 1069 RTSSGSAPEGAHHEMKSPSARSSPHSMASSWTSRRSSRNSLGRAPSLKRRSPSG 1128
DB 702 -----AKLEBK-PKG 711
QY 1129 ERRSLLSGEGQSDSEESSEEDRASPSAGSHRHGSLERAKSSFDLPDITQVGLHRT 1168
DB 712 EG---IPTTAKLVDEFEENVEVXDP-----YPSADPP-----743
QY 1189 ASGRSSASASHOONCKSASGRLARTLRTDQPOLDDDDNDGCLSKGEITQAVRSRPA 1248
DB 743 -----GDDEDEPEIYVSPRRRLAQL-767
QY 1249 CCRER-----DSWSAYIFPPQSRFLLCHRTTHKMDHVLVILFNCITIAMRPPKD 1303
DB 767 --KEKAVPIPEASSFFIFSPTNKVFLCHRIYATWTFNIFILLSSAALAE-----D 820
QY 1304 PHAEKFIPLTNSYI---FTAVFLAMTYKVALGCMCFEQAYLSSWVNLGLLVILYS 1360
DB 821 PIRAESVRNOILGFDIAFTSVFTYVILKMTTYGALFHKGSCRYFNIIDLVAVS- 880
QY 1361 IDLIVASVDSGTIKLGMRLVRLRLTLRPLRYISRAOGLKLVETIMSLKPIGNIVY 1420
DB 880 ---LISMGLEST--ISVAKILAVLVRPLRAINRAKGLKHVQCVFAITIGNIVLV 934
QY 1421 CCAFFIIFGLVQLFKGFEVCOGEDTRNITNKSACAASY-----RWY 1465
DB 935 TILQFMFAICIGVOLFKGKFFSC--NDLSKMT-EEECRGYYVYKXGDPTOMELRPMOI 991
QY 1466 RHYXNDNLGQALMSLFLVASKQWDVIMDGLDAVGVOOPIMNPNMMLYFISFLI 1525
DB 992 HNDHEBNVLSAMSLFTYSTFGWQOLYRALDSNEEDMGVYNNRVEMALFIIYIIL 1051
QY 1526 VAEFVLNMFVGVVVENFHCROHQBEEARREERKRLRLEKKRMLMDVYIASSGSAS 1585
DB 1052 IAFPMNMFVGFIVTF-----QEGGFEYKNC-----LDKNQRCV-----QYAL 1093
QY 1586 AASEAOCKPYSDYSRRLVHLCHLSHYDLFITGVIGLVNTYAMMEHYOQOLIDEAL 1645
DB 1094 KARPLRC---YIRKNPYQYVWYVYVYSYEFIMFALIMLNTICLGMORHQBSEEMNHS 1150
QY 1646 KICVYITVIVFESVFLKVAFGRRREFODRMNOLDLAIYLLSINGITLEEIEV----- 1700
DB 1151 DILNVAFTIIFTEMLIKLAFKARGFGDPWVDFDLIYIGSIDVILSEIDTFLASSG 1210

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QY 1700 -----NASLPINPTIIRMRVLRIRAVLKLKMAVGMALLDTVMAQALPOV 1745
DB 1211 GLXJAGGCGGNVDPDESARISAFRLFRVRL-----IKLLSRAGVRLTLWTFIKRSQAL 1267
QY 1746 GNIGLIFMLFIFALGVELEGLE-CEETHPCBGLGRHATFRNFGMAFLTLRVSTIGD 1804
DB 1268 IYVALLIYVLFYIAVIGMQMGKIALVDGTO---INRNNNFOTFFPOAVLLFRCAIGE 1323
QY 1805 MNNGIMKDL--RCDQDQES-----TCYNTVISPITYFSFVLTAQFVLNVYIAVLM- 1854
DB 1324 AMOEILLACYSKLDPESDVAPGEETC-GTNPAYTTFISYMLCAPLITNLEVAVIMD 1382
QY 1854 -----KHLESNKAEKAELEAE--LELEMKTISPOPHSPLGSPFLWP- 1896
DB 1383 NPDYILRMSIILGPHHLDLF-KAIAAEYDPEAKGRIKHLDVYTLRLRIQPLGEGKFCPH 1441
QY 1896 -----GVEGVNSP 1903
DB 1442 RVACKRLVGMNMP 1454

RESULT 8
US-08-455-543A-51
Sequence 51, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
City: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899

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QY 1817 CDQES-----TCYNTVISPIYFSGVLVLAQFVLNVYAVL-----1854
Db 1421 CDPESDYNPGEHFC-GNFAIVFISYIMCALITLNLVAMDMFDYLTIDMSTLGP 1479
QY 1854 KHEESNKEAEAELEAE--LELEKTLSPQPHSPGLSPFLMP-----GVEGVNSPD 1904
Db 1480 HHLDEF-KRINSEYDPEAKGRIKHLVDVTLRLRIOPLGFGKLCPRHVACKRLVAMMPL 1538
QY 1905 SPKPGAPHTTHIGASCFSL-----HPMVPHEEVPVPLG 1942
Db 1539 N-SDGTVMFNATLFLATYALKITEGNLQANEELRAVIKIKWKTSMKLLDQVVPAG 1597
QY 1943 PDLTVRK-----SGVSRTHSL-----1960
Db 1598 DDEVTVGKFYATFLIQDYFRFKRKEEGLYGKYPARKTTIALOAGRLTHIDIGPELIRA 1657
QY 1960 -----PNDSYMCRNG-----STAERSLGHGNG 1982
Db 1658 ISCDLQDDEPETKREEDDYFKRNGALLGNHVNHSDRRSLQQTWTRHPLHVORPS 1717
QY 1983 LPKAQ-----SGSLSHVSGPADISCIQLPKDVHYLLQ-----PHG-APTMGA 2025
Db 1718 IPPASDTKPLEPPAGNSV-CHNHNHNSIGKOVPTSTNANLNNAKAAHGRPSIGN 1776
QY 2026 IPKLPPPG-----RSPLAQPLR-----QAIKRTDLDVQ-----2057
Db 1777 LHVSENGHSHKHDRQRRSSVYKRRYETIRSDSGDQLPTICREDPEIHGFRD 1836
QY 2057 --GLGSRDLSEVSGPSCPLTRSSSEWG-----GSSIOVQORSG-----2095
Db 1837 PHCLGHOEFSESE--ECYEDSSPTWSRONVGYISRYPGRNIDSEPRGYHHPQGFLE 1892
QY 2095 -----IOSXSKHILRLAPCGGLEPNAKPPETRSSLELDTLSWISGDLPPSSOE 2147
Db 1893 DDDSPVCDRSRSPRRRLPPTPA-----SHRSSFNELCRROSSOEVPSS---1941
QY 2148 PLSPRDLKCYEVETOSCRPRRPSWLDQRRHSIAVSCIDSGSOPRLCPSPSSIG-GGPL 2206
Db 1941 PLRFP-----HRTALPLHMQOQIMAVAGLDSKAKGYSPSHSTRSWATP-1985
QY 2207 GGGSRPKKLSL--PSISIDPPES--OSSRPPCSGVCLRRARAASDKDPSVSP 2259
Db 1985 --PAPPPYRDWTPCYTPLLQVQSEALDQVNGSLP-----SLHSSWYTBEPDISTRFT 2036
QY 2260 LOSTASPSPKDTLSLGSIDPTMDPVLPPLPHHLSPPGADSSASMAFLKSPTA 2319
Db 2037 TPASLTVPSSFRKKNSDKQRSADSL-VEAVL--ISEGLGRVARDKRYVS-----A 2083
QY 2320 SSHE 2323
Db 2084 TKHE 2087

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COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO Version 1.5
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062 51:
INFORMATION FOR SEO ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-223-305C-51

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Query Match 12.7% Score 1579; DB 2; Length 2161;
Best Local Similarity 23.1%; Pred. No. 1,1e-117;
Matches 598; Conservative 366; Mismatches 748; Indels 872; Gaps 84;

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QY 31 ROGSGTERKDPGADSEAEGLPPALAPVFFYLSQDSRPRSNCULTVCPMP--FERVSM 88
Db 85 ROQYAKSKKQGNSSNR-----PARA--LFCLSLNPIRRACISIV--EWKPDFIL 133
QY 89 LVILLNCVTLGMFRPCEDIDACDQRCRILQAFDDFTFAFFAYEMVVKMALG-IGKKRY 147
Db 134 LAIPANCVALAIYIPPEPDSNSTN-HNLEKVEAFLLIFTVETFLKILAYGLLHPNAY 192
QY 148 LGDTWNRLDFFIYAGLWLEYSIDLQVNS-----FSAVRVVLRPLRA 190
Db 193 VRNQMNLDFVIYAVG--FVILDEOLITKETEGNHSKSGSGFDVKALRAFVLRPL 250
QY 191 INRVSMRIIVTLTLDLTPMIGVLLLCFVFPIFGIVQVLAAGLLRNKCLPENESLP 250
Db 251 VSGVPSLOVNLSTIKMAYPLHLHALLVLFVITIIYALIGLELFGKMHKTCFPA 307
QY 251 LSVLDPEYQTEENDESPFICOPRENGMRSRCSVPLRGEGGGCPCLSDITYSSSN 310
Db 307 --DI-----VAEDPAPCAFS-----GNGRQC-----TANG---331

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QY 311 TTCVMMNOYTYNCASGEHNPFGKAINFDNIGYAMIAIFOVITLLEGVDMFVMDAHSEF 370
Db 331 -----TECRSGWGPNGINGITNDFNAFALTVCQITMEGWTDLVWVMDAIGME 380
QY 370 YNFYIFILLIYGFEMINLCIVATQFSEKQRESQOLMEQRYRFLISNASTLASESEP 429
Db 381 WFWYFVSILIGSEFFVLVLVGLVSGESKEREKAKARGFOKLK-----EK 428
QY 430 GSCYEELKYLYVYIIRKARRLAQVRAIGVAGLLSSPARSGOEPQSGSCTRSHRL 489
Db 429 QOLEEDLNGYLDWITQ-----ADIDPENE-----454
QY 480 SVNHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRMLPPESTPTSGGPPRG 549
Db 454 -----EEGEGEKNTSMPTSET-----472
QY 550 AESVSHFYHADCHLEPVRCQAPPPRCSEASGRVYGSKVYPTVHTSPPEILDKALVE 609
Db 472 -ESVNT-----ENVSQ-----482
QY 610 VAPSPGPTLTSFNIPPGPFSSMHLLETQSTGACHSCCKISSPCSKADSGACGDCOPY 669
Db 482 -----EGENRGCGSLCQAIK-----499
QY 670 CARTGAGEPESADHVPDSDSEAYEFTQAOHSDLRDPHSRRORSIGPDAPESVYLA 729
Db 499 -----SKLSRRWRNRNRRRCR---AAVKSTFEY 526
QY 730 WRLICDFFRKIVDSKYFGRGIMAILVNTLSMGIEYHEOPELNNALEISNIVTSFAL 789
Db 527 WLVI-----VLVFNLTLTISEHNQPMWLTQIDIAKVALALFTC 568
QY 790 EMLKLKLVYGFPGITKPNYTFDGVY-----VISWEIVGOOGGLSVLRTFLMRY 842
Db 569 EMLKMTSLGQAFVSLFNRFDFCVGQITETILVELIEMSP-GISVFRVRLRT 626
QY 843 LKLVRFPALOROLVLMKTMNVATFCMLMFIIFISLIGMLBECKRASEDGTLP 902
Db 627 FKVYRHTSLSNLVASLNSMKSTASLILLLEFTIIFISLIGMOLFEGKKNFD-ETOT 683
QY 903 DRKNFSLMAIVTFOILTOEDMNKVLXNGM-----ASTSSWALYFALMTFGNYVL 966
Db 684 KRSTFDMFPOLLTVFOILGEDNNAVMYDGIAMVGPSSGMYCYTIFITLTCGYTL 743
QY 957 FNLLVALIVEGF-QAELIGKREDAQSOLCIQLFVNSOGGDATKSESEPDFSPVDG 1015
Db 744 LNVFLAIVNLDADSL-----NTAQKEAE-----EK 772
QY 1016 DRKKRLALVALGEHAELRKSILPLLIHTATPMSLPSKSSITGVGELSGSRRTSSGS 1075
Db 773 ERKK-----IARKESELENKKNKE-----VNOJANDKNVTITDDYR 809
QY 1076 AEPGAHHEKSPPSARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRRSPGSRSLLS 1135
Db 810 EE-----DEDKDYPPCDV-----PVGE-----828
QY 1136 GEOGESODEEESSEDEASGDHRRGSLREAKSSPDLPTLOVPGIHTASGRSSA 1195
Db 828 -----EEEEDEDEYVAPGRPRISLANKKETA-----PIP-----862
QY 1196 SEHQDCNGKASGRLATRTDPOLDGDDNDEGNLSKGERIQAWVRSLRPACCRERDS 1255
Db 862 -----EGS-----865
QY 1256 WSAVIFPPORFRLCHRTTHKMFHDVUVITFLNCITIAMERPKIDPHASERIFLTL 1315
Db 865 -AFFILSKTNPVIGCHKLNNHIFNLIVFIMLSALAEADP-IRSHSFNRTILGYE 922
QY 1316 NYIFTAVFLAEMTVKVALGCMCFEQAYLRSSNVLDGLVILSVIDILVMSVDSGTI 1375
Db 923 DYAFATLFTVEILLKMTTGAFIHKGAFCRNFTNLDMLVGVGSLSFSGIQ-----SSA 976
QY 1376 LGMRLVRLRLTLPRLVVISRAOGLKLVYETLMSLKPIGNIVVICAFIIFGILGVQL 1435

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Db 977 ISVKKILRVLRVLPRLAIRAKGLHVVQCVFALRTIGNTIMVITTLQIFMEFACIGVL 1036
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Db 1037 FKGFYRCTDEAKSNDECRGLFETLKDDVDVSPVREIMQNSDFNENVSAMALFT 1096
QY 1484 LASKDQWDMYMGDLAVGVDOQPINNHNPMLVIFISFLVAFVLMVGVVENEH 1543
Db 1097 VSTFEGMPALTKYKAIDSNENIGPIYNHVEISIFIIIIIVAFEMNIFGVYVTF 1156
QY 1544 KCRHOEEERAREERKRLRLERKRNMLDVLASSGSASAABEACKPY-----1596
Db 1156 -----QOGEKEYNKCE-----LDKNR-----OCVEYALKARPLR 1186
QY 1596 -YSDYFRLLVHNLCTSHYLDLFTVIGLVNVMAMEHYOQOILDEALKICVYFTV 1654
Db 1187 RYLPKNPYOKFMYVYVNSSPFEXMFFVIMLNTLCLAMQHYEQSKMFANDMLMVF 1246
QY 1655 IFVESEVFLVAFGRFRFODRBNQDLAIVLSTMGITLEIEYNAS--LPI-----1706
Db 1247 VTFVEMVLVIAFKPKGYFSDAMNFDLSLIVGSLIDVALSEADPTESBNVPVPTAPGN 1306
QY 1706 ---NEPTIRIRKVRIRIAVRLKLMKAVGMRLDPTVM---QALPOVGNLGLFMLPEI 1758
Db 1307 SEESNRISITFPRFLFRVYMLVYKLSRGSIRTLMTFTKFOALPYV---ALLIAMEFTI 1363
QY 1759 FALGVLELGDLECDTEHCESGLGHATFRNGMAFLFLFVSTGDNNGIMKDTL--RD 1816
Db 1364 YAVIGMOMGKVAAMDNNQ---INNENNFOFPOQAVLLFLFCARGEAMQEIIMLACLPGKL 1420
QY 1817 CDOES-----TCYNTMSPYIFVSFLVLAQFVAVVAVLVM-----1854
Db 1421 CPBEDYNNGEHTC-GSFAFVIFISYMCALITLIVFAVINDNFYLTRMSILGP 1479
QY 1854 KHLSESNKAKEAELEAE--LELEMKTLSPHSPPLSGSPFLP-----GVEGVNSPD 1904
Db 1480 HHLDEF-KRIMSEYDPEAKGRKIKHLDVYTLRLRIQPLRGFKLCPHRVACKRLVAMNPL 1538
QY 1905 SPKCAPHTTAIGAASFSL-----HPTWVPHPEVVPVLG 1942
Db 1539 N-SCGTVMFNATLFAVLTALKITEGNLEQANELRAVIRKIKMTSMKLLDQVPAG 1597
QY 1943 PDLITVRK-----SGVSRHSL-----1960
Db 1598 PDEVTYGVKFATFLQDFKFKRKEEGVYKYPRAKNTTIALDAGLTLHDIGPEIIRA 1657
QY 1960 -----PNDSYWCRNG-----STARSLSGRGWG 1982
Db 1653 ISCDIQODEPEBETKKEEDDVFKRNGALLGNHNVHNSDRSDSLQGTNTTHRPLHYGRS 1717
QY 1983 LPKAO-----SGSLSVHSQPADTSCLOPKOVHNYLQ-----PHG-APTWGA 2025
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QY 2026 IPKLPPG-----RSPLAORPLR---QAAIRTSILDVQ-----2057
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QY 2057 --GGSREDLISEVSGSPCPLTRSSFWG-----GSLIOVOQORSG-2095
Db 1837 PHCLGEDEYFSSE---ECYEDDSPTWSRONVGYRYGRNIDSERPRGHHQGFLE 1892
QY 2095 -----IOSKYSKHIRLPAPCPGLEPSWMAKDPEHTSSSLELDELNSIGDILPSSQEE 2147
Db 1893 DDDSPYVCDSRSPRRRLPLPTPA-----SHRSSNFECRLRROSSQEEVPPSS---1941
QY 2148 PLSRDLKCYVETOSCRRRPGSWLDEORRHSIAVSCDGSQPRLCSPSSIG-GOPL 2206
Db 1941 PIFP-----BRTALPLHLMQOQJMAVAGDSNAQYSPSHSIRSMATP-1985
QY 2207 GGPGRPKKKKSP---PSISIDPPES-----QGSRPSCSPGVCLRRRAPASDSKDPVSVP 2259

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Db 1985 --PAPPRDWTPCYTPILIQEAGEALDQVNGSLP-----SLHRSWTDEPDISTRTF 2036  
 QY 2260 LDSTASPSKKDTLSGLSSDPTDMDPVLPPLPHLSPPGADSSASMAFLKSEPTAA 2319  
 Db 2037 TPASLTIVSSSRNNKSDQKRSADSL-VEAVL--ISEGLGRVARDPKRVS-----A 2083  
 QY 2320 SSHE 2323  
 Db 2084 TKHE 2087  
 RESULT 10  
 US-08-808-793-4  
 Sequence 4, Application US/08808793  
 Patent No. 5858713  
 GENERAL INFORMATION:  
 APPLICANT: Soderlund, David M.  
 APPLICANT: Ingles, Patricia J.  
 TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
 TITLE OF INVENTION: AND USE THEREOF  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 STREET: Clinton Square, P.O. Box 1051  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/808,793  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,361  
 FILING DATE: 24-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/012,649  
 FILING DATE: 01-MAR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Braman, Susan J.  
 REGISTRATION NUMBER: 34,103  
 REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 716-263-1600  
 TELEFAX: 716-263-1600  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-808-793-4

Query Match 12.6%; Score 1576.5; DB 2; Length 2104;  
 Best Local Similarity 24.5%; Pred. No. 1.7e-117;  
 Matches 521; Conservative 371; Mismatches 704; Indels 533; Gaps 79;

QY 1 MDEEDGAGAESGGQPRST-----QINDISGAGGQ----- 33  
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 QY 33 GPSTEDP-----GSADEAGGLYPALAP-----VVEFTLSQ-----D 67  
 Db 61 GP---QPDPTLEQGVPIPVMGGSFPPELASTPLEDIDPYSNVLTFFVVISKGDIFRS 117

QY 68 SRPRSMCL-----RTVC-----NPMEEVSMVLILNCVTILGMFRCEDIIACDSQRCRI 116  
 Db 118 ASKAMLLDPENPIKRVAILIYVHLESLFTITILLNCILMIM-----PTPT 166  
 QY 117 LQAFDFIFAFVAVEMVYKVALG-IFGKKCYLGDTRNRLDFEVIAGMLEYSLDLOVNS 175  
 Db 167 VESTEVITFTGIYTESAVKVAARGFIIICPFYTLRDAMNMDFVIALAYVMGIDLGNL- 226  
 QY 176 FSAVTRVRLVPLRAINRPSKRIIVTLLDTPMLGAVLLLCFVFPIEGIVGVLWAG 235  
 Db 226 -AALRTFRVRLAKTVAYLPGLKTIVGAVIESVKNLRVILITMSEVFLMGLQITMG 284  
 QY 236 LKRNRC-----FLPENSLPLSVLDLEPYQTENEDESEPFICOPRENGMRCR 283  
 Db 285 VLTOKCIKRFPLDGSNGNLTIDNMFLHNSNSN--WFTENGESYVPC----- 331  
 QY 284 SVPTLRGEGGGPPCSLDIETYNSSNTTCV-----NMNQTITNSAGEHNPFGAINEF 338  
 Db 331 -----GNVSGAGCGGEDY-----VCLGGFQPNPNYDT-----SFD 361  
 QY 339 NTCYAMIAIEOYITLEGWVDIMYFVDAHSFYNTFYITILLIVGSFMINCLVIAIOF 398  
 Db 362 SEGMALSLFRLMTQDEWEDLYQHVLAAGPWHMFLFYIITFLGSFYVNLILIAVMSY 421  
 QY 399 SETKOR-----ESQLMR-----EQRYRELNSASTLASFSEPGSCYEELK 438  
 Db 422 DELQKKAEEEAEEEAIRAEAEAAAKAKLEERANVAQAQADAAADAAALHPENAK 481  
 QY 439 -----YLVYI-----LKAARLAQVSRALGVRAGLSSVYARGGQEPQSG 480  
 Db 482 SPYSCISELFEVGEKGDNDNKKEMSIKSYVE-----SESVYIQRPAPTT 531  
 QY 481 SCTRSRRLSVHLL-----VHHHHHHHHYHGLGTLR--VPRA--SPETIDORDANG 528  
 Db 532 APATKVRKSTTSLSPGSPNLRGSRSHKTYIRNGRGIGIGSDOKPLVLTQYDA 591  
 QY 529 SRRLMLPPSTPTPGSGPPGABSVSHFYHADCHLEPVRCQAPPPRCSEASGRVYSGK 588  
 Db 592 QQLHPYADSDNAVTPMSEENGALIVPAYV---CNL-----GSRHSYSYSHSR 636  
 QY 589 VYPTVHSPPELTKKALVAVAPSPGPTLTSFNTPPGFSSMKLLETOSTGACHSSC 648  
 Db 637 IYTSIH---GDLGGMAAGASTMKESKLSRN-----TNGSICG----- 676  
 QY 649 KISSPCKADSGACGPDSPCYCARTGAGEPESADHYMPDSDSEAYEFTQDA---QHS- 705  
 Db 676 -----ATNGG-----STAGGYPD-ANH-KEQDYEMGQDYDEAGKIKHHDN 717  
 QY 705 -----LRD-----PHSRRRGRSLGPPDAE-PS----- 725  
 Db 718 FLEIPVQOTIVVMKQVMVNLNDIIEQAAGRHSRASRGDEDDGDEFTFDIALEVIKGI 777  
 QY 725 SYLAFWRLICDIFRK-----IVDSKYFGRGIMAILVNTLSMGLEYHEQPEELTNALE 777  
 Db 778 EIFCYWD-CCWWMKKROEWVSFIVPDPVELFTTLCIVNTNMADHDHMDPELEKVLK 836  
 QY 778 ISNIVETSLFALEMLTKLVYGPFGYIKNPYNIFDGVIVVISWEIVGQG--GGSLVLT 836  
 Db 837 SGNYFTATFAIEASMKLMASPKRYFQEGMNIFDIYVALSLLEL-GLEGVQGLSVLRS 895  
 QY 837 FRLMRVLYVRLPALOROLVLMKTDNVATFCMLLMLEFIFFISLIGHITGCKRASER 896  
 Db 896 FRLIRVFKLAKSWPTLMLLISINGRTMGALNLTFLVLCIIFLFAVWGQLEKKNIDHK 955  
 QY 897 D---GDTLPBRKNPDSLMLAVIVFOILTOEDMNKYLNYNGMASTSSMAALYFALTMTFN 953  
 Db 956 DREFDHEIP-RNNTPTDMHSFMIVFRVLCGE-WIESMGDMYGVGVSCIPFLFATVIGN 1013  
 QY 954 YVLFNLVAIVIEGFOAEI-----GKREDASQGS-----CIQLPVN- 992  
 Db 1014 FVVLNLFALLLSNFGSSLSAPTADNDTNKIAEAFRIARFRKNVWVRNIAIDCFKLIRNK 1073

QY 992 -----SQCQATKSESEPFPSVODGDRKKRL-----ALVALGE-----HAE 1031  
Db 1074 LTNQISDOPSEHGD-----NELELGHDEIMGDLIKKMGKGTQLEVALIGMGMEITINGD 1128  
QY 1032 LRKSLPLIHTANTPMSLPKSS-----STCVGALSSGSGSRSTSSSSAEPGAHHMK 1086  
Db 1129 MAN-----NPKRKSFFINTTWNIGNSINHODNR-----LEHELN 1162  
QY 1087 SPPSARSPHSPWASAASWTSSRNSLSGRAPSLKRRSPGGERSLLSGEGOSODEE 1146  
Db 1163 -----HRELSTQDDDTASINSYGSHKNRP-FKDSHKSASFT---EGEERD--- 1207  
QY 1147 SEEDRASPAGDHRHRSLSLEFEAKSSFDLPDTLOVPLHRTASGRSSASEHODCKSA 1206  
Db 1207 VKRED-----LGUDE-----ELDEEAEAG----- 1225  
QY 1207 SGRRLARTLTDPPOLDG-----DDNDEGNLSKGERIQAM-----VRSRLPACCRERD 1234  
Db 1225 -----DEGOLDGIIITHAOND-----ELTDDYPRADCPDPSYKFPILAGDE 1268  
QY 1235 S--WSAYTFPPQSRPRLCHRTITTHKMDHVVVLIPLNCITIAMEREKIDPHSAERITL 1312  
Db 1269 SPFMQGW-----GNRLKTFOLIEKRYETAVITMILMSLALAEVHLDPDRVMDIL 1323  
QY 1313 TLSNITFAVLAENTVAVVAGMCFGQAVLRSSMNVLDGLVLIVYIDILVMSVSDG 1372  
Db 1324 YMDRIFIVIFLEMLKWLALG---KYVTNMCWLDVIMLSLILNVAW---SG 1376  
QY 1373 TKILGMLRVLLRTLRRLRYISRAQGLVLETMSLKPIGNIVYICAFIIFGILG 1432  
Db 1377 LNDIAVFRSMRTLRRLRAVSRMEGKVVVNLVQAIPSEIFVLCILFIMLFEIING 1436  
QY 1433 VOLKRGKFFVQC-GBDT---RNTNNSDCAEASYRWVRHKNYNDNGOALMSLEVLASK 1487  
Db 1437 VOLPAGKFKCKDNDVTLSEHIIIPNRNACKSENYTWENSAMNFDHVGNAVLCIFQVATF 1496  
QY 1488 DGWVDIMVGDGDAVGDOOPIMNHPMLLYFISFLILVAFVYVMEVGVVVENFHCKRO 1547  
Db 1497 KGWQIMNDAIDSREVDQPIRETNIYLYFEVFIFIFGSEFTINLPIGVIIIDNF----- 1552  
QY 1548 HOEEEARREERKRLRLKRRRLMLDVLASSSASASEAOCKRYSDYSRFLLV 1607  
Db 1552 NEOKKXKSGSEMFTEDOKKYNAM--KKMKSKKPLKAIIPRMRP-----QAIIV 1601  
QY 1608 HLCGSHLDLFTGVIGLVNTVAMEHYOQOPIIDELKICNYITFVIEVESYKLVAF 1667  
Db 1602 EIVDKKFDITIMLFISINMETLDRYDASEAYNNVLDKINGIFVIFSGECKLTFAL 1661  
QY 1668 GFRFPDDRNOQDLAVILSIMGITLEETJEVNASLPINFITIRIMVYLIAVLIKLM 1727  
Db 1662 RY-HYFREPMLFVYVYIISITGLVSDI--LEKYFVSPTLLEVVAVAKVGRVLRVKG 1718  
QY 1728 AVGRALDVTVMQALPOVGNLGLLEMLFFIFALGVELFEGDECEDETHPCEGLGRHA-- 1786  
Db 1719 AKGIRTLFLFLAMSLPALFNICILFLVMTIFALFGMSF-----MHKXSGINAVY 1771  
QY 1786 TFRFAGAFILFVSVSGMMNGIMKDTL--ROCD-----QESTCYNTVISPIYVSF 1836  
Db 1772 NFKFSGSMILLFOWMSTSAQMGDVLDAIINEECDDPPDNDKGYRNGSGATVITFLAS 1831  
QY 1837 VLAQVFLVAVVAVLAKHLEESNKEAKE 1865  
Db 1832 LVISFLIVIMYAVILENSQATVEDVOE 1860

RESULT 11  
US-07-745-206A-2  
; Sequence 2, Application US/07745206A  
; Patent No. 5429921  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark

APPLICANT: McQue, Ann  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2161 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-2

Query Match 12.6%; Score 1576; DB 1; Length 2161;  
Best Local Similarity 23.18% Pred. No. 2e-117;  
Matches 597; Conservative 365; Mismatches 750; Indels 872; Gaps 84;  
QY 31 RQGPSTKDPSSASSEADGLPYPLAVVFFYISQDSRPSWCLRTVCNFW--FERYSM 88  
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QY 89 LVILLNCTVIGFRCPCEDICADSCRCRILQAFDEIFAFEFVEMVYKVALG-IFGKKY 147  
Db 134 LAIFANCVALAIYIFPPDDNSNTN-HNLEVEYAFALITFVETFLKIAIAGLLHPNAY 192  
QY 148 LQDTNRLDFEIVAGMLEYSIDQNVS-----FSAVRTVRLPLRA 190  
Db 193 VENGNNLDEFVIVGL--FSVILEQLTKETEGNHSSGSGGFDVAKALRAFRLRLRL 250  
QY 191 INRVPSMRILVLLDILPMLGNVLLCFEYFFIYGIVQVLAGLNRNCFDEPNESLP 250  
Db 251 VSGVSLQVNLISITKAAPVLLHLLVLFVITIAITIGLELFGKXHKTCFFADS--- 307  
QY 251 LSVDEPYTOTENDESEPFISOPRENGMRSCRSVPTLRGEGGCPGCSLDYEYNSSN 310  
Db 307 ---DI-----VAEDPAPACAS-----GNGRCC-----TANG--- 331  
QY 311 TTCVMMNOYIYNSAGEHPKGAINFEDNIGYANIAIFOVITTEGWVDIMYFVDAHSF- 370  
Db 331 -----TECRSGWVGPGNGITNFDNFAMLTFOCITMEGWDVLYWMNDANGFE 380  
QY 370 YNEIFYILLIVGSPFMNLCVLVIATQSFTRQREQAKREQVRRLNSASTLASSEP 429  
Db 381 YFWYFVSLVIFGSPFYVNLVGLVSGFSEKREKAKARADFOFLR-----EK 428  
QY 430 GSCYEELIKYLVYLKRAARLAQVSAIGVAGILSSPVARSQGEPOPGSGCTSRHRL 489  
Db 429 QOLEEDIKGYLDWITQ-----AEDIDPENE----- 454  
QY 490 SVNHVVHHHHHHHHYHNGNLTLRVPASPEIODRDANGSRRLMLPPSPITRPSGGGPRRG 549

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Db 454 -----EEGEGEGRKNTSMPTSET----- 472
QY 550 AESVSHADCHLEPVCQAAPPRCPSGRTVSGKVPTVHTSPPEILLKDALVE 609
Db 472 -ESVNT-----ENVSG----- 482
QY 610 VAPSGPPLTASFNIPGPFSMMKMLLETOSTGACHSSCKISSPCSKADGACGDCOPY 669
Db 482 -----EGENGGCGSLCOAISK----- 499
QY 670 CARTGAGEPESADHYMPDSSEAYVEFTQDQSHDLRDPHSRRORSIGPDAPSSVLA 729
Db 499 -----SLSRMRMRNRNRNRRCR-----AAKSVTFY 526
QY 730 WRLICDTEFKIVDSKYFGGIMAILVNTLSKGIYHEQPELTNALEISNIVTSLFAL 789
Db 527 WLVI-----VLVELNLTITSEHYNQDPLTQIODIANKVILLAFETC 568
QY 790 EMLKLLVGPFGYTKNPYNIDVIV-----VISWEIYGOOGGGLVLFTRFRLMRV 842
Db 569 EMLVKKYSLGLOAYFVSLNRFDCVYCGGITETILVELEIMSPL--GISVFRVRLRTI 626
QY 843 LKLVRELPALQOLVYIMKTMNVATFCMLMFIIFISILGMLFGCKFASERDGTLP 902
Db 627 FVYTRMTLSLNVASLMSKMSIASLILLFLIIFISLGMOLFQKFNFD---ETQT 683
QY 903 DRKNEDSLMAIVYFOILLTOEDMKNVLYNGM-----ASTSSMAALFIALMTFGNTVL 956
Db 684 KRSTFNFQALLVFOILLTGEDMNAVMYDGIAMAGPSSGMIYVIFILITGNYTL 743
QY 957 FNLLVALIVEGF-QAEIQRKEDASQSLCIOLPVNSOGDATTSESEDFSPSVDCG 1015
Db 744 LNFELAIADNLTADASL-----NTQKEBAE-----EK 772
QY 1016 DRKRRLVALGHEALRKSLPLRIHTAATPMSLPKSSSTGVEALGSGSRSTSSGS 1075
Db 773 ERKK-----IARKELENKKNRKE-----VQIANDSKVTIDYR 809
QY 1076 AEPGAHHEKSPSPARSSPHSPWMASSWTSRRSSRNLGAPILKRSPGGERSLLS 1135
Db 810 EE-----DEDKDPYPCDV-----PVGE----- 828
QY 1136 GEGQESQDEESEDSPASGSDHRRGSLREAKSFDLPDLOVPGILHTASGRSSA 1195
Db 828 -----EEEEDEDEPVAGRPRISELNKEXIA-----PIF----- 862
QY 1196 SEHQDNGKSASGLARTLTPTDDPOLDGDNDENGLSKGERIQAWVRSLPACCHERDS 1255
Db 862 -----EGS----- 865
QY 1256 WSAYIPPOSRFLCHRITTHKMPDHVYVIFLNCITIAMERPKIDPDSABRFLTLS 1315
Db 865 -AFFILSKTPINVGCHKLINHIFITNLIVFIMLSAALADBP--IRSHSRNTITLGF 922
QY 1316 NYFTAVFLAEMTVKVALGMCGEQAYLRSSWNVLDELVLIVLISVILVSWVSOGTKI 1375
Db 923 DYAFATLFTVLEIKMTTFEAFILHKAFCNRYFNLLDMLVGVSVLSFGIO-----SSA 976
QY 1376 LGMRLVRLRLTRLPRLVIRASQALVYETLMSLKFISNIVYICAFIIFIGILGYOL 1435
Db 977 ISVYKILRVLRVLPRLAIRNARKGLKHVQCVVAITIGNIMIVTTLLOFMACIGVOL 1036
QY 1436 FKGFYFCQGEDFTN-----ITNKSQCAEASVY--WVSHKYNFDLQALGALSLTV 1483
Db 1037 FKGFYFCTBEAKSNPECCGLFLIYKGDVDSPVYERITWQSDNFEDVLSAMALFT 1096
QY 1484 LASKDGWVIMYDGLAVGVDOOPIMNHPMMLLYTISLLIYAFVLANKEGVVENVH 1543
Db 1097 VSTEGMPALLYKAIDNGENIGIYHNHVEISIFFIYIIVAFEMMNFVGVIVTF- 1156
QY 1544 KCRHOEBEERKREERKRLRLEKKRRNMLDDVIAGSSASASASEQCKPY----- 1596
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QY 1596 -VSDSRFLVNHLCITSHYLDLFTTGYIGLVNYVNAMEHYOQOPIDEALKICNYITV 1654
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QY 1655 IFVESVFKLVAFGRFRFRODRMNOLDLAIYVLSIMGITLEIEYVNAS--PI----- 1706
Db 1247 VLFVENYLVKVIAPKRGYSDAMNFDLSLIVGSIIDVALSADPTSEENVPVPTAPGN 1306
QY 1706 ---NPTIIRIMVRLIARVYKLLKMANVGRALDVTM---QALPOYGNLGLTFLLFEI 1758
Db 1307 SEESNRISITFFRLEFVYVRLYKLSRGEGIRLTLTFIKFOALPYV--ALLAMLEFI 1363
QY 1759 FALVYELGDLDECDTHCEGIGHATPRNGMAFLTFRSTGDNNNGIMKDTL--RD 1816
Db 1364 YAVIGMOMGKAMRDNNO---INRNNFOTPOAVALLFRATGEANOELMCLPGL 1420
QY 1817 CDOES-----TCYNTVISPITYVSFVLAQFVLYVNAVIAVM----- 1854
Db 1421 CDESDYNNGEHTC--GSNFAYIFISFYMLCAFLINLFVAVIMDNFDYLTRDWSILGP 1479
QY 1854 KHEESNKEAKEAELEAE---LELEMTLSPQSPHSPIGSPFLMP-----GVEGVNSPD 1904
Db 1480 HHLDEF-KRIMSEYDEAGRIKHLDVTLRLRIOPPLGFGKLCFHRVACKLYAMNPL 1538
QY 1905 SPRGAPHTTAHIGAASGFSLE-----HPTWVPHEEVPVPLG 1942
Db 1539 N-SDGYMFATLFAVLRATLAKITTEGNLEQANBELRAVTKIKWKTSSKLLDOVVPAG 1597
QY 1943 PDLTYRK-----SGVSTHSL----- 1960
Db 1598 DDEVYAKFYATFLIODYEKKFKRKEOGLVGRYPAKNTTIALQAGLRLHIGELIRRA 1657
QY 1960 -----PNSYMRNG-----STAEBSLGHGWS 1982
Db 1658 ISCDLODEPEETKREEDVEYKRNAGALLGNHYNHNSDRBSLOQTNTTHRPLHYQRS 1717
QY 1983 LPRKQ-----SGSILVSHQPADTSCILOPRDVHYLLO-----PHG-APTWGA 2025
Db 1718 IPRASDTERKLPFPAGNSV--CHNHNNHNSIGKOVPTSTANLNNANMSKAAGKRPISGN 1776
QY 2026 IPKLPPPG-----RSPLAQRPRLR---QAITDLSLDVQ----- 2057
Db 1777 LEHVSENGHSHKHDREPPRRSSVYKTRTYETVIRSDSGDEQLPTICREDPEIGHYFD 1836
QY 2057 --GLGSRDILLSEYSGPSCPLTRSSFWG-----GSSIOVQOBSG----- 2095
Db 1837 PHCLGEOEYFSSE---ECYEDDSSPTWNRONGYYSRYGRNIDSEDRGYHHNGFLE 1892
QY 2095 -----IQSKVSKHRLPAPCGLEBSWAKDPETRRSLELDTLSWISGDLPSQEE 2147
Db 1893 DDDSPVGYDSRSPRRRLLPPTPA-----SHRSSNFECILTRROSSOEVPSS--- 1941
QY 2148 PLSRDLKCYSVTQSCRRRPWSLDEORRHISAVSCDLSGSGOPRLCPSPSLG--GOLP 2206
Db 1941 PIFP-----HRTALPLHMOQJIMAVAGLDSASAOKYTSRSHSTRMATP- 1985
QY 2207 GGPSRPPKRLSP--PSISIDPPES-----QGSNPPCSPVCULRRRAPASDSKDPVSSP 2259
Db 1985 --PATPRYDMTFCYTLIOLVQESALDQYNGSLP-----SLHRSWYIDEDDISYRTE 2036
QY 2260 LDSTRAESPFRKDTLSLSSGSDPTMDPVLPPLPHHLSPPGADPSSASAAALAKSPTIA 2319
Db 2037 TPASLTVPSSFRNKNKSDKORSADSL-VEAVL--ISEGLGRYARDPRFVS-----A 2083
QY 2320 SSHE-2323
Db 2084 TKHE 2087

```

RESULT 12  
US-08-455-543A-49  
; Sequence 49, Application US/08455543A



Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2161 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-49

Query Match 12.6%; Score 1576; DB 2; Length 2161;  
Best Local Similarity 23.1%; Pred. No. 2e-117;  
Matches 597; Conservative 365; Mismatches 750; Indels 872; Gaps 84;  
QY 31 RGGPGSTENDPGSADSEAGLPALAPVVFYFLSDSRPRSMCLRTVCNPM--FERVSM 88

Db 85 RQYAKSKRGKGNSSNR-----PARA---LPLCLNNIRACISIV--EKKPDIIFIL 133  
QY 89 LVLLNCVTLGMRPCEDJACSORCRLQAFDDFLEAFENAVEMVKNVAGL-IGKKCY 147  
Db 134 LAIFANCVALAIYIPPEDDNSTN-HNLEKVEYALFIIFYETLTKITAGLLHPNAY 192  
QY 148 LGDTNRRLDFFVIAGMLEYSLDQNVS-----FSAVRYRVLRPLRA 190  
Db 193 VRNGWMLDFEVIYVGL--FVYLLEQLTKETEGNHSSKSGSGFVKLRARVRRLRL 250  
QY 191 INRPMSRLVTLTDTLPMGNVLLCFEYFFITGIYGVQVMAALLNRCELPENESLP 250  
Db 251 VSGVPSIQVYVLSIKAMPVLLHLLVLEVIYIYIIGLEIFIKMKRTCEFFADS--- 307  
QY 251 LSVLESPRYQTENEDSPFICQPRENGRCRSPVTLRGEGGPGPSLDYEYSSSN 310  
Db 307 ---DI-----VAEDPAPCAF-----GNGRQC-----TANG--- 331  
QY 311 TTCVMMNOYTTCSAGEHPFGAIFNPNIGYAMIAIFQVITLEGVDMFYVMDAHSF 370  
Db 331 -----TECRSGWGPNGGINTFNFAFAMLVFQCLIMEGMDVLYWMDAMGFE 380  
QY 370 YNEIFYILLIIVSFFMNLCLVIAIQESETKORESQMDQRRLFNSTLASESEP 429  
Db 381 LPVYFVSLVIGSFVNLVYGVLSGEFSKEREAKARGPQKLR-----EK 428  
QY 430 GSGYEELLKYLYILRKARRLAQVRAIGVAGLLSSPVARSQGPQSGSCTRSRRL 489  
Db 429 QOLEEDLKGYLDMITQ-----AEDIDPNE----- 454  
QY 490 SVHLVHHHHHHHHYHNGTGLRVPRASPEIQDRDANGSRRLMPPSTPTSGGPRG 549  
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QY 550 AESVSHFYHADCHLEPVRCQAPPRCPSEASGRVYVSGKYVPTYHTSPPELMDKALVE 609  
Db 472 -ESVNT-----ENVSQ----- 482  
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QY 730 WRLLCDTFRKIVDSKYFGIMAILVNTLSMGIEYHEOPELNLNALEISNIYFTSLFAL 789  
Db 527 WLVI-----VVFINTLTISSHEHNQDMLTIQDIDANKVLLALFTC 568  
QY 790 EMLKLIVYGPFGYIKNPNIFDGVYI-----VISWEIVGQGGGLSVLTFRLMRY 842  
Db 569 EMLVKMSISLGQAFVSLFNFRDFCVVCGGITELILVELIMSP--GISVFCVRLRLI 626  
QY 643 LKIVFLEPALQROLVYLMKTDNVAFCMLLMLEFIFESLILGHLNPGCKRASERDGTLP 902  
Db 627 FKVKRHTSLSLNVASLNSKSLASLLLLFLFIIFSLGQLRFGCKRNF--ETQ 683  
QY 903 DRKNFDSLMAIVTFQILQEDMKNVLYNGM-----ASTSSWALYFALMTFGVYL 956  
Db 684 KRSTFDFEPQALITVFIQLGEDMNAVYGIAMYGSSSGMIVCIYIFILICGNITL 743  
QY 957 FNLYAILIVEGF-QAEIIGREDASGOLSCIQLPVNSQGDARKSESDPFSPVDGGG 1015  
Db 744 LNVILAIADNLDAESL-----NTAQKEAE-----EK 772  
QY 1016 DRKRRLVNLGHEAELRKSLLPLLIHTATPMSLPKSSSTGVGALSGSRRTSSSS 1075  
Db 773 ERK-----IARKSELEKKNKPE-----VNDIANSDNKVTITDDYR 809  
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Wed Jan 19 08:15:00 2000

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Page 20

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QY 1316 NYIFLAVELAEVTVKVALGWCFGEOAYLRSSMWVLDGLLVISVIDILVMSVDSGTKI 1375  
Db 923 DYAFALITVELLKMFTFGAFLHKGACRNYFNILDLVGVSLVSGFIO-----SSA 976  
QY 1376 LGMALVLLRLRLRISRAOGKLVETLMSIKRIGNIVVIGCAFIIIEGIGVOL 1435  
Db 977 ISVVKILVRLRLRAINRAKGLKHVQCEVAIRITGIMIVTLLLOPMFACIGVOL 1036  
QY 1436 FKGFVFCOGEEDTRN-----ITNKSCEASYSR---VWRHKYFEDNLGOALMSLFV 1483  
Db 1037 FKGRYRCTDEAKSNPECRGFLILYKGDVDSPVYRERIMQNSDFNDVLSAMALFT 1096  
QY 1484 LASKDQWDIMTGLDAVGDOQPIAMENPMWLLYFISFLIYAFVYLMFVYVENFH 1543  
Db 1097 VSTFEGWALLKKAIDSGENIGPIYHNRVELSIFIIYIIIVAFEMNINIVGVIVTF- 1156  
QY 1544 KGRHOEEEARREKRLRLERKRRNMLDVIASGSASASAEACCKPY----- 1596  
Db 1156 ---QOGEKEYNCE-----LDKNOR-----QCVYALKARPLR 1186  
QY 1596 -YSDYSRFLVHLCTSHYDLFTTGVIGLVNTVAMEHQOQIDELDAIKONYITFV 1654  
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QY 1655 IVFESVFLVAFGRFRQDWRNOLDLAIYLSINGITLIEIENAS--PI----- 1706  
Db 1247 VETVEVNLVIAFKPKGIFSDAMNFDLSLIVGSIIDVALSADTESENVVPVPIATGN 1306  
QY 1706 ----NPTIIRIVRLIARVLRLKMAVGMALDVTM---QALPOVNLGLLEMLFEI 1758  
Db 1307 SEESNISTIFRFRVAVMLVLLSGESIRTLMTFKFQALDYV--ALLIAMLEFI 1363  
QY 1759 FALGVELFGDECTHPCCEGLGRHATFRNGMAFLIFRSTODNNGIMKDTL--RD 1816  
Db 1364 YAVIGWQMGKAYMRDNNQ---INRNNNFQTPPOAVLLFCATGEAMQETMLACLPGL 1420  
QY 1817 COGES-----TCYNTVISPILYSEVTLAQFVLYVNVVIAVM----- 1854  
Db 1421 CDSESINYNGEERTC-GSNFALYVIFSFYMLCAFLINLFAVINDNNDYLRDMSIIGP 1479  
QY 1854 KHLSESNKEAKEAELEAE--LELEMTLSPQSPSLGSPFLMP-----GVESVNSPD 1904  
Db 1480 HHLDEF-KRIMSEYDEAKRIKHLVDVTLRLRIQPLSGFKLCHRYACKRLVAMNPL 1538  
QY 1905 SPKPGAPHTAHGASGSLE-----HPTWPHREVEVPVLG 1942  
Db 1539 N-SDGTVMNATLFLAVLTALKIKTEGNEQANEELRAVIKIMWTKSKLLDQVVPAG 1597  
QY 1943 PDLLTVRK-----SGVSRTHSL----- 1960  
Db 1598 DDEVYVGKFAATFLIODYRKKKKRKEQGVYKPAKNTTIALQGLRLHLDIGEIRRA 1657  
QY 1960 -----PNSYMCRCNG-----STAESLGRKMG 1982  
Db 1658 ISCDLADDEPEETKREEDVFERKNGALLGNHVNHNVSNDRSLDQOTNTHRLPHVQPS 1717  
QY 1983 LPRKAO-----SGSILSVHSQPADTSCILQPKDVHYLLQ-----PHG-APTWGA 2025  
Db 1718 IPPASDTEKPLPPAGNSV-CHNHNHNNSIGKOVPISTANANLNAMSKRAAGKRPSIGN 1776

QY 2026 IPKLPPE-----RSLAQRRLR-----QALFTDLSLDOV----- 2057  
Db 1777 LEHVSNGHSHKHDREPPQRSSVKRTYETIYRSDSGDEQLPTICREDPELHGYFRD 1836  
QY 2057 --GLSREDLLSEVSGPCPLTRSSSEFWG-----GSSIOVOORSG----- 2095  
Db 1837 PHCLOEQEYFSE-----ECYEDDSPTWSRONGYGRYSPRNIDSRPRGYHHHOGFLE 1892  
QY 2095 -----IQSKYSKHTRLPAPQGLFEPWADPEPETSLSLELDELMSIGDILLSSQOE 2147  
Db 1893 DDDSEVCYDSRSPRRRLPPTPA-----SHRSSFNFECLRRQSSOEVPSS--- 1941  
QY 2148 PLSPBDLKVCYVEVQOSRRRGSWLDEQRHSIAVSCIDSGSOPRLCPSPSLG--GQPL 2206  
Db 1941 PLFP-----HRTALPLHMOQIIMAVAGLDSKXQKYSPSHSTRSWATP- 1985  
QY 2207 GGPGRPKKRLSP--PSISIDPPES-----OGSRPCCSPGYCLRRRAPASDKSPVSSP 2259  
Db 1985 --PAPPPYDWTPCYTPPLIOVQOSEALDQVNGSLP-----SLHRSWYTDPEPISYRTF 2036  
QY 2260 LDSTASPSPKDITSLGSLSDPTDMDPVLPTLPHLSPPGADPSSASMAFLKSP7AA 2319  
Db 2037 TPASLTVPSSPFKNKNSDKORSADSL-VEAVL--ISEGLGRYARDPKFVS-----A 2083  
QY 2320 SSHE 2323  
Db 2084 TKHE 2087  
RESULT 13  
US-08-223-305C-49  
Sequence 49, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McQue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2161 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-49

Query Match 12.6%; Score 1576; DB 2: Length 2161;  
 Best Local Similarity 23.1%; Pred. No. 2e-117;  
 Matches 597; Conservative 365; Mismatches 750; Indels 872; Gaps 84;

QY 31 RCGPSTEDPSADSEAGLEPYPALAVFFYTLSDSPRSCMLRTYCNPR--FERVSM 88  
 DB 85 ROQYAKSKQGGSSNR-----PARA--LFCISLNPDIRACISIV--EKKPFDITL 133  
 QY 89 IYLLNCVTLLGMRPCEDICDQRCRIQAFDFIFAFFAVEMVKKWALG-IFGKKCY 147  
 DB 134 LAIFANCVALLIYIPPEEDSNSTN-HNLEKEVAFLLIYETTLKIAAGLLHPAY 192  
 QY 148 LGDTNNRDLFFVIAGMLEYSLDLQNV-----FSAVTRVRLRLRA 190  
 DB 193 VANGNNLLDFEYIVGL--FSVILEOLTKEGNGHSSGSGGFVKALRAFRVRLRL 250  
 QY 191 IRRVSMRLVLLDLTLPMLGNVLLCFEYFIFGIYQVQMLGKLNKRFLENPSLP 250  
 DB 251 VSGVSLQVNLSTIKAVPLHLALVFLYITIAIGLEIFGKMKTKGFADS--- 307  
 QY 251 LSVDLFPYQTEDESPFISQPRENGMRSCRSVPLRGGGGGPPCLDYETYNSSN 310  
 DB 307 --DI-----VAEEDPACATS-----GNCRQC-----TANG--- 331  
 QY 311 TTCVMMNOYITNCSGEMNPRGAINFNIGYAMTIAFOYITLLEGWVDIMFYDANSF 370  
 DB 331 -----TECRSGWVPGNGITNPNFAMFLVQCITMEGMDVLYWMNDANGFE 380  
 QY 370 YNFIFILLITIGSEFMNLCLVYATQFSETKORESQLMEDQVRFLSNASTLASSEP 429  
 DB 381 LPMVYFVSLVIFGSEFVNLVGLVSGEFSKREKAKARGFOKLR-----EK 428  
 QY 430 GSCVEELIKLVYILRKARLAQVSAIGVAGLSSPVARSQOEPPSGSSCTRSRRL 489  
 DB 429 QOLEEDLKGYLDMITQ-----AEDIDPENE----- 454  
 QY 490 SVNHVHHHHHHHHYHNGTGLKVRASPELQDRDANGSRRLMPPSPPTPSGGPRRG 549  
 DB 454 -----EDGEGEKHNTSMPTSET----- 472  
 QY 550 AESVSHFYHADCHLEPVACQAPRPPCPSEASGRITVSGKVPYVHTSPPEILDKALVE 609  
 DB 472 -ESVNT-----ENVSG----- 482  
 QY 610 VAPSGPPTLTSFNIPGPFSSMKHLTQSTGACHSSCKISSPCSKADGACGPDSCPY 669  
 DB 482 -----EGENRGCCGSLQAIKSK----- 499

QY 670 CARTGAPESPESADHVPDSDSEAVYEFTQDAQHSDLRPHSRRRRSLGPDAPSSYLAF 729  
 DB 499 -----SKLSRRRRRRRRRRRCR-----AAVKSVTFY 526  
 QY 730 WRLICDTEFRKIVDSKYGREGIMAILVNTLSMGIEYHEQPEELTNALETISNYFTSLFL 789  
 DB 527 WLVI-----VLVEPLNTLTISSEHNQPDMLTQIODANKVLLALFLTC 568  
 QY 790 EMLKLIVGPFYIKNPYIFDGVIV-----VISWEIVGQGGGLSVLTFRILMRY 842  
 DB 569 EMLKMSLSLQAFVSLFNFRFCFVVCGITETLIVELIEMSP--GISVFRCVLLRI 626  
 QY 843 LKIVFLPALOROLVYMTKMDVAPECMILMFIETLSLGHLLGCKCFASRDEDTLP 902  
 DB 627 FKVTRHMTSLSNLVASLNSKSIASLLFLFLFIITLSLQGLGKFNED---ETQT 683  
 QY 903 DRKNFDSLMAIYVFOILTOEDMNKVLNGM-----ASTSSMALYFTALMTFGNYVL 956  
 DB 684 KRSTEDNEPQALLTVPQILUGEDMNAVMYDGMAYGGPSSGMIVCIYITLIFGNTYL 743  
 QY 957 FNLLVILVGEF-QAEITGRDASGOLSCIQLPVNSGGDATKSESEDPFSPSYDGDG 1015  
 DB 744 LNVFLATAVDNLDAESL-----NTAQKEAE-----EK 772  
 QY 1016 DRKRLALVALGEAEELKSLPLIHTATPMSLPKSSITGVGALSGSRRTSSSGS 1075  
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 QY 1136 GGEQSDDEESESSEDRASAGSDHHRGSLERKASFPDLPTLOVPCILHRTASGRSSA 1195  
 DB 828 -----EEEBEEDPEVAPGRPRRISELNKKEXIA-----PIP----- 862  
 QY 1196 SEHQDNGKSGSRLARTLRTDDPOLDDGDNDGELSGERIQAMVRSRLPACCRENDS 1255  
 DB 862 -----EGS----- 865  
 QY 1256 WSAIYIPPOSREFLCHRIITHKMFVHVLIIFLNCITAMERPKIDPNSAERITLTS 1315  
 DB 865 -AFFILSKTPIRIVGCHKLNHIFNLILVFLMSSALAEDEP-IRSHSRNIIIGVF 922  
 QY 1316 NYIFLAVFLAEMTVKYNVALGNCGEQAVYLRSSMNVYDGLVLIYSVIDLVSVSSGTRI 1375  
 DB 923 DYAFIATFVEYELIKMTTGAEFLHKGAFGRNYFNLDMLVGVSLVSFGIQ-----SSA 976  
 QY 1376 LGMRLVRLTLRPLRPLRVISRAQGLKLVETLMSSLKPIGNIVVICAFFIIFGLVOL 1435  
 DB 977 ISVYKILRLVRLRPLRALNRAKGLKHVQCVFVALRTIGNIMYITTLLOEFACIGVOL 1036  
 QY 1436 FKKEFVCOGEDTRN-----ITNKSQCAEASV--VWRHRYNPDNLQALMSLFV 1483  
 DB 1037 FKKEFYRCTDEAKSNDECRGLFIYKDGVDSPVYRERIMQNSPFNDVLSAMALFT 1096  
 QY 1484 LASKDGVDMIDGDLDAVVDQOPINNHNPMLLFIISLLIVAFVLMYGVVVENFH 1543  
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 QY 1596 -YSDYREFLYLHNLCTSHYIDLFTYVIGLVNVTAMAEHRYOQOILDEALKICYITV 1654  
 DB 1187 RYIPKNPYQYKFMYYVNSSPFYEMFVIMLNTLCLAMQHYSKMFNDAMDILNVETG 1246  
 QY 1655 IFVFESEFKLVAFFGRFRFQDRWNQDLALVYLSIMGITLEIEVNAS--LPI----- 1706  
 DB 1247 VFTVEMVLKVIAFKRGYISDAMNTFDSLIYAGSLIDVALSEADPTSENVVPVTPAIPGN 1306  
 QY 1706 ---NETIIRNRVRLIAFVILKLLMAVGMRLDVTM---QALPQVGNLGLLEMLLFFI 1758

1307 SEENRISTIFEFLEFRYMRVLKLLSNGEGIRTLMTIFFOALPYV---ALLIAMEFTI 1363  
1759 FAALGVELFGDLCEDETHPECEGRHATEFRNFQMAFLTEFRVSTGDNWNGIMKDTL- RD 1816  
1364 YAVIGMCFKVMARDNQ---INNNNFOTFFQAVALLFRCATGEMOIMLACLPGL 1420  
1817 CDOES-----TCYFTVSPYIFVFSVLTAAQFVLNVYVIAVL- 1854  
1421 CDPESDNPEEHTC-GSNFAIYFISFYMCAFLIINFEVAINOMEDYLTRDMSILGP 1479  
1854 KHLSESKKEKEKELEAE---LELEKTLSPDHPSPGLSPFMP-----GVEGNSPD 1904  
1480 HHLDEF-KRIWSEYDPKPKRIKHLVDVTLRLKROPPLGFKLCPIRVACKRLVAMNML 1538  
1905 SPKGPAPHTTAHICAGASGFLE-----HPTMPHPPEEVPVPLG 1942  
1539 N-SDGYVFNATLFAVLTALIKITEGNEBQANBELRAVIKIMKTSMKLLDQVVPAG 1597  
1943 PDLLTVRK-----SGVSRHSL----- 1960  
1598 DDEVYVKFYATFLIDYFRKKKKRQGLVGYKPAKNTTIALQAGLRLHDIGPEIRRA 1657  
1960 -----PNDSYMCRNG-----STAESLGHGNG 1982  
1658 ISCLQDEPERETKREEDDYFRKNGALLGNHVNHNVDKRDLSQOTNTHRLVHQRDS 1717  
1983 LPKAO-----SGSILSVHSQPADTSCILQPKDVHYLLO-----PHG-APTWGA 2025  
1718 IPPASDTEKPLFPAGNSV-CHNNHNSIGKQVPTSTNANLNANNSKAHGRPSIGN 1776  
2026 IPKLPPG-----RSPLAQRRLR-----QAIRFDSLDVQ----- 2057  
1777 LEHVENGHSHSHKHDREPORSSVKRTRYEYIRNSDGGEOPLTCREDPETHGFRD 1836  
2057 --GIGSREDLSEVSGSPCLTRSSSFWG-----GSSIOVQORSG----- 2095  
1837 PHCGEOGTFSE---ECYEDSSPTWMSRQNGYGRYGRNIDSRPGYHHPQGFLE 1892  
2095 -----IQSVSKHILPAPCPGLEPFSMAKQDPETRSSLELDTLWISGDLPSQOE 2147  
1893 DDDSPVCDYSRRSPRRRLPPTPA-----SHRRSFEFLRQSSQOEVPSS-- 1941  
2148 PLSPDLKKCVSVETQSCRRRPGSMLEORHSIAVSCDLSGSPRCPSPSLIG-GQPL 2206  
1941 PIFP-----HTALPLHMOQIYAVAGLDSKAKQKISPHSTSMATP- 1985  
2207 GPGSRPKKLSLSP--PSISIDPPES-----OGSRPPCSPGVCLRRAPASDSKDPVSSP 2259  
1985 --PATPPYRDMTPCYTPLIOVESEBALDQVNGSLP-----SLHRSWYTDDEPISYRTE 2036  
2260 LDSTVASSPKKDLISLGLSSDPDMPVPLTPLPHLSFGAGAPSSASNAAPLAKSTAA 2319  
2037 TPASLTVPSSFRNKNKSDKQSRADSL-VEAVL--ISEGLGRYARDPKFEVS-----A 2083  
2320 SSHE 2323  
2084 TKHE 2087

NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING-SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,363  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-51506  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0062  
TELEFAX: (619)238-0099  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-311-363-2

Query Match 12.68; Score 1576; DB 2; Length 2161;  
Best Local Similarity 23.18; Pred. No. 2e-117;  
Matches 597; Conservative 365; Mismatches 750; Indels 872; Gaps 84;

31 RQGPSTKEDGSDASEAGLPPALAPVVFYLSODSRPSCMLRTVCNPM--FEFVSM 88  
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89 IYLLNCVTLGFRCEDIACDSQRCRILQAFDEIFAFAVENVMKVALG-IFGRKY 147  
134 LAIFNCVALAIYIFPPDDNSNTHLEKVEYAFILIFVEFFLKTIYAGLLHPNAY 192  
148 LQDTNRLDFEIVTAGMLEYSLDQNS-----FSAYRVRYRLRLRA 190  
193 VANGNMLDFEIVIGL--FSVILEQLTKETEGNHSKSGGFVAKALRAFRLRLRL 250  
191 INRVSMRLIVTLDDTLPMLGNYLLCFEVEFFIGYGVOLMAGLLRNCFLPENSLP 250  
251 VSGVSLQVNLSTIKAMVPLHLILVLYITITAIIGLEFLGKMKHKTCFEADS-- 307  
251 LSVDLPEYVOTENDESPFISQPRENGMRCRSVPYTLRGEGGGGPPCSLDYEYNSSN 310  
307 ---DI---VAEEDPAPCAFS-----GNGROC---TANG-- 331  
311 TTCVANNQYITCSGAEHNPFGAINEPNIGYAWIAIFQVITLIGWVDIMFEVDAHSF 370  
331 -----TECRSGWVGPNGGINTFNENFAMLTFTVQCITMGWTDVLTWMDANGFE 380  
370 YNFIFILLIIVSFFEMILCVIATOFSETKORESOLEMDROVRLSNASTLASESEP 429  
381 LRVYTVSLYITGSEFFVNLVLTGVLSGEFSKEREKARAGDPQKRL-----EK 428  
430 GSCYEELLKYVLYILRKARRLAOLYSAIGVAGLSSPVARSQGOPOSSGCTRSHRL 489  
429 QOLEEDLKGYLDMITO-----AEDIDPENE----- 454  
490 VSNHLVNNHHNNHHNHLNGSLRVPRASPEIODDANGSRMLPPSTPTPSGGPPRG 549

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Db 454 -----EEGEGEGRKNTSMPTSET----- 472
QY 550 AESVSHFADCHLEPVRCQAPPCPSEASGRTVSGKVYPTVHTSPPEILKDKALVE 609
Db 472 -ESVNT-----ENVSQ----- 482
QY 610 VAPSPPTLTSPNIPGPFSMHKLELTQSTGACHSSCKTSPSCRADSGACGPDSCPY 669
Db 482 -----EGENRGCCGSLQALSK----- 499
QY 670 CARTGAGEPESADHYMPDSEAVEFEODQSHDLDPHRSRORSLSGDAEPSSYLAF 729
Db 499 -----SKLSRMRMRNRNRRCR-----AAVSTTFY 526
QY 730 WELICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHOPELNTALEISNIYFTSLFAL 789
Db 527 WLVI-----VLVFTLTITISEHYNQDMLTQIODANKVLLALFTC 568
QY 790 EMLKLLVYGPFGYIKNRYNIFDGIY-----VISWMEYGOQGGSLVLRFRMLRY 842
Db 569 EMLVMTSLGLQAFVLSLNRFDCEVCGGITETITLVELEIMSP-GLSVFRCVLLRI 626
QY 843 LKLVFELPALQOLVINKTMDNATFCMLMFIFFISLGMHLFGCKPASERGGDTLP 902
Db 627 FKVTRHMTSLSNVJSLNSKMSIASLLFLFIIFSLGMQLFGKFNFD---ETQF 683
QY 903 DRKNEDSLMLVYVFOILTQEDMNKVLXNGM-----ASTSSMAALYFALMTFGVYL 956
Db 684 KRSTIDNPPOLVYFQLTGEDMNAVMDGIMAYGGPSSGMYCIFYLFIPLFCGYTL 743
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Db 828 -----EEEEEDEDEPPAGPRPRRISELNMEKIA-----PIP----- 862
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QY 1236 WSAYFFPOSRFRLCHRIITHKMDHVVLIIFLNCITIAMERPKIDPSARIFLTLS 1315
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QY 1316 NIIETAVLEAETVYVVALWCFGEQAVLRSSMVNDGLLVLISVIDLILVMSVDSGTXI 1375
Db 923 DYAFALITVELLKMTFGAFLHGAFCRNYFMDLMLVGVSVLSVFGIQ-----SSA 976
QY 1376 LGMFLVRLTLRLPLRVISSAQGLKLVETLMSLKPIGNIVVICAFILFIGILGVOL 1435
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QY 1544 KCRQOHEEELARRERKRLRLLEKKRRMLMDVYIAGSSASASEQCPY----- 1596
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QY 1655 IPWVESVFKLVAFGRFRFPQDNRNQLDAIVLISINGITILEEVNAS--LPI----- 1706
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QY 1706 ---NPTIIRIMRLVRLIARVYLKLMKAVGRALDDTYM---QALPOGVNGLFMLFEI 1758
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QY 1759 FALGVELFGDLEDETHPEEGTGRHATFRNFGMAELTFLEFRVSTGDNMGINKDTL-RD 1816
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QY 1817 CDOES-----TCYNTVISPITYEVSFLVLAOFVAVNYAVIAM----- 1854
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QY 1854 KHLSENRKAEKAELEAE--LELEKTLSPQHSPLGSPFLMP-----GVEGVNSPD 1904
Db 1480 HHLDEF-KRIMSEVDPEAKGRKHLVDVTLRLRLOPPLGFGKLPBRVACKRLVAMNML 1538
QY 1905 SPKGPAPHTAHIGAAGFSLE-----HPTWVPHPEVPVPG 1942
Db 1539 N-SDGTWENATLFAVYRIALKITBESGNEOANEELRANYIKKIMKTSKMLDQVVPAG 1597
QY 1943 PDLTLVRK-----SGVSRTHSL----- 1960
Db 1598 DDEVYGVFYATFLQDYFRKFKRKEQGLVGYPAKNTTIALQAGRLHLDIGPEIRRA 1657
QY 1960 -----PNDSTMCNG-----STAESLGRHNG 1982
Db 1658 ISCDLQDDEPETKREEDDYFKRNGALLGNHVNHNVSDRSLQOQNTTTHRLHVQPS 1717
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Db 1718 IPPASDTEKPLFPAGNSV-CHNHNHNSIGKQVPTSTANLUNNANMSKAHGRKSIGN 1776
QY 2026 LPKLPPG-----RSLPAQPLR---QALRTDSLQVQ----- 2057
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QY 2095 -----IQSKVSKHRLPAPCPGLEPSPWAKDPPETRSSLELDELTSWISGDLBPSSQEE 2147
Db 1893 DDESPVUCDSRRSPRRRLPPTPA-----SHRSSNFELCLROSSQOEVPSS-- 1941
QY 2148 PLSPADLKCYVETQSCRRRPGSWLDEORHSAIVSCUDSGSQPLCPSPSLG-GOPL 2206
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QY 2320 SSHE 2323
Db 2084 TNRH 2087

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RESULT 15  
 07-08-793-3  
 ; Sequence 3, Application US/08806793

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Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
INVENTOR: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2105 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-793-3
Query Match 12.6%; Score 1572.5; DB 2; Length 2105;
Best Local Similarity 24.5%; Pred. No. 3,6e-117;
Matches 521; Conservative 370; Mismatches 705; Indels 533; Gaps 79;

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Job time: 2070 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2000, 19:59:19 ; Search time 88.8 seconds

(without alignments)  
9299.550 Million cell updates/sec

Title: PCT-US99-19675-1

Perfect score: 7129  
Sequence: 1 atgacgagagagagagatg.....gtccgcacacagagagctg 7129

Scoring table: IDENTITY\_NUC

Searched: 207703 seqs, 57918364 residues

Database: Issued\_Patents\_NA:\*

Word size: 0

Number of hits that pass the threshold: 415406

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- 2: /cgn2\_6/pdata/2/ina/5B.COMB.seq:\*
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- 4: /cgn2\_6/pdata/2/ina/5D.COMB.seq:\*
- 5: /cgn2\_6/pdata/2/ina/PCUTS9.COMB.seq:\*
- 6: /cgn2\_6/pdata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 2          | 135.8 | 1.9         | 5904   | 3  | US-08-193-078B-3  |
| 3          | 135.8 | 1.9         | 5904   | 3  | US-08-223-305C-3  |
| 4          | 135.8 | 1.9         | 5904   | 3  | US-08-149-097D-3  |
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| 6          | 134.8 | 1.9         | 5975   | 1  | US-08-314-083B-1  |
| 7          | 134.8 | 1.9         | 5975   | 2  | US-08-435-675B-1  |
| 8          | 134.8 | 1.9         | 5962   | 6  | 5386025-5         |
| 9          | 132   | 1.9         | 5904   | 1  | US-07-745-206A-6  |
| 10         | 132   | 1.9         | 2338   | 2  | US-08-455-543A-31 |
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| 13         | 131.6 | 1.8         | 5975   | 2  | US-08-336-257A-3  |
| 14         | 126   | 1.8         | 1789   | 3  | US-08-455-543A-29 |
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| 34 | 122.4 | 1.7 | 7635 | 3 | US-08-223-305C-23 | Sequence 23, Appl |
| 35 | 122.4 | 1.7 | 7635 | 3 | US-08-149-097D-1  | Sequence 1, Appl  |
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| 37 | 109.6 | 1.5 | 6513 | 1 | US-08-338-702-7   | Sequence 7, Appl  |
| 38 | 109.6 | 1.5 | 6513 | 1 | US-08-337-339-7   | Sequence 7, Appl  |
| 39 | 109.6 | 1.5 | 6513 | 1 | US-08-724-095-7   | Sequence 7, Appl  |
| 40 | 109.6 | 1.5 | 6519 | 3 | US-08-808-793-24  | Sequence 24, Appl |
| 41 | 109.6 | 1.5 | 6513 | 5 | PCT-US95-14262-7  | Sequence 7, Appl  |
| 42 | 109.6 | 1.5 | 6513 | 5 | PCT-US95-14378-7  | Sequence 7, Appl  |
| 43 | 107   | 1.5 | 7808 | 3 | US-08-149-097D-22 | Sequence 22, Appl |
| 44 | 107   | 1.5 | 7791 | 3 | US-08-149-097D-23 | Sequence 23, Appl |
| 45 | 102.6 | 1.4 | 7032 | 3 | US-08-149-097D-24 | Sequence 24, Appl |

## ALIGNMENTS

RESULT 1  
US-08-455-543A-3  
Sequence 3, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/175,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Feldman, Stephanie L.  
REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5904 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..5904  
US-08-455-543A-3

Query Match 1.9%; Score 135.8; DB 2; Length 5904;  
Best Local Similarity 53.8%; Pred. No. 6e-22; Indels 42; Gaps 3;  
Matches 377; Conservative 0; Mismatches 282;  
QY 2230 aaatacttggccgggaatcatgatacgcacccctggtcaatacactcaagatgggcatc 2289  
DB 1645 AATGCTTCTACTGCTGCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704  
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QY 2857 aactatgtctcttaacctgt 2897  
DB 2296 AACTATATCTCACTGATGTGTTCTTGCCATTCGTGTGA 2336

Patent No. 5846757  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McGue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN  
STREET: 1660 UNION STREET  
CITY: SAN DIEGO  
STATE: CA  
COUNTRY: USA  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193,078B  
FILING DATE: 07-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/868,354  
FILING DATE: 10-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-53607  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5904 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..5904  
US-08-193-078B-3  
Query Match 1.9%; Score 135.8; DB 3; Length 5904;  
Best Local Similarity 53.8%; Pred. No. 6e-22; Indels 42; Gaps 3;  
Matches 377; Conservative 0; Mismatches 282;  
QY 2220 aaatacttggccgggaatcatgatacgcacccctggtcaatacactcaagatgggcatc 2289  
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RESULT 3  
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 Sequence 3 Application US/08223305C  
 Patent No 5851824  
 GENERAL INFORMATION  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384

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RESULT 4  
US-08-149-097D-3  
Sequence 3, Application US/08149097D  
Patent No. 5874236  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,097D  
FILING DATE: 05-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/105,536  
FILING DATE: 11-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US92/06903  
FILING DATE: 14-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/914,231  
FILING DATE: 13-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/868,354  
FILING DATE: 10-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-55038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 238-0999  
TELEFAX: (619) 238-0062  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5904 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..5904  
US-08-149-097D-3

Query Match 1.9%; Score 135.8; DB 3; Length 5904;  
Best Local Similarity 53.8%; Pred. No. 6e-22;  
Matches 377; Conservative 0; Mismatches 282; Indels 42; Gaps 3;

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QY 2290 ggtaccacagagagccgag 2349  
Db 1705 GAGCAGTCAACAG 1764  
QY 2350 accagcctcttgccttggagatgctgtaactgtgtcgaagtgcccttgactac 2409  
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RESULT 5  
US-08-404-354B-1  
Sequence 1, Application US/08404354B

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: Patent No. 5618720
: GENERAL INFORMATION:
: APPLICANT: Ellis, Steven Bradley
: APPLICANT: Williams, Mark E.
: APPLICANT: Harpold, Michael Miller
: APPLICANT: Schwartz, Arnold
: APPLICANT: Brenner, Robert
: TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/404,354B
: FILING DATE: 15-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/314,083
: FILING DATE: 28-SEP-1994
: APPLICATION NUMBER: US 07/914,231
: FILING DATE: 13-JUL-1992
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 08-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-53192
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-238-0999
: TELEFAX: 619-238-0062
: TELEX:
: INFORMATION FOR SEQ. ID NO.: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5975 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 79..3700
: OTHER INFORMATION:
: US-08-404-354B-1

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Query Match 1 %; Score 134.8; DB 1; Length 5975;  
 Best Local Similarity 47.0%; Pred. No. 1e-21;  
 Matches 747; Conservative 0; Mismatches 772; Indels 69; Gaps 8;

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## RESULT 6

US-08-314-083B-1  
 : Sequence 1, Application US/08314083B  
 : Patent No. 5686241  
 : GENERAL INFORMATION:  
 : APPLICANT: Ellis, Steven Bradley  
 : APPLICANT: Williams, Mark E.  
 : APPLICANT: Harpold, Michael Miller  
 : APPLICANT: Schwartz, Arnold  
 : APPLICANT: Brenner, Robert  
 : TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 : NUMBER OF SEQUENCES: 3  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Brown, Martin, Haller & McClain  
 : STREET: 1660 Union Street  
 : CITY: San Diego  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 92101-2926  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ Version 1.5  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/314,083B  
 : FILING DATE: 28-SEPT-1994  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/914,231  
 : FILING DATE: 13-JUL-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/603,751  
 : FILING DATE: 08-NOV-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seidman, Stephanie L.  
 : REGISTRATION NUMBER: 33,779  
 : REFERENCE/DOCKET NUMBER: 6362-53191  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 619-238-0999  
 : TELEFAX: 619-238-0062  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 5975 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : FEATURE:  
 : NAME/KEY: Coding Sequence  
 : LOCATION: 79...5700

OTHER INFORMATION:  
US-C3-314-083B-1

Query Match 1.9%; Score 134.8; DB 1; Length 5975;  
 Best Local Similarity 47.0%; Pred. No. 1e-21;  
 Matches 747; Conservative 0; Mismatches 772; Indels 69; Gaps 8;

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Qy 4804 ttccgctcctctgccaacacctgtgtacacagcactacccctgagccctctcatcagtcgt 4863
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Db 3928 ATCGGATGAGATGTTTGAAGATCG 3955

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RESULT 7
US-08-435-675B-1
; Sequence 1, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwartz, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435.675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53193
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 79...5700
OTHER INFORMATION:
US-08-435-675B-1

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Query Match 1.9%; Score 134.8; DB 2; Length 5975;
Best Local Similarity 47.0%; Pred. No. 1e-21;
Matches 747; Conservative 0; Mismatches 772; Indels 69; Gaps 8;

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Qy 3760 gattccgtgtggtggtcctatatttctcctcctcgaagtggttcgtctcgtgtgtcaccg 3819
Db 2401 GAAGCAGACTCTCTTCATCTCATCTCAGTCCACCAATAGAGCGCTGTGTCAGTGCACCG 2460
Qy 3820 atcatcaccacaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3879
Db 2461 ATGCGCAAGCGCAGCTGTTGATCCAGACTTCACTGCTGTTCATCTGCTGCTGCTGCTGCT 2520
Qy 3880 accatcgtatgtgagcgccccaatgtgacccccaacagcgtgagcgcatctcctgacc 3939
Db 2521 GCGTGCGCGCGGAGGAGCCCATCGGG---CGAGTCCGTGAGATCGATCTTGGCA 2577
Qy 3940 ctctccaactcatctcgaagcagcttctctcgtcgtgaatgaagtgagtggtgtgtgtgtga 3999
Db 2578 TATTGTGATTTGCTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637
Qy 4000 ctggcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4059
Db 2638 TACGGCGCTTCTGCAAGAGGCTCTTTCGCGGCACTTCAATCAATCTGGAAGCTG 2697
Qy 4060 ttgctgtgtcctatctcgtcatcgaacatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4119
Db 2698 CTGCTGTGCGCGTGTCTCATCTCATCTGATGCTGAGTCCAGCAACATCTCGGTGTA 2757
Qy 4120 aagatctgtgcatgtcgaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4179
Db 2758 AAGATCTGAGAGTGTCAAGGCTGTCCGGCCCTCGAGC-----C 2799
Qy 4180 atcacccggcccaaggagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4239
Db 2800 ATCAACAGAGCCAAAGGCTTGAAGCAAGTGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 2859
Qy 4240 attgcaacattgtgtcatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4299
Db 2860 ATCGGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2919
Qy 4300 cagctctcaagggaagttcttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4341
Db 2920 CAGCTCTCAAGGCAAGTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2979
Qy 4342 accaggaactactaacaatccgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4386

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|----|------|---|------|
| OY | 4440 | ccgtttgtgtgcgctccaagaatgtgttggtttacatcaatgtaagtgtggtcggatgc       | 4459 |
| Db | 3396 | ccctttacccgctccacccttccgaagggtggccacagactgctgtracccgctcatcgaactc  | 3455 |
| OY | 4500 | tgtgggtgtgtatcaagcagcccaatcaatgaacacaaacccctgtgattgtctataactcat   | 4559 |
| Db | 3456 | ccacacgagagacaaaggagcccccatttccaaactaacctgtggagatctccattcttccat   | 3515 |
| OY | 4560 | ctcttcctccctatcggtgagcctttttcccgaaacatggtttgtggcggtgtgtgtga       | 4619 |
| Db | 3516 | catctacatcatatcatctccctcttcttcattgatgaacatcttgcggcgcttgcacatgct   | 3575 |
| OY | 4620 | gaacttcataaagtgcagaaagcacaagcaggaaggagagagcgagcggtgaaggaa         | 4679 |
| Db | 3576 | caccttttcagagag-----cagggggagcagagatcacaagaactgtgagcttgacaagaa    | 3629 |
| OY | 4660 | gcgactacggaagctctggaagaaaagaaagaaatctaatgttggacgatgttaattgtctc    | 4739 |
| Db | 3630 | ccacgcgacagtgcttgaaat-----  | 3651 |
| OY | 4740 | cggcagctcgaagcagcgctgtgcacgaagccagtgcaagccctactactgtactactc       | 4799 |
| Db | 3651 | -----cgccctcaaggccgccccttcggagagatnattcccaaa                      | 3692 |
| OY | 4800 | gagattccggtccttgcacaacactgtgtacagacataactgtgaccttctatcac          | 4859 |
| Db | 3693 | ccagaccacagtaacaaatgtgtgacgtggcaactccactcttctgagatctcatgtt        | 3752 |
| OY | 4860 | tgtgtatcgtggttgaaagtggttgcataatgagcattgagaaattacagcaagcccgat      | 4919 |
| Db | 3753 | cgctctatctctgcttcaacacacatctgcttggccatgcacactagcgccaaagctgcct     | 3812 |
| OY | 4920 | cctgacgaagctctgaaatctgtcaataatcaatcttaccgtaactcttgtcttgaagtc      | 4979 |
| Db | 3813 | gttcaaatgccatgaacatctccatcagatgcttctacagcgcttctcacgctggaat        | 3872 |
| OY | 4960 | agtttcaacttgtgaccttggcttcgcgcgttcttccaggaagtgaaacagct             | 5039 |
| Db | 3873 | gatcttgaaagctcatgtcccttcaaacccaaagggttactttagatccctggaaatgttt     | 3932 |
| OY | 5040 | ggaactgtgctattgtctctgtccatcatatgagcacaacacatgtgaaagattgaagtcaa    | 5099 |
| Db | 3933 | tgaacttccctatcgttaatttgacacataaattgaacgtatctcagtagagataatcagc     | 3992 |
| OY | 5100 | tgc-----ttgcgtgccatcaacccacatcatcgc                               | 5132 |
| Db | 3993 | tgaacatccccaatgctctccctctatgaacgcagagaaatctccggatctcatcattac      | 4052 |
| OY | 5133 | tatactgaggtgtgtccgcatctgttcgaattcctgaagctgtgaagatgtgcgtgtgcat     | 5192 |
| Db | 4053 | ctttcttccgctgtttccgggtcatatgccttctgttgaaacttctaagccgtggagagggat   | 4112 |
| OY | 5193 | gcgggcaactgtctgacaagtgatcagagcgcttgcacagtgaggagtggaactgtgaactct   | 5252 |
| Db | 4113 | ccggacgctgctgtagaacttcatcaatcagatcttccacagccctcctctatgtggccctctct | 4172 |
| OY | 5253 | cttatgtatattgttttcaactcttgcaagctctggggtgtggaactctttggagactgtga    | 5312 |
| Db | 4173 | gatctgtatgtcgttttcatcttaccgggtatcggagatcgaaggttttggaaaattgac      | 4233 |
| OY | 5313 | gtgtatagacaacacctgttgagggtcttggtgcagcatgacacatttagaactttgg        | 5372 |
| Db | 4233 | cctgatatgataac-----cagagagatcaacccgaatacaacaaattttcagacgttccc     | 4282 |
| OY | 5373 | tatggccttctbgacccctctccagatcctcacatgtgtgacaactgtgaattatattga      | 5433 |
| Db | 4284 | ccagagccgtgtgcttcccttcaaggtgtgcccacccggagagccctggcagagatcatgct    | 4343 |
| OY | 5433 | ggacacccctccggagc   | 5448 |
| Db | 4344 | ggcctgcatgccagcc  | 4359 |

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Query Match

1.98; Score 132; DB 2; Length 2338;

Best Local Similarity 47.3%; Pred. No. 3e-21;  
Matches 830; Conservative 0; Mismatches 770; Indels 156; Gaps 8;

|    |      |   |      |
|----|------|---|------|
| Oy | 3756 | ggaagattcigtgrogcctaattcttcctccctcagttcaagtttctgctctgtgtca        | 3815 |
| Db | 250  | gccagaaaccagggcgtttttatcttcaagcttcaaacagaaagtttgcctcagtgcca       | 309  |
| Oy | 3816 | ccggaatcatccccaagaatgtttgacacagtgctcctgcatactcctctcaacy           | 3875 |
| Db | 310  | ccgcattgttcattgaacagattcttaccacacctatctcttcttatttctgtcagacg       | 369  |
| Oy | 3876 | tatcaccatcgtatagagcgccccaataattgaccccaacagcgtcgaagcacttcc         | 3935 |
| Db | 370  | cattttccctgcgtctgagggaccgggtccacgacacacctctcttaggaacattaa         | 426  |
| Oy | 3936 | gaacctctcaactacatcttcaacggaagcttttctagctgaaatagatgaagtgct         | 3995 |
| Db | 427  | gtttattttgattgttttttttaccacctattttcacattgaaattgctctgaatgac        | 486  |
| Oy | 3996 | ggaactggcgtggtgtcttttgggagcgagcctactctgcagcagcttgaatgtctga        | 4055 |
| Db | 487  | tccattatggcgctttctttgacaaaggggtttcttctgcgggaacttaactcaatcttga     | 546  |
| Oy | 4056 | cggctgtcgtgtgcatactcctgcatacgcgaatccctgttccatagtctccgaacgg        | 4115 |
| Db | 547  | ccgtgtgggggtcagcgtgtccctcattc-----tcccttggscattca                 | 588  |
| Oy | 4116 | caccaagaatccttggcaltgcatgtgaagtgctgcggtcgtcgtcgtcgaacctcgtccactag | 4175 |
| Db | 589  | gtccagtgcaattcaatgtcgtggaagattcttgacagtcctgcgagctactcagccctcag    | 648  |
| Oy | 4176 | gttcaatccggggcccccaggaacgtgaagcgtgtgtgaaagactctgaatccactaa        | 4235 |
| Db | 649  | ggccattcaacagggcccaagggcctaaagcctgaagctatgtgtgttgcgccattcg        | 708  |
| Oy | 4236 | accgaatggcaacatgtgtgcatattgtctgtgctcttcatcatatttgaattccgg         | 4295 |
| Db | 709  | gaacctcgggaactgtgattgttcacacacctgctgacgttcatgtttgcctgcattcg       | 768  |
| Oy | 4296 | gttgaagctctcaagaaggaaatcttcgtgtgtcaaggt-----ga                    | 4337 |
| Db | 769  | ggtcagctcttccaagggaanagctgttgcacctgttcagacgttccaaagcacagagcc      | 828  |
| Oy | 4338 | ggaacaaagaaacatcactacaatccagctgcgtcgtgaagcaactacc-----            | 4388 |
| Db | 829  | ggaaatgcaagggaactacatcagctgacagtgcaaaagcgggaggtgacaccccatcattca   | 888  |
| Oy | 4388 | -----gatgggtccggcaacagtaacaaacttgaacaacctggccaggtctgaatgc         | 4439 |
| Db | 889  | accocccagactggggagaaacagaaagtttgacttttgacattgtttcggagccatgattggc  | 948  |
| Oy | 4440 | ccgttttgtgtgcgtccccaagaatgtgtgtgtgacatcatgtatgtatggcgtgctgc       | 4499 |
| Db | 949  | cctcttcacccgttccacgtttgcaaggggtggccagaaagctgctgtaacgctccattcagctc | 1008 |
| Oy | 4500 | tgtgtgtgtgattgaagaccccatctatgtacaacaacccctggatgtcgtatactcat       | 4559 |
| Db | 1009 | ccaaacggaaagacaagggcccccatttcaacaaactgctgagatcttccattcttctcat     | 1068 |
| Oy | 4560 | ctctctctcctacatcgttgccttcttctgtcgaacaatgtttgtggcggtgtgtgtga       | 4619 |
| Db | 1069 | catctacatcatcatcatatcccttctttcatgtatgaacattcttcgtggccttgcattcgt   | 1128 |
| Oy | 4620 | gaacttccaatgaatgcagacagcaaccaggaaggaaggaaggaagcggtgcgttgaagaa     | 4679 |
| Db | 1129 | cactttttcagag-----cagggggagcaggaagttacaaagaaactgtgagctggacaagaa   | 1182 |
| Oy | 4680 | gcgcactcggaggtcgtgagaaaaaaggaaggaatctaattgttgaagatgaattgcttc      | 4739 |
| Db | 1183 | ccagcgacactgcgtgtgaaah-----1204                                   |      |
| Oy | 4740 | cgcgcactcagcagcgcgttgcgtcagaagcccgatgcagagcctactactctgactactc     | 4799 |

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| 1204 | -----CGCCCTCAAGGCCCGGCCCTTCGGAGGTACATCCCAAGA                           | 124  |
| QY   | 4800 gagatctcgagctccttgcacacacctgtgttaccagacactatcgaccttcatac          | 4859 |
| 1246 | CCAGACACAGTACAAAGTGTGTACGTGTCACACTCCACTACTTGTGAGTACTGATGTT             | 1305 |
| QY   | 4860 tgggttcaatcgaggctgaaagtgtgtactatgtgcattgacattacacagccccagat       | 4919 |
| Dh   | 1305 CGTCTCATCTCGTCACACACCACTCTCCGTGGCCATGACAGCACTACGCGCAGAGCTGCT      | 1365 |
| QY   | 4920 cctggacagagctctgaaagatcgtcaattacactttaccgttcatttgtctttgagtc       | 4979 |
| Dh   | 1366 GTTCAAAATGCGCATGACATCAATCTCAACATGCTCTTCACTGGCGCTTTTCCAGCTGGAGAT   | 1429 |
| QY   | 4980 agtttccaacttbtgagcctttgtcttcgcgcgtttcttcttcacagaaagttgaacagct     | 5039 |
| Dh   | 1426 GATCTGTAAGCTATMTGCTTCAACACCAAGGGTTACTTTAGTATCCTGGAAATGTTTT        | 1485 |
| QY   | 5040 gtaacctgtctatbtgtctctgtctccatcatatggacatcacactgtgagagatbtgagtc    | 5099 |
| Dh   | 1486 TCACCTTCTCATCTCAATATGGACGCAATATGACGTCACTTTCAGTAGACTAATTCAGC       | 1545 |
| QY   | 5100 tgc-----ttgcgtgccatacaaccacacatcatcg                              | 5132 |
| Dh   | 1545 TGACATATCCCAATGCTCTCCCTCTATGAACGAGAGGAAATCTCCGCACTCCATCTCCATAC    | 1605 |
| QY   | 5133 tatcatgagggtgtctccgacattctcgaagttctgaagctgtttgaagatcgctgtggcat    | 5192 |
| Dh   | 1606 CTCTTCGCGCCTGTTTCCGGGTATAGGTCTGTGGTAAGCTGCTGACCCGTGGGAGGGCAT      | 1665 |
| QY   | 5193 gctgggcaactgttgcacaggttgatgcagagcccttgcacagctgtggaaactgtggaacttct | 5252 |
| Dh   | 1666 CCGGACGCTGCTGTGGACCTTCAATCAAGTCTTCCAGGCGCTTGCCTATGTGGCCCTCT       | 1725 |
| QY   | 5253 cttaatgttatgttt     | 5312 |
| Dh   | 1726 GATCTGATGCTGTGCTTCTTCACTACCGGCTGATCCGGATGCGAGGTGTTTGGGAAATATGC    | 1785 |
| QY   | 5313 gtgtgatgagacaacacctgtgaaggctgtgtgcgcatgacacactttagaacttttg        | 5372 |
| Dh   | 1786 CCTGAAATGATAC-----CAGCAGATCAACCGGAAACAACAATTTCAAGACCTTCCC         | 1836 |
| QY   | 5373 tatgtgcttcttaacctcttcagagtccttcaactgtgtacaaactgaaatgttatatgaa     | 5432 |
| Dh   | 1837 CCAAGCCGTGCTGCTCTCTCTTCAAGTGTCCACCGGGAGGCGTGTGGCAGACATCATGCT      | 1896 |
| QY   | 5433 ggaacaccttcggagc  | 5448 |
| Dh   | 1897 GGCTGTGATGCCAGGC  | 1912 |

RESULT 11  
US-98-223-305C-31  
Sequence 31, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:

[illegible]

|    |      |  |      |
|----|------|--|------|
| Db | 547  | CTCTGCTGTTGGTACGGTGTCTCCCTCATP-----TCCTTTGGATCA                  | 588  |
| QY | 4116 | caccagaatccttggagatgctgagggtgcgcgcgtgctgcgacccctgcctcaatcg       | 4175 |
| Db | 589  | GTCACAGTCATCAATAGTCGTGTAAGATCTTGCGAGTCTCTCGAATCTCAGGCCCTCGAG     | 648  |
| QY | 4176 | ggtcaatgcgcggcccaaggagactgaagctggtggtgtagagactgtatgtacatccctaa   | 4235 |
| Db | 649  | GGCCATCAAGAGGCCAAGGGGCTAAAGATGTGGTTTCAGTGTGTGTTTGTGCCATCCG       | 708  |
| QY | 4236 | accattggacaacttgtgtcaatttgccttgccttcttcacatlitttggaaletcgg       | 4295 |
| Db | 709  | GACCATGGGAACATCGTATTGTACCAACCCCTGGTCAGTTCAATGTTGCTCGATCCG        | 768  |
| QY | 4236 | ggtgcagctcctcaaggaggaaagttcctgtgtgtaaggt-----ga                  | 4337 |
| Db | 769  | GGTCCAGCTTTCAGAGGAAGCGCTGTACACCTGTTCAACAGATTCAGAGCAGACAGCG       | 828  |
| QY | 4338 | ggacaccagaagaataactaactaacaataacgcagtcgcctgagacaagctacc-----     | 4388 |
| Db | 829  | GGAAATGCAAGGGCAACTACTACGTACAAAGACGGGAGGTTGACCAACCCATCATCCA       | 888  |
| QY | 4388 | -----gaggggtccggacacaagtaacaactttgacaacctgggccaaggtctgalytc      | 4439 |
| Db | 889  | ACCCCGCAGCTGGGAGAGAACAGCAAGTTTACATTGTACAAATGTTCTGGCAGCATGATGC    | 948  |
| QY | 4440 | cctgtttgtgctgcgtcccaaggatggttgggttgcacatcatatgatggtgcctgagtc     | 4499 |
| Db | 949  | CCCTTTACCCCTTCACCTTCACCTTCAGAGGGTGGCCACAGGCTGCTGTACCGCTTCATGC    | 1008 |
| QY | 4500 | tgtgtgtgtgatacgaagcccatctatgaacacacaaccccttgatgctgtacatctcat     | 4559 |
| Db | 1009 | CCACACGGAAACAAAGGGCCCATCTTACATCTACCGTGTGAGATCTTCATCTTCTCAT       | 1068 |
| QY | 4560 | ctctctctccctcatcgctggcctcttcttgcctgaacatggttggcgctgtgtgtgga      | 4619 |
| Db | 1069 | CATCTACATCATCATCATTCATGCCCTTCTTCATGATGAACATCTTCGGGCTTCGTATCGT    | 1128 |
| QY | 4620 | gaactcacaatgagcagacacgaaccaaggagagagagcgagcgcggtgtggaggaa        | 4679 |
| Db | 1129 | CACCTTTTACAGAG-----CAGGGGGGAGCGAGGTATCAAGAACTGTAGCTGGCAAGAA      | 1182 |
| QY | 4680 | gggactaaggaggtctggagagaaagaggaagtaactaatgttggacgagttaattgcttc    | 4739 |
| Db | 1183 | CCAGCGACAGTGGGGAAAT-----   | 1204 |
| QY | 4740 | cggcagctcagccagcgctgcgtgcagagaagccagtcgcaagccctactactctgactac    | 4799 |
| Db | 1204 | -----CGCCTTCAGAGGGCCCGCCCTCGGAGATCAATCCCAAGAA                    | 1245 |
| QY | 4800 | gagatccggctcctctgttccaacaacctgtgttacacgcaactaccctggaccccttcaaac  | 4859 |
| Db | 1246 | CCAGCACCCAGTACAAAGTGTGTACGGTGCACCTCCACTCTTCGTGATCTGATGTT         | 1305 |
| QY | 4860 | tgtgtgcatacgggcctgaagcogtgcactatgagccatgagaaacttacaagcagccccagat | 4919 |
| Db | 1306 | CGTCCATCACTGCTCAACACCAATCTGCTTGGCCATGCAACACTTACGGCAGAGCTGCT      | 1365 |
| QY | 4920 | cctggagcaggtcctgaagatctgaacttacaactttacacgttcaatcttgtcttggagtc   | 4979 |
| Db | 1366 | GTTCAAAATCGGCATGAGCAATCTGCAACATGTCCTTACATGGCCCTTTCACCGTGGAGAT    | 1425 |
| QY | 4980 | agtttcaaatgttgccctttggtcttcgcgcggttcttccagagaaagtgtgaacagct      | 5039 |
| Db | 1426 | GATCTCGAAGCTCATATGCTCTCAACCAACCAAGGTTATTTAGTATCCCTGGAAATGTTT     | 1485 |
| QY | 5040 | ggagcccggtatgtgctcttgcatacatgaggatcaaacctgtaagagatgaggtctaa      | 5099 |
| Db | 1486 | TGACTTCTCATCTGTAATGGCAGCATATATGACGTATTTCTAGTGAACATAATTCAGC       | 1545 |
| QY | 5100 | tgc-----ttgcgtgccatacaaccacacatccgcg                             | 5122 |
| Db | 1546 | TGAACATACCAATGCTCTCCCTCATGAAAGCAGAGAGAAATCTCCCGCATCTCCATCAC      | 1605 |

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|----|------|--|------|
| QY | 5133 | tatactgaggggtgcctccgcacattgtctgaagtcgaagctggttaagaatgctgttggaat        | 5192 |
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| Db | 1606 | ctttcttccgcctgattccgggcatgacgctcttgctgaagactctatgcccgtggggaaggcat      | 1665 |
|    |      |  |      |
| QY | 5193 | gcgggactgctgtgacaacggtgatgacgagccctgcgcccacaggtgaggaaacttggaactct      | 5252 |
| Db | 1666 | ccggacgcctgctgtgggacattctatcaatgaagtccttccagagccctgcctctatgtggccctcct  | 1725 |
| QY | 5253 | cttcactgtatctgttttcaactctttgagctcgcggcctggagacctcttttgagacctga         | 5312 |
| Db | 1726 | gatcctgatgcctgctttctttcatctatcagcggggtgattcgggaatccagagcttttggsaaattgc | 1785 |
| QY | 5313 | gtgtgatgtgaacacacacctgtgaggtgttggtcggcatgcacaccttaagaaactttg           | 5372 |
| Db | 1786 | cctgatattatnac-----cacagagatcaaacccgaacaacactttcaacaccttgc             | 1836 |
| QY | 5373 | tatgacctttcttgacctctcttcgagctcagctcactgtgtgacaactgaaatgatatataa        | 5432 |
| Db | 1837 | ccagcccgctgctctcctcttttcaagctgtgcacacggggagagccttgacagacatattctct      | 1896 |
| QY | 5433 | ggacacacctccggagac   | 5448 |
| Db | 1897 | ggcctgcattgccagcc  | 1912 |

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1      RESULT 12
2      US-08-311-363-6
3      ; Sequence 6, Application US/08311363
4      ; Patent No. 5876958
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Harpold, Michael
7      ; APPLICANT: Ellis, Steven
8      ; APPLICANT: Williams, Mark
9      ; APPLICANT: Feldman, Daniel
10     ; APPLICANT: McCue, Ann
11     ; APPLICANT: Brenner, Robert
12     ; TITLE OF INVENTION: Human Calcium Channel Compositions and
13     ; TITLE OF INVENTION: Methods
14     ; NUMBER OF SEQUENCES: 32
15     ; CORRESPONDENCE ADDRESS:
16     ; ADDRESSEE: Brown, Martin, Haller & McClain
17     ; STREET: 1660 Union Street
18     ; CITY: San Diego
19     ; STATE: California
20     ; COUNTRY: USA
21     ; ZIP: 92101-2926
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: Patentin Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/311,363
29     ; FILING DATE:
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: US 07//45,206
32     ; FILING DATE: 15-AUG-1991
33     ; ATTORNEY/AGENT INFORMATION:
34     ; NAME: Seidman, Stephanie L.
35     ; REGISTRATION NUMBER: 33,779
36     ; REFERENCE/DOCKET NUMBER: 6362-51506
37     ; TELECOMMUNICATION INFORMATION:
38     ; TELEPHONE: (619)238-0999
39     ; TELEFAX: (619)238-0062
40     ; INFORMATION FOR SEQ ID NO: 6:
41     ; SEQUENCE CHARACTERISTICS:
42     ; LENGTH: 5904 base pairs
43     ; TYPE: nucleic acid
44     ; STRANDEDNESS: unknown
45     ; TOPOLOGY: unknown
46     ; MOLECULE TYPE: DNA (genomic)
47     ; US-08-311-363-6

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|-----------------------|-----------------|--------------------|-------------|--------------|
| Query Match           | 1.98;           | Score 132;         | DB 3;       | Length 5904; |
| Best Local Similarity | 47.38;          | Pred. No. 4.5e-21; |             |              |
| Matches 830;          | Conservative 0; | Mismatches 770;    | Indels 156; | Gaps 8       |

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| Db | 2697 | gccaaagcgaacggcgtttttcaicttccagcttaacaaaggttccgtccagtcga        | 2755 |
| QY | 3816 | ccggatctatccccaagaagatttgacatgtgtctctgtcatcatcttcccaatg         | 3877 |
| Db | 2757 | ccgcattgtcatatgacacagattcttccaccaactgattcttcttattctgtcagac      | 2811 |
| QY | 3876 | tatcaacatcgatagtagcccccacaatttgacccccacagcgtcgtagcgactcttc      | 3935 |
| Db | 2817 | catttccctggcgtgtgagaccgggtccagcacactcttcttagaaccatna---ttct     | 2877 |
| QY | 3936 | gacccctccacaatacatcttcaacgagtccttctagtgaatgacagtgaagtgtgt       | 3995 |
| Db | 2874 | gtttttattttatattgttttttacacacattttccacctattgaaattgctctagatgac   | 2933 |
| QY | 3996 | ggcactggccgtgtgtcttggtagagcagcctacccgtgcagcagctgtgaatgtctga     | 4055 |
| Db | 2934 | tcccttatggcgctttcttgacaaaggctttcttccggaaacttcttaacatcttga       | 2995 |
| QY | 4055 | cgagctctgtgtctcatctccgtcatcgacaactcctgtctctcatgtctccagacggt     | 4115 |
| Db | 2994 | cctgctgtgtgtcagcgtgtccctcattc-----tccctttggcatcca               | 3035 |
| QY | 4116 | caccaagaatctctgcatgtcgtgaagggtcgtgcgtcgtgcggaacccctgcacatag     | 4175 |
| Db | 3036 | gtccagtgcatcaatgtctgaaagattctgcagatcttcgacagtaactagcccttgag     | 3095 |
| QY | 4176 | ggtatcaagccgggccaggaagtgaagctgtgtgtagaagactctgaigtcatccctaa     | 4235 |
| Db | 3096 | ggcattcaacaggcccaaggcgcttaaaagcattggttcagtgatgtgtgtgtgcgcatcgg  | 3155 |
| QY | 4236 | aacctgtgcaacatgtgttcaattgtcgtgtcctcttcatcatatttgaatctcgg        | 4295 |
| Db | 3156 | gacctatcggaacatcgtgattgttcacacacctctgcagttcatgtttgctcgtcattgg   | 3215 |
| QY | 4296 | ggtgcagctcttcaagggaagttctctgtgtgtcaaggt-----ga                  | 4337 |
| Db | 3216 | ggtccagcttcttcaagggaagcgtgtacacctgttcagacatttccaagcacagagcc     | 3275 |
| QY | 4338 | ggacaacggagaactctcaacaatccgaactgcgtgtggcccaatcac-----           | 4388 |
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| QY | 4388 | -----gatgggtccggaacacagtaacacttgaacaaccgtggccagctcgtatgc        | 4439 |
| Db | 3336 | accocgcagctgggagacagcagcaagtttgcattttgacattgtttggcagcatgatgc    | 3395 |
| QY | 4440 | ccgttgtgtcgtgcctccaaggatgtgttggttgaatcatgtatgtatgtgtgcgtgagtc   | 4499 |
| Db | 3396 | cccttttaccgcttccacacttgcamaagggtggccagagctgcgtacccctccatcgactc  | 3455 |
| QY | 4500 | tgtgtgtgtatcagcagcccatctgaacacacacccctgagatcgtctataactcat       | 4559 |
| Db | 3456 | ccacacgggaagacaaaggcccatctacaaatcagctgtggagatctccattctttcat     | 3515 |
| QY | 4560 | ctctctctctcatatcgtgtgccttcttctcctgaacatgttgtgtggcgtgtgtgtga     | 4619 |
| Db | 3516 | catttatcatatcatatcatgccttcttctatgtatgaacattcttgcggcttcgtatcgt   | 3575 |
| QY | 4620 | gaacttccataagttgcagacagacacaggaaggaaggaagcgcggtctgagga          | 4679 |
| Db | 3576 | caactttcagagc-----caaggggagcagagatgacaaactgtacgttcgacaaagaa     | 3629 |
| QY | 4680 | ggcactcgtgagcgtgtgagaaaaagagaagaatcctaattgttgacgtatgaattgtcttc  | 4739 |
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Oy 4740 cggagctcagccagcgtcgtcagagagccagtgcaagccctactactcactc 4799
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Oy 5040 gtagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 5099
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Oy 5100 tgc-----ctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 5132
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Oy 5133 taccatgaggtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 5192
Db 4053 cttcttccgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 4112
Oy 5193 gctggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 5252
Db 4113 ccgagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 4172
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Db 4173 gatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 4232
Oy 5313 gctgtatgagacacacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5372
Db 4233 cctgatatgac-----cacagacatcacccggaacacacacacacacacacac 4293
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Db 4284 ccagcccgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 4343
Oy 5433 ggaacacctcgggagc 5448
Db 4344 ggcctgcatgcccagc 4359

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RESULT 13  
US-08-336-257A-3  
Sequence 3, Application US/08336257A

GENERAL INFORMATION:  
APPLICANT: JAY, SCOTT D  
APPLICANT: ELLIS, STEVEN B.  
APPLICANT: HARPOLD, MICHAEL M.  
APPLICANT: CAMPBELL, KEVIN P.  
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,257A  
FILING DATE: 07-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 54898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 238-0999  
TELEFAX: (619) 238-0062  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5975 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: Genomic DNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 79..5700  
OTHER INFORMATION: "product="Alpha-1 subunit of animal calcium channel"  
US-08-336-257A-3

Query Match 1.8%; Score 131.6; DB 2; Length 5975;  
Best Local Similarity 46.9%; Pred. No. 5.6e-21;  
Matches 745; Conservative 0; Mismatches 774; Indels 69; Gaps 8;

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4444 ttgt 4503  
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4504 ggt 4563  
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4624 ttccataagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 4683  
3280 TTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3333  
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3392 ACCCATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3450  
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4864 gtcacggagcgtgag 4923  
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4924 gtagagagcgtgag 4983  
3568 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3627  
4984 ttcaactgt 5043  
3628 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3687  
5044 ctggt 5103  
3688 ACTTTCCTGCTCCAGCGGGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3747  
5104 tgcgtgccatlaaaccccccatacctcgtatcagagagagagagagagagagagagagag 5163  
3748 CAG 3807  
5164 ctgaagcgtgtgag 5223  
3808 ATCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3867  
5224 ctgcccagaggtgag 5283  
3868 TTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3927  
5284 ctgagcgtgag 5311  
3928 ATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3955

RESULT 14  
US-08-455-543A-29  
; Sequence 29, Application US/08455543A

Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 2...1789  
OTHER INFORMATION: No. 5792846e "CNS 1.30"  
US-08-455-543A-29





Query Match 1.8%; Score 126; DB 3; Length 1789;  
Best Local Similarity 50.1%; Pred. No. 6,4e-20;  
Matches 469; Conservative 0; Mismatches 410; Indels 57; Gaps 4;

QY 3756 gcgagatcctcgtcgcgcctatcttcctcctcagtcgaagttcgtctcgtcgtca 3815  
DB 499 GCCAGAACCCGCGCTTTTCATCTTCAGCTTACACAGAGTTTCGCCAGTGC 558  
QY 3816 ccggtatcaccccaagaagatggttgacagtggtctcgtcgtcctcctcactg 3875  
DB 559 CCGCATGTGTAATGACAGATCTTACCAACCTGATCTCTTCTTCATCTGCTCAG 618  
QY 3876 tataacatcgctatggagcgcacccaaatgaccccccacagcgtgagcgcactcct 3935  
DB 619 CATTCCTGCTGCTGAGAGCCGCTCAGACACCTCTTCAGSACATA---TCT 675  
QY 3936 gacctctcaactaactctcagcagcagtcctctcgtgaatgacagtgagtggt 3995  
DB 676 GTTTTATTTGATATTTGTTTACCATTTTCACCATTTGAAATGCTCTGAGATGAC 735  
QY 3996 ggcactggcgtgctcttgaggagcagcctacgtgcagcagcgtgagtggtgga 4055  
DB 736 TGCTTATGGGGCTTCTTGCAACAAGGTTCTTCTGCGGAACTACTTCAACATCTGGA 795  
QY 4056 cgagctgctggtcgtcctcgcgtcagcactcgtgctcgtcgtcgcagcagcgg 4115  
DB 796 CTGCTGTGTGTCAGCTGTCTCCCTATC-----TCTTTGGCATCCA 837  
QY 4116 caaccaatccttgagcagtggtggtggtggtggtggtggtggtggtggtggtggt 4175  
DB 838 GTCCAGTGCATCAATCTGTAAGATCTTGCGAGTCTGCGAGTCTGCGCCCTGAG 897  
QY 4176 ggtcatcagccgggcccaggaagctgagtggtgagagactgagtcacccctcaa 4235  
DB 898 GGCCTATCAACAGGCGCTAAAGCATGTGTCAAGTGTGTGTGTGTGTGTGTGTGTGT 957  
QY 4236 acccatggcaaatggtggtcgtgctgctcctcctcctcctcctcctcctcctcct 4295  
DB 958 GACCATCGGGAACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1017  
QY 4296 ggtgcaagctctcaagggaagttcctcgtggt-----cagggtga 4337  
DB 1018 GGTTCAGCTCTTCAAGGAAAGCTGTACACCTTTCAGACAGTTCACAGACAGAGGC 1077  
QY 4338 ggcacccaggaacatacctaacaatcgcagctgctgagggccagctacc----- 4388  
DB 1078 GGAATGCAAGGCACTACATCAGTACAAGAGGAGGTGACCAACCCCATCATCCA 1137  
QY 4388 -----ggtgggtcgcgagcaagtaacttgacaacctgggcccagctcctgattc 4439  
DB 1138 ACCCCGAGCTGGGAGAACAGCAAGTTTGACTTGTGACAAATGTTCTGGCAGCATGATGC 1197  
QY 4440 cctgtttgtgcttgccccaaggatggttggtgagcatcatgatatgagctgagtc 4499  
DB 1198 CCTCTTACAGCTCTCCACCTTGGAAGGTGGCCAGAGCTGCTGTACCCCTCATGACTC 1257  
QY 4500 tgtgggtggtatcagcagcccatcatgaaaccaacccctgagtgctatacticat 4559  
DB 1258 CCACACGGAAGCAAGGCCCATCTACAACTACCTGTGAGATCTCATCTTCTTCAT 1317  
QY 4560 ctccttcctcctcctcgtggtcctcttgctcgaacatggttggtgggtggtggtgga 4619  
DB 1318 CATCTACATCATCATCATGCTCTTCTTCATGATGAACATCTTCTGCGGCTTGTGATCGT 1377  
QY 4620 gaattccataagtgacagacacccaggaaggaga 4655  
DB 1378 CACCTTTAGAGCAGGGGAGCAGAGATACAAGAA 1413



GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: January 15, 2000, 17:23:57 : Search time 34.74 Seconds  
(without alignments)  
1987.625 Million cell updates/sec

Title: PCT-US99-19675-2

Perfect score: 12469  
Sequence: 1 MDEEEDGAGAESGQPSRFT.....LREEGKGESPWPRRLTPGA 2374

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SwissProt\_38:\*

Word size: 0

Number of hits that pass the threshold: 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID         | Description        |
|------------|--------|-------------|--------|----|------------|--------------------|
| 1          | 11719  | 94.0        | 2254   | 1  | CCAG_RAT   | 054988 ratu        |
| 2          | 5860   | 47.0        | 2044   | 1  | CCAG_HUMAN | 095180 homo sapien |
| 3          | 3388.5 | 27.2        | 766    | 1  | CCAG_HUMAN | 043497 homo sapien |
| 4          | 1709.5 | 13.7        | 2327   | 1  | CCAG_MOUSE | 055017 mus musculu |
| 5          | 1706.5 | 13.7        | 2339   | 1  | CCAG_HUMAN | 000975 homo sapien |
| 6          | 1688.5 | 13.5        | 2259   | 1  | CCAG_RABIT | 002343 oryctolagus |
| 7          | 1688   | 13.5        | 2336   | 1  | CCAG_RAT   | 002294 ratu        |
| 8          | 1678   | 13.5        | 2223   | 1  | CCAG_DROM  | 056599 discopyle o |
| 9          | 1670.5 | 13.4        | 2272   | 1  | CCAG_MOUSE | 061390 mus musculu |
| 10         | 1669.5 | 13.4        | 2312   | 1  | CCAG_HUMAN | 015878 homo sapien |
| 11         | 1663   | 13.3        | 2339   | 1  | CCAG_RABIT | 005152 oryctolagus |
| 12         | 1649.5 | 13.2        | 2222   | 1  | CCAG_RAT   | 007652 ratu        |
| 13         | 1608.5 | 12.9        | 1873   | 1  | CCAG_HUMAN | 060840 homo sapien |
| 14         | 1608   | 12.9        | 1966   | 1  | CCAG_HUMAN | 022316 cyptinus ca |
| 15         | 1604.5 | 12.9        | 1852   | 1  | CCAG_MOUSE | 001815 mus musculu |
| 16         | 1587   | 12.7        | 2036   | 1  | CCAG_MOUSE | 022316 cyptinus ca |
| 17         | 1586.5 | 12.7        | 2036   | 1  | CCAG_MOUSE | 022316 cyptinus ca |
| 18         | 1585   | 12.7        | 2203   | 1  | CCAG_HUMAN | 014524 homo sapien |
| 19         | 1583   | 12.7        | 2171   | 1  | CCAG_RABIT | 027732 ratu        |
| 20         | 1580.5 | 12.7        | 2516   | 1  | CCAG_DROME | 024770 drosophila  |
| 21         | 1578   | 12.7        | 2169   | 1  | CCAG_RAT   | 022002 ratu        |
| 22         | 1577.5 | 12.7        | 1873   | 1  | CCAG_HUMAN | 013698 homo sapien |
| 23         | 1568   | 12.6        | 2163   | 1  | CCAG_HUMAN | 001668 homo sapien |
| 24         | 1568   | 12.6        | 2019   | 1  | CIN5_RAT   | 025452 musca domes |
| 25         | 1563.5 | 12.5        | 1687   | 1  | CCAG_MOUSE | 092944 mesocricetu |
| 26         | 1558.5 | 12.5        | 1610   | 1  | CCAG_MOUSE | 073700 gallus gall |
| 27         | 1557   | 12.5        | 2190   | 1  | CCAG_CHICK | 000655 homo sapien |
| 28         | 1541.5 | 12.4        | 2505   | 1  | CCAG_HUMAN | 035500 drosophila  |
| 29         | 1536.5 | 12.3        | 2131   | 1  | CIN4_DROME | 056698 discopyle o |
| 30         | 1535   | 12.3        | 2326   | 1  | CCAG_DROM  | 008104 ratu        |
| 31         | 1533.5 | 12.3        | 1951   | 1  | CIN3_RAT   | 013936 homo sapien |
| 32         | 1531   | 12.3        | 2221   | 1  | CCAG_HUMAN | 004774 ratu        |
| 33         | 1530   | 12.3        | 2005   | 1  | CIN2_RAT   | 004774 ratu        |
| 34         | 1518   | 12.2        | 2164   | 1  | CCAG_MOUSE | 004774 ratu        |
| 35         | 1516   | 12.2        | 1840   | 1  | CIN4_RAT   | 013390 ratu        |
| 36         | 1511.5 | 12.1        | 2424   | 1  | CCAG_RABIT | 027884 oryctolagus |
| 37         | 1511.5 | 12.1        | 2009   | 1  | CIN1_RAT   | 004774 ratu        |
| 38         | 1510.5 | 12.1        | 2212   | 1  | CCAG_RAT   | 054282 ratu        |
| 39         | 1508.5 | 12.1        | 1851   | 1  | CCAG_DROME | 091645 drosophila  |

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|-----|--------|------|------|---|------------|--------------------|
| 40  | 1439   | 12.0 | 1836 | 1 | CIN4_HUMAN | P35499 homo sapien |
| 41  | 1472.5 | 11.8 | 1820 | 1 | CIN4_ELEBL | P02719 electrophor |
| 42  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 43  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 44  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 45  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
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| 49  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 50  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
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| 52  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 53  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 54  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 55  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 56  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 57  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
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| 67  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
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| 96  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
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| 99  | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |
| 100 | 1463.5 | 11.7 | 1522 | 1 | CIN1_LOLBI | 005973 loligo blae |

FT REPEAT 68 398 I.  
 FT REPEAT 730 968 II.  
 FT REPEAT 1242 1519 III.  
 FT REPEAT 1564 1822 IV.  
 FT DOMAIN 1 80  
 FT TRANSMEM 81 101  
 FT DOMAIN 102 119  
 FT TRANSMEM 120 141  
 FT DOMAIN 142 150  
 FT TRANSMEM 151 170  
 FT DOMAIN 171 175  
 FT TRANSMEM 176 193  
 FT DOMAIN 194 213  
 FT TRANSMEM 214 234  
 FT DOMAIN 235 370  
 FT TRANSMEM 371 395  
 FT DOMAIN 396 744  
 FT TRANSMEM 745 765  
 FT DOMAIN 766 778  
 FT TRANSMEM 779 800  
 FT DOMAIN 801 806  
 FT TRANSMEM 807 825  
 FT DOMAIN 826 833  
 FT TRANSMEM 834 857  
 FT DOMAIN 858 868  
 FT TRANSMEM 869 889  
 FT DOMAIN 890 940  
 FT TRANSMEM 941 965  
 FT DOMAIN 966 1251  
 FT TRANSMEM 1252 1274  
 FT DOMAIN 1275 1292  
 FT TRANSMEM 1293 1313  
 FT DOMAIN 1314 1323  
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 FT TRANSMEM 1614 1635  
 FT DOMAIN 1636 1642  
 FT TRANSMEM 1643 1661  
 FT DOMAIN 1662 1675  
 FT TRANSMEM 1676 1699  
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 FT TRANSMEM 1714 1734  
 FT DOMAIN 1735 1794  
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 FT DOMAIN 1823 2058  
 FT TRANSMEM 290 295  
 FT DOMAIN 496 506  
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 FT DOMAIN 354 354  
 FT SITE 924 924  
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 FT CARBOHYD 173 173  
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Query Match 94.08; Score 11719; DB 1; Length 2254;  
 Best Local Similarity 97.98; Pred. No. 0;  
 Matches 2241; Conservative 1; Mismatches 12; Indels 34; Gaps 2;

QY 1 MDEEDGAGAEESGGPRSTQTLNDISGAGRGSGSTKEDSGADSEAGLPPALAPV 60  
 DB 1 MDEEDGAGAEESGGPRSTQTLNDISGAGRGSGSTKEDSGADSEAGLPPALAPV 60  
 QY 61 FFYLSQDSRPSRCWCLRTVCNPFERVSMLVILNCVTLGMFPCEDIAQSORRILOAF 120  
 DB 61 FFYLSQDSRPSRCWCLRTVCNPFERVSMLVILNCVTLGMFPCEDIAQSORRILOAF 120  
 QY 121 DDFIFAFVAVVYKMAVGIFGKKCYLGDITWNRIDDFIYAGMLESLDLQNSFSFAVR 180  
 DB 121 DDFIFAFVAVVYKMAVGIFGKKCYLGDITWNRIDDFIYAGMLESLDLQNSFSFAVR 180  
 QY 181 TVRVLRPLAIRVPSMRILVTLDDTLPLMGNVLLCFEYFFIFGIVGOLMAGLLRNR 240  
 DB 181 TVRVLRPLAIRVPSMRILVTLDDTLPLMGNVLLCFEYFFIFGIVGOLMAGLLRNR 240  
 QY 241 CPLEPENSPLSVLDLEPYQTEENEDESPFCISQPRENMRSCRSVPTLRGEGGGPDSL 300  
 DB 241 CPLEPENSPLSVLDLEPYQTEENEDESPFCISQPRENMRSCRSVPTLRGEGGGPDSL 300  
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 DB 301 DYTYSNNTTCVMMNOYITNCSSAGEHNPFGALINFDIGAMTAITOVITLBEWDIM 360  
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 DB 361 YFVMDASHFYNYFILLIIVGSFMINCLVIVIAOTFSETKORESQLMRQVFLSNA 420  
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 DB 421 STLASSEPGSCYEELKLVYTLKKAARLQVSRALGVRLGLSSPVASGGQPSG 480  
 QY 481 SCTSRHRRLSVHLLVHHHHHHHHYHNGTLRVPRASPEIODRDANGSRRLMLPPSTP 540  
 DB 481 SCTSRHRRLSVHLLVHHHHHHHHYHNGTLRVPRASPEIODRDANGSRRLMLPPSTP 540  
 QY 541 TPSSGPPRGAESVSHYADCHLEPVRCOAPPPRCSSEASGRTVSGKYVPTVHTSPPE 600  
 DB 541 TPSSGPPRGAESVSHYADCHLEPVRCOAPPPRCSSEASGRTVSGKYVPTVHTSPPE 600  
 QY 601 ILKDKALVEAPSPGPTLTSENIIPGPPSSMHKLEIOTSGACHSSCKTSSPCSKADSG 660  
 DB 601 ILKDKALVEAPSPGPTLTSENIIPGPPSSMHKLEIOTSGACHSSCKTSSPCSKADSG 660  
 QY 661 ACPGDSQPCYARAGABEPESADHVPDSSEAVYEFTOAQSDDLDPHSRRQRSLGPD 720  
 DB 661 ACPGDSQPCYARAGABEPESADHVPDSSEAVYEFTOAQSDDLDPHSRRQRSLGPD 720  
 QY 721 AEPSSVLAIFRLICDIFRKLVDSKYTRGIMTAIIVNTSMGIEHDEOBEELTNALISN 780  
 DB 721 AEPSSVLAIFRLICDIFRKLVDSKYTRGIMTAIIVNTSMGIEHDEOBEELTNALISN 780  
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 DB 781 IVFTSLALMLKLIVYGPFGYIKPNYINFDGVIVISWEIVGQGGGLSVLRTFRIM 840  
 QY 841 RVKLIVFELPALQROLVVLNKTMDNVATFCMLMLFIFISILGMLFQCKRASERGGT 900  
 DB 841 RVKLIVFELPALQROLVVLNKTMDNVATFCMLMLFIFISILGMLFQCKRASERGGT 900  
 QY 901 LPDRKNFDSLMAIVYVQTLTQEDMKNVLYNGMASTSSMAALYFALTMTFGYVFNLL 960  
 DB 901 LPDRKNFDSLMAIVYVQTLTQEDMKNVLYNGMASTSSMAALYFALTMTFGYVFNLL 960  
 QY 961 VAILVEGFOAEIIGKREDASGQLSCIQLPVNSOGGATKSESEDFSPSVDSGDGRKKR 1020  
 DB 961 VAILVEGFOAEIIGKREDASGQLSCIQLPVNSOGGATKSESEDFSPSVDSGDGRKKR 1020  
 SQ SEQUENCE 2254 AA; 250405 MW; 338F5789 CRC32;

QY 1021 LAVALGEHAELRKLRLPILITHTATPMSLPRKSSSTGVBALGSGSRFTSSSGSAPGA 1080  
 DB 998 LAVALGEHAELRKLRLPILITHTATPMSLPRKSSSTGVBALGSGSRFTSSSGSAPGA 1057  
 QY 1081 AHHEMKPPSARSSPHSPWMASSWTSRRSSRNSLGRAPSLKRSPGGERSSLLSGGQE 1140  
 DB 1058 AHHEMKPPSARSSPHSPWMASSWTSRRSSRNSLGRAPSLKRSPGGERSSLLSGGQE 1117  
 QY 1141 SODEEESSEDRASPASDRHRGSLEREAKSSFDLPTQVGLHATASGRSASEHOD 1200  
 DB 1118 SODEEESSEDRASPASDRHRGSLEREAKSSFDLPTQVGLHATASGRSASEHOD 1177  
 QY 1201 CNKGSASGRRLARTLRTDDPOLDDGDDNDEGNLSKGERIQAMVRSRLPACCREDMSAYI 1260  
 DB 1178 CNKGSASGRRLARTLRTDDPOLDDGDDNDEGNLSKGERIQAMVRSRLPACCREDMSAYI 1237  
 QY 1261 PPPQSRRLCHRLTHKMFDPVLYIIFLNCITIANERKIDPHSAERITLTSNYIFT 1320  
 DB 1238 PPPQSRRLCHRLTHKMFDPVLYIIFLNCITIANERKIDPHSAERITLTSNYIFT 1297  
 QY 1321 AVELAEMTVAVVALGMCFGQAVLRSSMNYLDGLVLISYIDILVMSVSDSGIKIGMR 1380  
 DB 1298 AVELAEMTVAVVALGMCFGQAVLRSSMNYLDGLVLISYIDILVMSVSDSGIKIGMR 1357  
 QY 1381 VLRLRLTLPRLVISAQGLKLVETLMSLKPIGNIVVICAFFITFGLGVQLFKGE 1440  
 DB 1358 VLRLRLTLPRLVISAQGLKLVETLMSLKPIGNIVVICAFFITFGLGVQLFKGE 1417  
 QY 1441 FVQGGEDTRITKSCAERASYRWVHKYFNQDGLGALMSLFLVASKDGMVIMYGLDA 1500  
 DB 1418 FVQGGEDTRITKSCAERASYRWVHKYFNQDGLGALMSLFLVASKDGMVIMYGLDA 1477  
 QY 1501 VGVDOOPIMNHNPMMLYFISFLIYAFVLMFVGVVVENFHKROHDEEAPRREK 1560  
 DB 1478 VGVDOOPIMNHNPMMLYFISFLIYAFVLMFVGVVVENFHKROHDEEAPRREK 1537  
 QY 1561 RLRLRKKRRNMLDYIASGSSASASAPACKPYSDYSRRLVYHDLTSYHDLFT 1620  
 DB 1538 RLRLRKKRRNMLDYIASGSSASASAPACKPYSDYSRRLVYHDLTSYHDLFT 1586  
 QY 1621 GVLGVWVWVMAHEHYQOPIIDELALICNYITFYFVFSVSKYLAFCGRREFODRMO 1680  
 DB 1587 GVLGVWVWVMAHEHYQOPIIDELALICNYITFYFVFSVSKYLAFCGRREFODRMO 1646  
 QY 1681 DLAIYVLSIMGITLLEIEVNASLPINPITIRIMVRLIARVAKLMAVGMALHTYMO 1740  
 DB 1647 DLAIYVLSIMGITLLEIEVNASLPINPITIRIMVRLIARVAKLMAVGMALHTYMO 1706  
 QY 1741 ALPOVONIGLILMLLFFITFAALGVELFGDLEDETHPCGGLRHATFRNGAFTLFRV 1800  
 DB 1707 ALPOVONIGLILMLLFFITFAALGVELFGDLEDETHPCGGLRHATFRNGAFTLFRV 1766  
 QY 1801 STGDWMNGIMKDTLRDCDESTCYNTVISPIYFVSFVLTAQVLANVYAVLAKLEESN 1860  
 DB 1767 STGDWMNGIMKDTLRDCDESTCYNTVISPIYFVSFVLTAQVLANVYAVLAKLEESN 1826  
 QY 1861 KAKKEBALEALELEMLKTLSPQHPSPGLSPGLMPGEGVNSPDSKPGAHHTAHIGAA 1920  
 DB 1827 KAKKEBALEALELEMLKTLSPQHPSPGLSPGLMPGEGVNSPDSKPGAHHTAHIGAA 1886  
 QY 1921 SGEFSLHPHVPHEEVPVPLGPDILYTRAKSVSTHSLPNDSTYCRNGSTAESLARG 1980  
 DB 1887 SGEFSLHPHVPHEEVPVPLGPDILYTRAKSVSTHSLPNDSTYCRNGSTAESLARG 1946  
 QY 1981 WGLPRAOGSILSVHOPADTSCILQLEPKDYVLLQHPGAPTGAIPPLPPGSRPLAOR 2040  
 DB 1947 WGLPRAOGSILSVHOPADTSCILQLEPKDYVLLQHPGAPTGAIPPLPPGSRPLAOR 2006  
 QY 2041 PLRRAAARTDSLDVQIGSRDLSEVSGPSCPLTRSSSWGSSIQVQORSGIQSKVS 2100  
 DB 2007 PLRRAAARTDSLDVQIGSRDLSEVSGPSCPLTRSSSWGSSIQVQORSGIQSKVS 2066

QY 2101 KHIRLPAPCGLEPSPWADPPETNSLELDTLMSISGDLIPSSOEPLSPRDKKCYV 2160  
 DB 2067 KHIRLPAPCGLEPSPWADPPETNSLELDTLMSISGDLIPSSOEPLSPRDKKCYV 2126  
 QY 2161 ETQSCRRRPGSWLDEORHSHIAVSCLDGSGOPRLCPSSSLGGQPLGPGSRPKKTLSP 2220  
 DB 2127 ETQSCRRRPGSWLDEORHSHIAVSCLDGSGOPRLCPSSSLGGQPLGPGSRPKKTLSP 2186  
 QY 2221 SISIDPESSGSRPPCSBGVCLRRRAPASDSDKSPSSPLDSTAASPPKDTLSLGLS 2280  
 DB 2187 SISIDPESSGSRPPCSBGVCLRRRAPASDSDKSPSSPLDSTAASPPKDTLSLGLS 2246  
 QY 2281 SDPTMDP 2288  
 DB 2247 SDPTMDP 2254

RESULT 2  
 CCAH\_HUMAN STANDARD; PRT; 2044 AA.  
 AC 095180;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL, ALPHA-1H SUBUNIT.  
 GN CACNA1H.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC TISSUE=HEART.  
 RX MEDLINE; 98333998.  
 RA CRIBBS L.L., LEE J.-H., YANG J., SATIN J., ZHANG Y., DAUD A.,  
 RA BARCLAY J., WILLIAMSON M.P., FOX M., REES M., PEREZ-REYES E.;  
 RT "Cloning and characterization of alpha1h from human heart, a member  
 of the T-type Ca2+ channel gene family.";  
 RL Circ. Res. 83:103-109(1998)  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOPORM ALPHA-1G  
 GIVES RISE TO T-TYPE CALCIUM CURRENTS. T-TYPE CALCIUM CHANNELS  
 BELONG TO THE "LOW-VOLTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY  
 BLOCKED BY NICKEL AND MIBERRADIL. A PARTICULARITY OF THIS TYPE OF  
 CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A  
 VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING  
 FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND  
 SUPPORT CALCIUM SIGNALING IN SECRETORY CELLS AND VASCULAR SMOOTH  
 MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING  
 PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING  
 AS WELL AS IN CELL GROWTH PROCESSES.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY, HEART AND BRAIN.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- PTM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE  
 CHANNELS ARE ACTIVATED BY CAM-KINASE II.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: AF051946: AAC67239.1; -  
 DR PF00520: Ion.trans: 4.  
 KW Ionic channel: Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel: Glycoprotein: Repeat: Multigene family;  
 KW Calcium-binding: Phosphorylation.

FT REPEAT 86 421 I.  
 FT REPEAT 778 1017 II.  
 FT REPEAT 1280 1557 III.  
 FT REPEAT 1601 1862 IV.  
 FT DOMAIN 1 99 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 100 118 S1 OF REPEAT I.  
 FT DOMAIN 119 138 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 139 159 S2 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 160 168 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 169 183 S3 OF REPEAT I.  
 FT DOMAIN 184 192 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 193 211 S4 OF REPEAT I.  
 FT DOMAIN 212 231 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 232 252 S5 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 253 293 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 394 418 S6 OF REPEAT I.  
 FT DOMAIN 419 792 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 793 813 S1 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 814 826 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 827 848 S2 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 849 854 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 855 873 S3 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 874 881 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 882 905 S4 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 906 916 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 917 937 S5 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 938 989 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 990 1014 S6 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 1015 1289 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1290 1312 S1 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1313 1330 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1331 1351 S2 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1352 1361 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1361 1381 S3 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1382 1395 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1396 1417 S4 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1418 1427 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1428 1451 S5 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1452 1528 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1529 1554 S6 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1555 1615 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1616 1636 S1 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1637 1650 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1651 1672 S2 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1673 1679 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1679 1698 S3 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1699 1712 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1713 1736 S4 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1737 1750 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 1751 1771 S5 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1772 1834 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 1835 1862 S6 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1863 2044 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 42 POLY-GLY.  
 FT DOMAIN 519 529 POLY-HIS.  
 FT DOMAIN 1105 1108 POLY-ALA.  
 FT DOMAIN 1582 1585 POLY-ARG.  
 FT SITE 377 377 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 973 973 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1503 1503 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT CARBOHYD 191 191 POTENTIAL.  
 FT CARBOHYD 270 270 POTENTIAL.  
 FT CARBOHYD 1465 1465 POTENTIAL.  
 FT SEQUENCE 2044 AA: 229115 MW: 2059B9EC CRC32:

Query Match 47.0%; Score 5860; DB 1; Length 2044;  
 Best Local Similarity 58.0%; Pred. No. 1.9e-289;  
 Matches 1265; Conservative 175; Mismatches 465; Indels 276; Gaps 44;

7 GAGAESGQPSFTQINDLSGAGRGPG-----STEKDPS-----ADSEAGLPYP 54  
 23 GVGSGVPEPR-----GAGTRGGGGFELGVSPESEPAERCAELGADEE-GRVPYP 72  
 55 ALAPVFEFFYLSQDSRPSWCLRTVCNPFWEYSMLVLLKCYTLGMRPREDIACDSORC 114  
 73 ALAAVFFELCQTRPRSWCLRTVCNPFWEYSMLVLLKCYTLGMRPEDECCSERC 132  
 115 RLLOAFDFEFAFVEVVMVALGLFGKCYGDTGNRLDFEVIAGMLEYSIDLQNY 174  
 133 NLEFADFETFAFVEVVMVALGLFGKCYGDTGNRLDFEVIAGMLEYSIDLQNY 192  
 175 SFSAVRTVRLPLRAINRVPMSRLVTLDTLPMIGNVLLCFEYFFIGIVGOLMA 234  
 193 SLAIRTVRLPLRAINRVPMSRLVTLDTLPMIGNVLLCFEYFFIGIVGOLMA 252  
 235 GLNRNCELPEFSLPSVD-LEPTYTENDESPFICSPREMGMSCRSVPTLRBEGG 293  
 253 GLNRNCELPEFSLPSVD-LEPTYTENDESPFICSPREMGMSCRSVPTLRBEGG 309  
 294 GGPSCSLDETNY-----SSNNTCVNMNQYTYNCAGEHNEFKAGINEDNIGYAMIA 346  
 310 VMPFCLHEATYQDAEGVGAARACINMNOYIYVNCSSGDSNHNAGININDCYAMIA 369  
 347 IFQVITLEGWDMYFVMDAHSFYFIILLIIVGSEFMINLCVATGATOFSETKORES 406  
 370 IFQVITLEGWDMYFVMDAHSFYFIILLIIVGSEFMINLCVATGATOFSETKORES 429  
 407 QLMRQRAVFLSNASTLASFSPGSCYEELIKYILIRKARLAQVRAIGRAGLLS 466  
 430 QLMRQRAVFLSNASTLASFSPGSCYEELIKYILIRKARLAQVRAIGRAGLLS 489  
 467 SPVARSQEPQPSGQTSRHR-----LSVHNLV-HNNHHNNHNYLNGTLRVPRAS 518  
 490 DPAVAGGPR-----GHRQRAGRHTASVHNLVHNNHHNNHNYHFSGRPRGPE 541  
 519 PETQPDANGSRRLM--PPESTPPSGPRGASVSFYHADCHLEPVACQAPRPPC 576  
 542 PGACD-----TRLVAGAPSPSPRGPR--DAESVHSIYHADCHLEPVACQAPRPPC 594  
 577 SEA-----SGRTVSGSKVYVHTSPPELTK-----DKALVEYA-----PSPGP 616  
 595 SHRCQPOGHRAGH-----HELPHDPAALGGOROHOROTGEVGRWTAHRHGRGP 647  
 617 PLTSTNIPPGPESSMHKLETOGTGAC--HSS-----KTISSPCSKADSGACGDCSPY 669  
 648 LSLNS-----PDPEKIPVHAGEHGLQAPGHLGSLVPCPLPSP--PAGTLCELSKSPY 701  
 670 CART-GAGEPESADHWPDSSEAVEFEFQDAOHSLDRP-----HSSR 712  
 702 CTALDPEBELSGSSGSDGVEFEFQDAOHSLDRP-----HSSR 761  
 713 RORSLEPDEPSSVLAFLMLICDTFRKIYDSKYFGGIMATILVNTLSNGLEYHQPDEL 772  
 762 AQQRAP-GEPMGMLVNTFSGLKLRIYDSKYFGGIMATILVNTLSNGLEYHQPDEL 820  
 773 TNALEISNIVTSLALEMLIKLVLYGPGYKPNPIFDGYIYVSWEIVGQGGGLS 832  
 821 TNALEISNIVTSMFLMLIKLVLYGPGYKPNPIFDGYIYVSWEIVGQGGGLS 880  
 833 VLRTFRMLRLKLVRLPALROLVYLMKTMNVAFECMLMLFIFISILGMHFGCKE 892  
 861 VLRTFRMLRLKLVRLPALROLVYLMKTMNVAFECMLMLFIFISILGMHFGCKE 940  
 893 ASERD-GDTLPDRKNFDSLMAIVTFOILLTOEDMKNVLYNGASTSSAALYFALMTF 951  
 941 SLKIDIGDTPDKRNDLSLMAIVTFOILLTOEDMKNVLYNGASTSSAALYFALMTF 1000

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OY 952 GNYVFLNLLVALVLEGOAEIGKREDASQGLSCIQLPVNSOGGDATESEPPDF----- 1008
DB 1001 GNYVFLNLLVALVLEGOAEIGKREDASQGLSCIQLPVNSOGGDATESEPPDF----- 1008
OY 1008 -----SBSVDDGDRKRRALVALGAEELRKSLLPLLIHTATMSLPKSSSTG 1058
DB 1047 LQTELEKMCSTAVPENGWREACPLPSSCAQLPRLPLPRAHSMWQ-----PASQTLG 1103
OY 1059 VGEALGSGSRRTSSSGAEPGAHHEMS-----PPSARSSPHSPASASWTSRRSRNSL 1115
DB 1104 V-----AAAPGTRHHEHRTSLRQPKFSLCPLG-----SGANSSRRSSMSLSL 1146
OY 1116 GAAPLKRKRSRSGERSSLLSGEGODEEESSEEDRASPAGSHRRGSLERPAKSFED 1175
DB 1147 GAAQOAPACOCGERESSLLSEBGKSTDEEDRARGSPRATPLRAESID----- 1199
OY 1176 LFDTLQVGLHRTASGRSASEHODCNKGSAGRLARTLFTDDPOLGDDDDNENGLSKG 1235
DB 1199 -PRPLRP-----PPAYQVRDQGVVALPSDFLRLDSHREDAELDDSEDSCC 1248
OY 1236 ERIQAMVNSRLPACCRER--DSMSAYIFPPQSRLCHRIITHKMFHVVYIIFLNCI 1293
DB 1249 LRLHVLVLPYKFORCSRPRPGSTLYLFSPONRFRVSCQKVIITHKMDHVVYIIFLNCY 1308
OY 1294 TIAEMRPKIDPSARIFLTLSTNYFTAVFLAEMTVKVVVALGMCQGOAYLRSSMNYLDG 1353
DB 1309 TIALERPDIIDPSTERVLSNFTIIFAEAMKVVVALGSLGSEHAYLQSSMNYLDG 1368
OY 1354 LVLVLVIDIVSVSDSGTKILGLMRLVLLRLPLRLVISAQGLKLVETLMSLKP 1413
DB 1369 LVLVLVIDIVSVSDSGTKILGLMRLVLLRLPLRLVISAQGLKLVETLMSLKP 1428
OY 1414 IGNIVVICAFFIIGIIGVOLFCKGFVCGGDEPTNTNDCAEASYRVRHRYVEDN 1473
DB 1423 IGNIVVICAFFIIGIIGVOLFCKGFVCGGDEPTNTNDCAEASYRVRHRYVEDN 1488
OY 1474 LGOALMSLFLVASKDGVNDIYDGLAVGVDOQPIIMNPMMLYIFSLIYAFVLYNM 1533
DB 1489 LGOALMSLFLVASKDGVNDIYDGLAVGVDOQPIIMNPMMLYIFSLIYAFVLYNM 1548
OY 1534 FGVVAVENHCKROHOREEERAREERERLEKRRRLMDVYIAGSSASASEQCK 1593
DB 1549 FGVVAVENHCKROHOREEERAREERERLEKRRRLMDVYIAGSSASASEQCK 1596
OY 1594 PYSDYSRFLVHHLCTSHYLDLFTIGVIGLVNVTAMMEHYOQOLIDEALKICNYFT 1653
DB 1597 PYSDYSRFLVHHLCTSHYLDLFTIGVIGLVNVTAMMEHYOQOLIDEALKICNYFT 1656
OY 1654 VIFVESVYKLVAFGRFRFPQDRMNQDLAVLISMGITLLEEVNASLPINTIRIM 1713
DB 1657 VIFVESVYKLVAFGRFRFPQDRMNQDLAVLISMGITLLEEVNASLPINTIRIM 1716
OY 1714 RVLRLARVLLKLMAVNGRRLDITVQALPOVNGILGFLMFLIFPAGLVELEGDELC 1773
DB 1717 RVLRLARVLLKLMAVNGRRLDITVQALPOVNGILGFLMFLIFPAGLVELEGDELC 1776
OY 1774 EHRPEBGGRATFRNEGMAFLITLFRVSTGNNWIMKDTIADC---DOESTCNYVISP 1830
DB 1777 EHRPEBGGRATFRNEGMAFLITLFRVSTGNNWIMKDTIADC---DOESTCNYVISP 1836
OY 1831 IFFVFLVLAQFVLNVVAVLMLKLEESNKEAELEAELEKKTLSPOPHSLG 1890
DB 1837 VYFVFLVLAQFVLNVVAVLMLKLEESNKEAELEAELEKKTLSPOPHSLG 1894
OY 1891 PLMLGVEGVNSPDSFKGAPHTTAHIGAAGFSLEHFTYMPHREEVYVPLGDLTVRK 1950
DB 1894 PLMLGVEGVNSPDSFKGAPHTTAHIGAAGFSLEHFTYMPHREEVYVPLGDLTVRK 1957
OY 1951 SGVSRTHSLPNDSYMCRNGSTA-----ERSLGHGMLPKAOGSSILTSOPADT 2001
DB 1918 VAVSRHSLPNDSYMCRNGSTA-----ERSLGHGMLPKAOGSSILTSOPADT 2002
OY 2002 SCILLOPKDVH-----YLDPHGAPITGALPKLPPPERPSPLAORPLRROAIRTDS 2052

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DB 1975 CASLQIPLAVSPARSGEPHALSPRCT-----ARSPSLRLLCQEAHVHTDS 2022
OY 2053 LD--VQGLSGREDLLSEVSGP 2071
DB 2023 LKGRLLALGTWIIQSLVRRP 2043

RESULT 3
CCAG: HUMAN STANDARD; PRT; 766 AA.
AC 043497; 043498;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL, ALPHA-1G SUBUNIT
DE (FRAGMENTS).
GN CACNA1G.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
FN [1]
FP SEQUENCE FROM N.A.
FC TISSUE-BRAIN:
RX MEDLINE: 98154730.
KA PEREZ-REYES E., CRIBBS L.L., DAUD A., LACERDA A.E., BARCLAY J.,
KA WILLIAMSON M.P., FOX M., REES M., LEE J.H.;
RT "Molecular characterization of a neuronal low-voltage-activated
RT T-type calcium channel."
RL Nature 391:896-900(1998).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1G
CC BELONGS TO THE "LOW-VOLTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY
CC BLOCKED BY NICKEL AND MIBEFRADIL. A PARTICULARITY OF THIS TYPE OF
CC CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A
CC VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING
CC FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND
CC SUPPORT CALCIUM SIGNALING IN SECRETORY CELLS AND VASCULAR SMOOTH
CC MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING
CC PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING
CC AS WELL AS IN CELL GROWTH PROCESSES.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, IN PARTICULAR IN
CC THE AMYGDALA, SUBTHALAMIC NUCLEI, CEREBELLUM AND THALAMUS.
CC MODERATE EXPRESSION IN HEART; LOW EXPRESSION IN PLACENTA, KIDNEY
CC AND LUNG.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- FTM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE
CC CHANNELS ARE ACTIVATED BY CAM-KINASE II.
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF029228; AAD12731.1; -.
CC DR EMBL: AF029229; AAD12732.1; -.
CC DR PFAM: PF00520; Ion_trans.1.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Calcium channel; Glycoprotein; Repeat; Multigene family;
CC FM

```

Calcium-Binding: Phosphorylation.

| Query Match   | Best Local Similarity | 27.2%   | Score 3388.5 | DB 1 | Length 766 |
|---|-----------------------|---|--------------|------|------------|
| Matches 686; Conservative 22; Mismatches 57; Indels 337; Gaps 3;        |                       |   |              |      |            |
| QY 1188 TASGSSASSEHDDCGKSGASGRLARTLTDPPOLDGDDNDENGLSKERIQAWVRSLP 1247   | 1188                  | TASGSSASSEHDDCGKSGASGRLARTLTDPPOLDGDDNDENGLSKERIQAWVRSLP 1247   |              |      |            |
| DB 1 TASGSSASSEHDDCGKSGASGRLARTLTDPPOLDGDDNDENGLSKERIQAWVRSLP 60        | 1                     | TASGSSASSEHDDCGKSGASGRLARTLTDPPOLDGDDNDENGLSKERIQAWVRSLP 60     |              |      |            |
| QY 1248 ACCREDSWSAYIFPPOSFRLCHRIITHKMFHDVYVYIFLNCITAMERPKIDPISA 1307    | 1248                  | ACCREDSWSAYIFPPOSFRLCHRIITHKMFHDVYVYIFLNCITAMERPKIDPISA 1307    |              |      |            |
| DB 61 ACCREDSWSAYIFPPOSFRLCHRIITHKMFHDVYVYIFLNCITAMERPKIDPISA 120       | 61                    | ACCREDSWSAYIFPPOSFRLCHRIITHKMFHDVYVYIFLNCITAMERPKIDPISA 120     |              |      |            |
| QY 1308 ERFELLSNYITFAVFLAMTVKVAALGWCFCGEQAYLRSSNMVLDGLVLISVIDILVSM 1367 | 1308                  | ERFELLSNYITFAVFLAMTVKVAALGWCFCGEQAYLRSSNMVLDGLVLISVIDILVSM 1367 |              |      |            |
| DB 121 ERFELLSNYITFAVFLAMTVKVAALGWCFCGEQAYLRSSNMVLDGLVLISVIDILVSM 180   | 121                   | ERFELLSNYITFAVFLAMTVKVAALGWCFCGEQAYLRSSNMVLDGLVLISVIDILVSM 180  |              |      |            |
| QY 1368 VSDSGTKILGMLRVLLRLTLRLPLRVISRAQGLKIVETLMSLKPIGNIYVYICAFPII 1427 | 1368                  | VSDSGTKILGMLRVLLRLTLRLPLRVISRAQGLKIVETLMSLKPIGNIYVYICAFPII 1427 |              |      |            |
| DB 181 VSDSGTKILGMLRVLLRLTLRLPLRVISRAQGLKIVETLMSLKPIGNIYVYICAFPII 240   | 181                   | VSDSGTKILGMLRVLLRLTLRLPLRVISRAQGLKIVETLMSLKPIGNIYVYICAFPII 240  |              |      |            |
| QY 1428 FGLISVOLKRGKRFVCGGSDTNTITKSCCAEASRYRWHRKXNPNLGOALMSLVLSK 1487   | 1428                  | FGLISVOLKRGKRFVCGGSDTNTITKSCCAEASRYRWHRKXNPNLGOALMSLVLSK 1487   |              |      |            |
| DB 241 FGLISVOLKRGKRFVCGGSDTNTITKSCCAEASRYRWHRKXNPNLGOALMSLVLSK 300     | 241                   | FGLISVOLKRGKRFVCGGSDTNTITKSCCAEASRYRWHRKXNPNLGOALMSLVLSK 300    |              |      |            |
| QY 1488 DGVNDIMYDGLDAVGDQOPIMNHNPMMLYFISFLIYAFVLMVGVVVENFHCRO 1547      | 1488                  | DGVNDIMYDGLDAVGDQOPIMNHNPMMLYFISFLIYAFVLMVGVVVENFHCRO 1547      |              |      |            |
| DB 301 DGVNDIMYDGLDAVGDQO----- 320                                      | 301                   | DGVNDIMYDGLDAVGDQO----- 320                                     |              |      |            |
| QY 1548 HOEEERARRRERKRLRLERLEKRRNMLDVIYASGSASASAEPCKPYISDSRRLVH 1607    | 1548                  | HOEEERARRRERKRLRLERLEKRRNMLDVIYASGSASASAEPCKPYISDSRRLVH 1607    |              |      |            |
| DB 320 ----- 320  | 320                   | ----- 320   |              |      |            |
| QY 1608 HLCSTHYDLFITGVIGLVNVTNAMEHYQOQLIDALKICNYIFTVIFVESVEKLVAF 1667   | 1608                  | HLCSTHYDLFITGVIGLVNVTNAMEHYQOQLIDALKICNYIFTVIFVESVEKLVAF 1667   |              |      |            |
| DB 320 ----- 320  | 320                   | ----- 320   |              |      |            |
| QY 1668 GFRRFQDRWNQDLAIIVLLSINGITLLEIEVNASLPINPTIIRIMRYLRIARVCLKLM 1727 | 1668                  | GFRRFQDRWNQDLAIIVLLSINGITLLEIEVNASLPINPTIIRIMRYLRIARVCLKLM 1727 |              |      |            |
| DB 320 ----- 320  | 320                   | ----- 320   |              |      |            |
| QY 1728 AVGMRALDITVMAQLPOVGNLGLFMILFFIFALGVELFGDECDETHPCBGLGRHAF 1787   | 1728                  | AVGMRALDITVMAQLPOVGNLGLFMILFFIFALGVELFGDECDETHPCBGLGRHAF 1787   |              |      |            |
| DB 320 ----- 320  | 320                   | ----- 320   |              |      |            |
| QY 1788 RNFGMAFLTLFVSTGDNMGIMKDLRDODSTCYNTVISPFIYVSEVLTAQFVLNV 1847     | 1788                  | RNFGMAFLTLFVSTGDNMGIMKDLRDODSTCYNTVISPFIYVSEVLTAQFVLNV 1847     |              |      |            |
| DB 320 ----- 327  | 320                   | ----- 327   |              |      |            |
| QY 1848 VIAVLMKLEESNKEAKEALELELEKTKLSPQHPSPFGSPFLMPGVEGVNSPDSRK 1907    | 1848                  | VIAVLMKLEESNKEAKEALELELEKTKLSPQHPSPFGSPFLMPGVEGVNSPDSRK 1907    |              |      |            |

RESULT 4

CCAB-MOUSE STANDARD: PRT: 2327 AA.

QY 328 VIAVLMKLEESNKEAKEALELELEKTKLSPQHPSPFGSPFLMPGVEGVNSPDSRK 387

QY 1908 PGAPHTTAHGAAGSFSLEHPTWVPHPEVVPVLGPDLLVYRKSGVSRTHSLPDSYMR 1967

DB 388 PGALPAHAHASASHFSLEHPTWVPHPEVVPVLGPDLLVYRKSGVSRTHSLPDSYMR 444

QY 1968 NOSTERISLGHGWLKPAQSGSITSVSOPADTSCITQLEPKVDHYLLOPHGAPTGAIP 2027

DB 445 HGSITAGPLGHGWLKPAQSGSITSVSOPADTSCITQLEPKVDHYLLOPHGAPTGAIP 504

QY 2028 KLPPEGRSPLAQRPLRQAARTDSDVQGLSREDLSEVSGSPCLTSSSGWSSSI 2087

DB 505 KLPPEGRSPLAQRPLRQAARTDSDVQGLSREDLSEVSGSPCLTSSSGWSSSI 564

QY 2088 QVOQSGISQSKVSKIRLPAPCGLEPSMAADPPETRSLELDLSELSGDL-PSOE 2146

DB 565 QAOHRSRSHSKISKMTPEAPCPGEPNMGKGPETRSLELDLSELSGDL-PSOE 624

QY 2147 EPLSPDLKCYSVETQSCRRRPGSMLEDEORRHSIYVSCLDGSGQPLCPSPSSLGQPL 2206

DB 625 EPLSPDLKCYSVETQSCRRRPGSMLEDEORRHSIYVSCLDGSGQPLCPSPSSLGQPL 684

QY 2207 GGPSPRKKKLSPPSISIDPPESGSPPCSPGVLRRAPASDSKDPVSPLDSTAAS 2266

DB 685 GGPSPRKKKLSPPSISIDPPESGSPPCSPGVLRRAPASDSKDPVSPLDSTAAS 744

QY 2267 PSPKKDLSLGSISDPDMDP 2288

DB 745 PSPKKDLSLGSISDPDMDP 766

RA HONG T., BIRNBAUMER L., "Nucleotide sequence polymorphism of mouse alpha B.", Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases. [2]

RA MATTEI M.-G., LAZDUNSKI M., "Molecular cloning of a murine N-type calcium channel alpha 1 subunit. Evidence for isoforms, brain distribution, and chromosomal localization.", FEBS Lett. 338:1-5(1994).

CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS (I<sub>h</sub>) AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CITX-GVIA) AND BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN





Query Match 13.7%; Score 1709.5; DB 1; Length 2327;  
 Best Local Similarity 24.2%; Pred. No. 4.1e-79;  
 Matches 645; Conservative 391; Mismatches 805; Indels 829; Gaps 98;

27 GAGGROGFGSTKDPGSDSEAEGLPYPALAPVVF-----FYLSQDSRP 70  
 25 GAGGAGGPGGGLPPGGVLYKOSIAORARTMALNPVKNCFVNRSLFVFESEENV 84  
 71 RSMCLRTVCNMFPERVSMTVLILNCVTLGMFRPCEDACDSORCRILQAFDD--EFAF 127  
 85 KRYAKRTIEMPERFEMLIATIIANCIVALT-----EQHLPODDKTPMERBDDDEPIYGI 140  
 128 FAVEMVYKVALG-LEFKCYLGDTWRNLDFFIYAGMLEYS---LDLONVSSAVTVR 163  
 141 FCFEAGIKIILAFVFKHGYLKNGMNMDVNVVLTGILATAGTDFDLR-----TLRAVR 195  
 184 VLRLPRLANRVPMSMLITLLDILPMLGNVLLCFEVEFFIYGVQVQVQVQVQV 243  
 196 VLRLPLKLVSGIPSLQVVLKSTIKKANVPLDGLLFFAILMFAIIGLEFFYMGKFKACF- 255  
 244 PENFSLPLSVLDLERYUTENEDESEPFICOPRENGMRSRCSVPTLRGEGGPPCSLDYE 303  
 255 -----PMSIDEPY-----GDFPCGKDP 273  
 304 TYNSSSNTCVNMNOYTNCNAGEHNPFGKALINDNIGAMIAIFQVITLGGWVDIYFV 363  
 274 AFQCDGDEEC---REYWP-----GPNFGITNEFNILFALLTYFOCTIMGWTDILYNT 323  
 364 MO-AHSFNFYFILLIIVGSPFMINICLVATQFSETKORES-----OLMREQRYRF 416  
 324 NDAAGNTWMLTFLIILIGSFFMLNVLGVLSGEFAKERERVRRAFLKLRQOQOE- 383  
 417 ISNASTLASFSEPGSCYEELLKYUYILKKAARLQVSRALGVRAGLSSPVARSQEP 476  
 383 -----RELNGYLEMIFKAEVMLEED-----KNAEEK 410  
 477 OPSGSTRHRLSYHNLHNNHNNHNNHNLGNGTLVRPRASPELQDANGSRRLMP 536  
 411 SPLDYLRKATKSRDLH-----AEEGEDR----- 438  
 537 PSTPTPSGPRGASVSHFYHADCHLBPVRCQAPRPRCPSEASGRTVSGKVPYVHTS 596  
 438 ----- 438  
 597 PPEILLKALVYVAPSPPTLTFNIPRPFSSMHKULETOSTGACHSSCKTSSPCSK 656  
 438 -----FVDL-----CAGSPPAR 450  
 657 ADSGACGPDSCPCARTGAGEPESADHVAPDSDEAVVEFTQAOHSDLRPHSRORS 716  
 451 AS-----LKSGETESSYF-----RRKEK- 470  
 717 LGDPAEPSSVLAFWRLICDTPFKIYDSKTFGKGMIAIIVNTLSMGIEYHEDEPPELLNAL 776  
 470 -----MFRFF-----IRMVAKAGSFYVWVLCVVALNTLCVAMVHYNOPORLTAL 514  
 777 ELSNIYETSLFALMELTKLLVYGPFGYIKNPYNIPDGVIYVVSWEIYQO-----QGGL 831  
 515 YFEFEFLGLFTEMLKMGIGLPRSYFSRNCEDFGVIVSIEYVMAAKPSTSGI 574  
 832 SVLRTFLMKVLFVLFALOROLVLMKTNDVATFCMLMLDFEFISILGMLFGCK 891  
 575 SVLRALRLRIFKVTUWYMSLRNLVSLNSKMSIISLFLFLFVYFALLGMLFGGQ 634  
 892 FASERGGDILPDKKNDLSLMAIVYFQIITQEDMKVLYLNGM-----ASTSMNAALFTI 946  
 635 FNFODEPT-----TNDTFPPAALIVFQIITGEDMNAVMHGISOGVSKMGESSFTFI 690  
 947 ALMTFGVYVFNLLVAILVVGCF-QAEIIGK-----REDASGO-----LSCI 986  
 691 VTLFGNTLLNVLAILANDNLNAOELLTKDEBEEMEAANOKIALOKAEVAVSPMSGA 750

967 QLPVNSGGDATKSSSEPD-----FFSPVDGDDGRKKRLATVALGE-HAELR 1033  
 751 NISIAARQNSAKASWEGQASOLRLONLRASCALXSEMDPEERLRYASTRIVRDMK 810  
 1034 KSLPPLIILH-----TAATPMS-LP-----KSSSTGVG----- 1061  
 811 TMMDRPIVVEPBGDLRQPVGSKSPECTEATESADLPRHRRHRDCKTISATAPAGEQ 870  
 1061 ---EALGSGSR---RTSSGSAE-PGA-----AHHEKMSPPSARSPPSPMSA 1102  
 871 DRTSETEGAREERARPRRSKETPGADTQVCEERSRHRHRSPEBA--TEREPPRHR 928  
 1103 SGMTSRRSRNSLGRAPSLKRSPGERRSLSGE---GQESODEESSEDRASPAGSD 1159  
 929 AHRHADSKE--GAPVL---VPKGERAHRHGRPTGPRAENNEEPTRHRA----- 978  
 1160 HHRGSLEREAKSFDDLDTLOVPGELHRTASGRSSAE-----HOCNCKSA 1206  
 978 -RHK-----VPTLOPPE-REAAKESNAVAGDKETRNHOPKEPHCOLAIAV 1023  
 1207 SG-----RLARTL--RTDDPOLDGDND----- 1229  
 1024 TGVGLHMLPSTLOKQVDEQPDADNQRNVTBMGSQSDPTVHAVPTLGPGETPVV 1083  
 1229 -EGNL-----SKGER-----IQAMVRSRLPACCRERDSWAVIFPPQSRFLCHRIT 1275  
 1084 PGGNNMLEGQAGKKEADVDLRRGPRIVYS-----SMCLSPTNLLRRFCHYIV 1136  
 1276 THRMEDVYLVITFNLCTITAMERKIDPHSAERIFLLNSVTFNAVLAEMTVYVALG 1335  
 1137 TMRFEVNLVILASTSLAAEDP-VRTDSFRNNALYMDIIFGVTFEVMKMDLG 1195  
 1336 WCFGEQAYLRSSWNVLDGLVLIVYDI-LVSMVDSGTKILGLMRLVRLTRTRPVI 1394  
 1196 LLHPATYRDLNMLIDFVYSGALVAFRFSFGMSGKNDINTKSLRYLVRPLKTI 1255  
 1395 SRAQGLKLVETLMSLKPIGNIVVICAFFIIFGILGVQFKGFYVCOGE-----DT 1448  
 1256 KRLPKLKAFFDCVANSKLVNLLIYVLMFIFIVAVIOLKGFYFCTESKELERDC 1315  
 1449 RN--LTKSDCAEASR-VWRKYNFDNLGOALMSFLVASGDVADLMYDGLDAVGDQ 1505  
 1316 RGQVLYEKEVEADPRQMKKTIDHDVLMALLILFTVSTEGSPMWLKHSDVATYEDQ 1375  
 1506 QPTMNHNPMLLYFISFLIVAFVLMFVGVVENEHFKROHDEEERARRERKRLRL 1565  
 1376 GSPGFMELSTIYVYVFPPEFVNFVALLITF-----QEGDKVMSE-----CSL 1425  
 1566 EKKRNLMDDVJASGSSASASEAQKPYSDYSRFLVHLHCTSHYDLFITGVGL 1625  
 1426 EKNER-ACIDFAT-----SAKPLTRYMP--ONKSFQKVTWVAVSPPEFFIIMATIAL 1476  
 1626 NVYTMAMEHYQPOLIDEALCKNTFYTVFVESEFKLVAFGRFRFODRBNQDLAIY 1685  
 1477 NYVYLMKFTADAYEYELMKLCINIVFTSMFGECLIKIANGVLYNFDANVDFVTV 1536  
 1686 LLSIMGTIEIEIVNASLPIIPTIRINRVLRIARVLLKKAAGRRALLDVQALQV 1745  
 1537 LGSITDLVTEIANNF---IN--LSFLRLFRARAILKLRQGYTRILLMTFVVSFKAL 1590  
 1746 GNLGLFMLLFFPALGVLPGLDCEHHPDEGGRATPRNGMAFLTLFVSTGDN 1805  
 1591 PYVCLLTLMLFFYVAILIGVQVFNALDDO--TSINRHNERTFLOALMLLFRSITGA 1647  
 1806 WNGIMKDTL--RDOD--QESTYNTVISPIYFVSFLTAQVLYVNVYVIAVLMKHLSESN 1860  
 1648 WHEIMLSCLNRACDDPHANSEC-GSDFAVYFVSTIFLCSFLMLNLFVAVIMDNFEYLT 1706  
 1861 KEAK-----EBALEALEF-----LKM-KTLSQPHSPIG-----SPTL 1893  
 1707 RDSISLPHHLDDEFIRVAYEADPAACGRISYNDMFEMLKHMSP---PLGLKCKCPARVA 1762  
 1894 WPGVEGVNSPDSRPGARPHHTAHIGAAGFSLE-----HPTMVVHPREVP----- 1939

Db 1763 YKRLVBMNPISENEDMTVHTSTLMALIRLLEIKLAPACTGKCOCAELKEISSWYAN 1822  
 QY 1939 -----VPLGPDLLTV-----RKSQVSRHSPLPNDSYMCNRGSTAE 1973  
 Db 1823 LPQKTLDLVPHKPRDEETVGVKVAALMIFEDFYKQNKTTROTQHQAAG----- 1871  
 QY 1974 RSLGHRGWLKRAQSGSLVSHSQPADTSCILQPKVDVHLLQHGAPVTCATPKLPPPG 2033  
 Db 1871 -----GL-----SOMGPRVSLFHPYKAT-----LEOTOPAVLNGA----- 1900  
 QY 2034 RSLPAQR---PLRQAAIRTDLSLDVQ-----GLGSRDLSEVSGP-----SCPLTRS 2078  
 Db 1900 RVFLRQKSAISLNGCAIQOESIKESLSWGTQRTODALYEANAPLERGHSALPIVQGS 1959  
 QY 2079 SSFVGSGSIQVQGRS-----GIOS--KVSCHILPA---PCGILEP----- 2115  
 Db 1960 -----GTLAVDVQOMNMTLRGPDGEPGPGLSOGRAASMPRLAETOPAPNAPSMKRSIST 2015  
 QY 2115 -----SWAKDPP-----ETRSLELDTL-----LSWIS 2137  
 Db 2016 LARPHGTOLCSTYLDPRPSQASHHHHCHRRRCKKORSLKGPBLSDVPCGASTA 2075  
 QY 2138 GDLPSQSEPLSPRLDKCTVETOSGCRPRPSWIDEORHSIVASCIDSGSQ--PRLC 2195  
 Db 2076 GPGIAPHGEGSTACRORRCKOERGRSQE--RRQPSSSSEKQRF--YSCDRFGSREPPOLM 2130  
 QY 2196 PPSF-----SLGGGPL-----GGPSRPRKKTSP--PSIS 2223  
 Db 2131 PLSLSHPTSTALEPAPHQGGSGSVNGSPLMSTSGASITPGRGGRQOLPOTPLTPRPSIT 2190  
 QY 2224 -----IDPESQSGRPPCSPG-----VCLRRAPASD-----SKDSVSS 2258  
 Db 2191 YKTANSSPVHFAQSGSLPAFSPGRLSRGLSEHNALLQKRPLOPLAPSGRISGDPYLOQ 2250  
 QY 2259 PLDSTAASPKKDTLSL-----SGLS 2281  
 Db 2251 RLDSASAHPLPEDTLFEFAVATNGRSS 2280

RESULT 5  
 CCAB HUMAN  
 ID CCAB HUMAN STANDARD: PRT: 2339 AA.  
 AC 000975;  
 DT 01-OCT-1996 (rel. 34, Created).  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL I1) (B11).  
 DE CACNA1B OR CACNA1A5 OR CACHS.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).  
 RC TISSUE-BRAIN;  
 RA MEDLINE: 9233586.  
 RA WILLIAMS M.E., BRUST P.F., FELDMAN D.H., PATTHI S., SIMERSON S., MAROUFI A., MCCUE A.F., VEICELEBI G., ELLIS S.B., HARPOD M.M.;  
 RT "Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel.";  
 RT Science 257:389-395(1992).  
 RL [2]  
 RP SEQUENCE OF 1-94 FROM N.A.  
 RC TISSUE-LUNG FIBROBLAST;  
 RA KIM D.S., JUNG H.H., PARK S.H., CHIN H.;  
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B

CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.  
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-SUBUNIT AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -I- ALTERNATIVE PRODUCTS: INTEGRAL MEMBRANE PROTEIN.  
 CC -I- ALTERNATIVE PRODUCTS: TWO ISOFORMS THAT DIFFER IN THEIR C-TERMINAL REGION. ALPHA-1B-1 (SHOWN HERE) AND ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING  
 CC -I- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.  
 CC -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -I- PFM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.  
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DR EMBL: M94172; AA51897.1; -  
 DR EMBL: M94173; AA51898.1; -  
 DR EMBL: U76666; AAC51138.1; -  
 DR MIM: 601012; -  
 DR PFM: PF00520; Ion.trans. 4.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.  
 FT REPEAT 82 359  
 FT REPEAT 468 712  
 FT REPEAT 1137 1419  
 FT REPEAT 1456 1711  
 FT DOMAIN 1 95  
 FT TRANSSEM 96 114  
 FT DOMAIN 115 132  
 FT TRANSSEM 133 152  
 FT DOMAIN 153 163  
 FT TRANSSEM 164 183  
 FT DOMAIN 184 187  
 FT TRANSSEM 188 206  
 FT DOMAIN 207 225  
 FT TRANSSEM 226 245  
 FT DOMAIN 246 331  
 FT TRANSSEM 332 356  
 FT DOMAIN 357 482  
 FT TRANSSEM 483 501  
 FT DOMAIN 502 516  
 FT TRANSSEM 517 536  
 FT DOMAIN 537 544  
 FT TRANSSEM 545 562  
 FT DOMAIN 563 573  
 FT TRANSSEM 574 592  
 FT DOMAIN 593 611  
 FT TRANSSEM 612 631  
 FT DOMAIN 632 684  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S1 OF REPEAT I (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT S2 OF REPEAT I (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S3 OF REPEAT I (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT S4 OF REPEAT I (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S5 OF REPEAT I (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT S6 OF REPEAT I (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S1 OF REPEAT II (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT S2 OF REPEAT II (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S3 OF REPEAT II (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT S4 OF REPEAT II (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT S5 OF REPEAT II (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 685 709 S6 OF REPEAT II (POTENTIAL).  
FT DOMAIN 1151 1151 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1152 1169 S1 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1170 1185 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 1186 1205 S2 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1206 1217 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1218 1236 S3 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1237 1246 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1247 1265 S4 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1266 1284 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1285 1304 S5 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1305 1391 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1392 1416 S6 OF REPEAT III (POTENTIAL).  
FT TRANSMEM 1417 1471 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1472 1490 S1 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1491 1505 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1506 1525 S2 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1526 1533 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1534 1553 S3 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1553 1563 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1564 1582 S4 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1583 1601 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 1602 1621 S5 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1622 1683 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1684 1708 S6 OF REPEAT IV (POTENTIAL).  
FT TRANSMEM 1709 2339 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 2050 2054 POLY-HIS.  
FT TRANSMEM 2118 2122 BINDING TO THE BETA SUBUNIT (BY  
FT DOMAIN 379 396 SIMILARITY).  
FT NP\_BIND 451 458 ATP (POTENTIAL).  
FT SITE 314 314 CALCIUM ION SELECTIVITY AND PERMEABILITY  
FT SITE 663 663 (BY SIMILARITY).  
FT SITE 1365 1365 CALCIUM ION SELECTIVITY AND PERMEABILITY  
FT SITE 1655 1655 (BY SIMILARITY).  
FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY  
FT MOD\_RES 1719 1719 (BY SIMILARITY).  
FT CA\_BIND 1737 1748 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
FT CARBOHYD 256 256 BY SIMILARITY.  
FT CARBOHYD 1563 1563 POTENTIAL.  
FT CARBOHYD 1675 1675 POTENTIAL.  
FT VANSPLIC 2164 2339 POTENTIAL.  
FT GSGVNSGSLSTSGASTPGSGRGLPOTPLTPRSITTK  
FT TANSPIHFAQTSLSAFSGRLSKLSHNNALQDPIS  
FT QPLAGSRIGSDPYLGQRLDEASVHALPEDTLFEAVAT  
FT NSGRSSRTSYVSLQSHPRLRVNHYHCTLIGSSGRAR  
FT HSYHPPDDHMC -> AGSAVGEPNTPCCRETSPASMPDL  
FT ALELALTLTWSVTVTRPLSPCLRTSLSRRLPPTRAP  
FT PGLPCCP (IN ISOFORM ALPHA-1B-2).  
FT SEQUENCE 2339 AA; 262494 MW; 16679780 CRC32; -

Query Match 13.7%; Score 1706.5; DB 1; Length 2339;  
Best Local Similarity 24.2%; Pred. No. 5.9e-79;  
Matches 645; Conservative 370; Mismatches 844; Indels 805; Gaps 91;

QY 27 GAGGROGPESTKEDPGASDAEAGLEPYPALAVYF-----FYLSQDSRP 70  
DB 25 GAGGAGGPGPGLOPQORVLYKOSIAORATMALYNPIPVKONCFYKRSLEFVSEDRV 84  
QY 71 RSMCLRTVCNPMWERYSMVLINCVTLGMPCEDIACDSORCHILAFDD---FIAF 127  
DB 85 RYAKRITMPPEYITLITANCIVLAL-----EOHLPDGKTMSESLDTEYFIIGI 140  
QY 128 FAVENVVKNVALG-IFGKCYLGDTRNRLDFEVIAGMLEYS---LDLQNVSESAVTR 183  
DB 141 FCEAGAKITIALGFEVHKSYLRNGVMVDEYVVLGLATAGTDFDLR-----TLRAVR 195  
QY 184 VLRPLRINRVSMRLIVLLDTPMLGNNVLICFFVFFIGYGVOLMAGLLANRCL 243  
DB 196 VLRPLVSGISLQVLYLKSIMKAMVPLLIQILGLFALIMFAIIGLEFYMKGFHACF- 255

QY 244 PENISLPLSVLDLEPYTOTENDESPFICQPRENGMRSCHSVPTLRGEGGGPGPCSIDYE 303  
DB 255 -----PSTDAEAPV-----GDFPCGKEAP 273  
QY 304 TYNSSNTTCVNMNOYVNCGAGEHNPFGKAINPDNIGYAMIAIFQVITLEGWDIMYFV 363  
DB 274 ARLCGDEEC---KEYW-----GNFGITNDNLFLALYFQGITMEGWDILYNT 323  
QY 364 MD-AHSFYNFYLILLIVGSEFMINCLVYATOSEYKORSE-----QLMREQVRF 416  
DB 324 NDAAGNTVMNLYFPLILIGSFMLNLVLGVLGSEFAKERREVRNRRAPLKLROQDIE- 383  
QY 417 LSNASTASPEPGCYELLKLYLILRKARLAQVRAIGVAGILLSPVARSGQEP 476  
DB 383 -----RELNGYLEMIFKAEEVMALED-----RAMEEK 410  
QY 477 QPSGCTSHRRLSVHNLVHHHHHHHHYHLGNTLRVPRASPEIODRDANGSRRLMLP 536  
DB 411 SPLDVLKKAATKKSNDLH-----AEEGEDRFAD----- 441  
QY 537 PSTPLPSGGPRGASVSFTHADCHLEPVRCQAPPRCPSEASGRVYSGKYVTVHTS 596  
DB 441 ----- 441  
QY 597 PPELILKQALVEVAPSPGPPTLSFNIPGPFSSMKLLETOSTGACHSSCKISSPCSK 656  
DB 441 -----LCANGSPFAR 450  
QY 657 ADGACGPDSCPCYARTGAGEBESADHYMPDSSEAYEFTQDAHSDLRDPHSRRORS 716  
DB 451 AS-----LKSGTSSSYF-----RRREK- 470  
QY 717 LGPDAEPSSVLAFWMLIDITPRKIYDSKYFGRGIMAILVNTLSGIEYHPOPELINAL 776  
DB 470 -----MRFEE-----IRRWYKQSFYVWLVCAVALNLVYAMHYQPRLLITL 514  
QY 777 EISNIFVSLFMLEMLKLKLYVPGYIKNPYNIDGVIVYSWEIYGO-----QGGL 831  
DB 515 YFAEYFVLQFLTEMSIKMGIGRPSYRSPNCDFGVISYVEVYMAIKPGSPGI 574  
QY 832 SVLRFRLRVKLIVFLDALQRLVLMKTYMDNVAITCMILMFIFESLIGHLPCK 891  
DB 575 SVLRALRLIRIKVTKYWSLSRLNVLVSLNSKRSIISLFLFLFIVFALLGQLEGGQ 634  
QY 892 FASERGDPLPRKNDLSLMAIVTFOILQEDKNKVLVNGM-----ASTSSMAALYFI 946  
DB 635 FNFQDETPT---YNDTFPAALIVYFOLLIGEDNNAVMYHIESQGVSKGMSSFEFI 690  
QY 947 ALMTFQNYVLFMLVAILVEGF-QAEIEIGK---REDAAGQ-----LSCI 986  
DB 691 VLFIFQNTYLLNVLFLAIVDNLANOELTKDEEMEAQKTLAKAKAEVAYEAPMSAA 750  
QY 987 QLFVNSOGGDAIKSESEPFPSVDGDDRKRLALVALGHAELRSLPLLIHTAA 1046  
DB 751 NISIAKQONSAAKARVWE-----QASQRLQNLTRASCALYSNDPBERLPA 800  
QY 1047 TPMSLPKSSSTGVE-----ALGSGSRRTSSSGSABEGAA-----HH-ENKS 1087  
DB 801 TTHRLPRDKMTHLDRVLVELGRDARGVGKARPEAAEAPEGVPPRRHHNRDKXT 860  
QY 1088 P-----PSANS---PSPVSAASWTSRRSSRNSUGRAPSLLKRSPS 1127  
DB 861 PAAGDODRAAPKAESGEGAREERPRPHRSKSEA--GPEARSERKGP-----GPE 913  
QY 1128 GERRSLISGGGQSOOE-----ESSPEDRASPAQSHHRRGSLE---REKSSF 1174  
DB 914 GGRHHRRGSPDEAAREPRRHARHODPSKECAGAKERRARHRRGGRAPRAAESG- 973  
QY 1175 DLPLTLQVPG-LHRTASGRSSASE--HODCNKSSAGRLA-----RTLTDPPOLDG 1223  
DB 973 -----DEPARRRRARHKKQAPHAENVEKETTEKEATEKAEALVEADKEREKLNHQPREDH 1026





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QY 562 RTVSGKXVPTVHTSPPEILKDKALVEAPSPPTLTSTFNIPGPPSSMKLLETQST 641
DB 429 -----DEHCVDIS-----437
QY 642 GACHSSCAISSPCSAADGACGPPCYCARTGAGEPESADHVMPDSDSEAVYEFQDAQ 701
DB 437 -----SVGTPLARASIKSAKVDGASY-----FR 459
QY 702 HSDLDRSRRRRSLGDAEPSSVLAFWRLICOFKIVDSKTFGKCIAMIAIIVNTLSM 761
DB 460 HKE-----RLRISVRAHVSOQVYVIVLSLVALNACV 493
QY 762 GIEHEOPEELTNALETSINIVFTSLFALEMLIKLIVGPFGYIKNPYINFGDVIWISW 821
DB 494 AIVHNQOWMLTHLYAEFLGLFLEMLKMKMGKPRLYFHSNCFEGTVASIF 553
QY 822 EIVGO-----OGGIVSVTRFLRMYLKVLPALORQVLVLMKTDNVATFCMLMLF 876
DB 554 EVWMAIFRPGTSFISVLRALRLRIFRITKYMASLRVLVLSMSSMKSIISLFLFLF 613
QY 877 IIFSIILMHLFGCKFASERDGLTPDRKNFDSLMAIVYFOILTOEDMKNVYNGM-- 935
DB 614 IVEFALLMQLFGGRF--NFNDG-----TSANFDTPPALIMTVFOILLTGEDMNEVWYNGIRS 669
QY 935 ---ASTSSMAALYIALMTFGNYVLFILVALIVEGF--QAEELGK---REDAAGQLSCI 986
DB 670 OGVVSGMMSAVYFIVTLFGNYTLNLNVLAIANDNLANQELKDKQDEEAFNOQHAI 729
QY 987 QLPVNSGGODTKSESEPDFSPVDDGDRKKLAL-----1024
DB 730 -----OKAKVSPMSA---PSIERDRRRRHMSMEBRSSHLERRRRHHMSWEQR 781
QY 1024 -----VALGEHAELKRLPLIHTAATPM-----SLPSSSTGVGEALG-- 1065
DB 782 TSOLRRHMQSSQALNKEAPRPNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLN 841
QY 1065 SGRSRTSSSASBPAAHHEKSPPS--ARSSPHSPMSA-----ASSWT---1107
DB 842 KCEBHVSRGSLKGDCCO--RSLPLSGRREP--PMLARCHGNCPEALQETAGGEIVYT 898
QY 1107 ---SRSSRNSLGRAPSLKRSPSGERRSILSGGQSOEBESSEDRASPPGSDH 1160
DB 899 FEDRARROQRORSRHRRVTEAKESSASRS-----RSVQSRSLDEGASTEGERSH 951
QY 1161 RHRS-----LERKASSFDLPILQVP-----GLHRTAS-----GRSSA 1195
DB 952 EARSHGKREPTIHEERADLRRTOSLWPKSGLAGLDEAGTPLYLSPGCVKKEAA 1011
QY 1196 SEHODCKGKASGRL-----ARTLRTDDPOL-----DGGDD 1226
DB 1012 PTEOHADGSEPALGLHVOUDVGRALISOSEPDLSCTATDKVYTESTDYVAIPDAEPL 1071
QY 1227 NDE-----GNLSKGE-----RLOAMVRSRLPACCREDSMSA--YIIPQSR 1266
DB 1072 VDSIVAHIGKKTGEGASPRQEAEMKEADETEKQKKERRASGKAVPHSSMFTSTSNP 1131
QY 1267 FLLCHRIITHKMFHDVAVIIFLNCITIAMERPKIDPISAERIFLTLISNYTAAFLAE 1326
DB 1132 IRRACHYVVALRYFEMCILLVIAASSIALAEDPVLINSERNV--LRYDYFTGVTFTTE 1190
QY 1327 MYKVAVALGCGFGEQAVLSSMWVLDGLVLISVIDI--LVSWSDSGTIKLMLRVLRL 1385
DB 1191 MYTKMIDOGILLIDGSYFDLWMIIDFVVVVGALVAFALAMGLTKKGRDITIKISLRYL 1250
QY 1386 RILRPLRVISRAQGLKLVYETLMSLKPIGNIVICAFIIFGILGYOLEKGFVC-- 1444
DB 1251 RVLRLPKITIKRLPKLAVDCVVTSLKNVNTIIVYKLMFIFAVIAYAVOLEKGFVC 1310
QY 1444 QGDDTNR-----ITKSCDAEASV--WVRHKYFNEDNLQALMSLEVLASKDGWDIMYD 1496
DB 1311 SSKDTEKECIGNVVDHEKKNMEVKGREMKRHEFHYNIMAILLTLFTVSTGCMQVOYLQH 1370

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CY 1497 GLDVGVDQOPINNNPMLLFIISFLIVAFVLMVEGVVENEHCKROHEEERAR 1556
DB 1371 SVDTTEDEKSPSRNSKREMSIFVYVFEVPEFVNIIFALLIITF-----QOQDKM 1423
QY 1557 REEKRRLREKKRRNMLDVIASGSSASASAEQCKRP--VSDYSR--FRLLVHLLCTS 1612
DB 1424 MECSL-----EKNERACIDFALSA-----KPLTRMPONRHTFOYRWHVAVS 1467
QY 1613 HYIDFTIGVIGLVNTVMAHEYOQPOLIDEALKICNYLFTYIFVEESYFKLVAGFRRE 1672
DB 1468 PSFETIMAMIALHVVLMKXYASPCYELAKTLNIAFTWVSELCVKIAGFVNY 1527
QY 1673 FODRNQOLALVILSIMGITLEEIVNANSLPNIPIIRIMVRLIARVLKILKAVGM 1732
DB 1528 FHDWNIEFIVYISITIEIVLDEKLVNTGFNNFSLKLFRA--ARLIKLRQGYIR 1584
QY 1733 ALIDVMAQALPOVNGILFLMFLFIFALAGVELFGDLECD--ETHPCGSLGRHATFRMG 1791
DB 1585 ILLMTFVGSFKALPYVCLLIAMLFFIYALIGMOVGNIRLDEESH---INRHNHRSFF 1640
QY 1792 MAFLTFRVSTGDNNGIMKTTL--RDOD-----QESTCYTVIISPITYVSVLTA 1840
DB 1641 GSIIMLFRSATGEAMQETMLSCLEKCEPDTPASGOQESPRGCTDLAYVYFVSIFFC 1700
QY 1841 OFVLVNVVIAVLMKLEESNKEAK-----EEALEALE-----LEMKTL 1880
DB 1701 SFLMLNFAVAMIDNFEYITRDSILGHHLDEFVRAVEYDRAACGRIHYTEWEMTL 1760
QY 1881 -SPQHSPLG-----SPLMPGVGVNSP-----DSPKGAPIHTAHGAASG-- 1923
DB 1761 MSP-----PLGICKRCPKAVAKRLVIANMMPVAEDMTVFTLMAILLRTALDIYAKGA 1816
QY 1923 ---FSLHPTNY--PHPE-----VVPYLPBDLITVRKSGVSRTHSLPNDSYMCRN 1968
DB 1817 DRQOLDSELOKETTALIWPLHSOKMLDLVPMRKASD--LTVEKIVAA--MMIMDYKOSK 1872
QY 1969 GSTAERSLGHROWGLPKAOSGSLSVSHSPADTSCIIOLPRDNYVLILOPHAPVGAIPK 2028
DB 1873 VAKORROL-----EOKNAPMFORMEPS-----SLPEET--IANAKALP---CLPQ 1913
QY 2029 LPP-----PGRSPLAQRPLRROAIRTD-----SLDVQIGLSREDLSEVSG 2070
DB 1914 GPBAGLGRSGCPAPSPPLSPQIFQUTCMDPADDDGQFOEDRSILVTPDGSRRSFTIIR 1973
QY 2071 PSCPLTRSSFW-----GSSIOYQORSIQS--KVKKHRLPAPCGLEPSWAKDP 2120
DB 1974 ---KRSSSSWLEEFESMERSSDNTYKRRRSYHSLSLSAH--RL-----2013
QY 2121 PETRSLELDELWISGDLPSQOEPLSPRODKCYSVETOSCRRRPSWLDQORHS 2180
DB 2013 -NSDSGKHSDTHRSG--GREKRSKERHLSADVSRCSSEB---RGAQADW--DSPERRH- 2065
QY 2181 IAVGCLDGSQPLRCPSPSSLGQPLGPGSRPKKLSPSISIDPPEGSGRPPCPGV 2240
DB 2065 ---PSRSPBGRGQSPSRGQTSLSSESSIPSVSDISTPRHSKRLPVP-- 2112
QY 2241 CLRRSAP-----ASDSKQPS--VSSPLD-----STASGSPKKTLSLSGLSSDPTMDPVL 2290
DB 2112 ---APRPLASTYSLKQOPSNFSPADSSQGSLLASPALSSAOGVL-----BESSD---2160
QY 2291 PTLPHLSPGADPSSASMAAFIKSPTAASSHAPHLPPSSVAGDDEQNF 2340
DB 2160 ---SPRAGOSHASPQRISEPTLA--LHEDSH--ASDCGEELITF 2199

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RESULT 7
CCAB_RAT ID CCAB_RAT STANDARD; PRT; 2336 AA.
AC G02294;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-1999 (Rel. 38, Last annotation update)
DB VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM

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DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL  
 DE III) (BIII).  
 GN CACNA1B OR CACNA1S OR CACNA5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eukarya; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE: 92279265.  
 RA DUBEL S.J., STARR T.V.B., HELL J., AHLJANIAN M.K., ENYEART J.J.,  
 RA CATERALL W.A., SNUITCH T.P.;  
 RT "Molecular cloning of the alpha-1 subunit of an omega-conotoxin-  
 RT sensitive calcium channel.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5058-5062(1992).  
 RN [2]  
 RP SEQUENCE OF 1516-1679 FROM N.A. (CLONE RBB-10).  
 RX MEDLINE: 90239020.  
 RA SNUITCH T.P., LEONARD J.P., GILBERT M.M., LESTER H.A., DAVIDSON N.;  
 RT "Rat brain expresses a heterogeneous family of calcium channels.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).  
 RN [3]  
 RP PHOSPHORYLATION.  
 RX MEDLINE: 94171759.  
 RA HELM J.W., APPLEBYARD S.M., YOKOYAMA C.T., WARNER C., CATERALL W.A.;  
 RT "Differential phosphorylation of two size forms of the N-type calcium  
 RT channel alpha 1 subunit which have different COOH termini.";  
 RL J. Biol. Chem. 269:7390-7396(1994).  
 RN [4]  
 RP BETA-SUBUNIT BINDING DOMAIN.  
 RX MEDLINE: 94150724.  
 RA PRAGMEL M., DE WAARD M., MORI Y., TANABE T., SNUITCH T.P.,  
 RA CAMPBELL K.P.;  
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II  
 RT cytoplasmic linker of the alpha 1-subunit.";  
 RL Nature 368:67-70(1994).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B  
 CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS  
 CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED  
 CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-  
 CC IITIA (OMEGA-AGA-IITIA). THEY ARE HOWEVER INSENSITIVE TO  
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN  
 CC DIRECTED MIGRATION OF IMMATURE NEURONS.  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: THERE SEEMS TO BE TWO ISOFORMS THAT DIFFER  
 CC IN THEIR C-TERMINAL REGION; THEY ARE PROBABLY PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC use by non-profit institutions as long as its content is in no way

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 CC -----  
 CC DR EMBL: M92905; AAA42014.1; -  
 CC DR PFAM: PF00520; Ion.trans; 4;  
 CC DR Ionic channel; Transmembrane; Repeat; Multigene family;  
 CC KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 CC KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.  
 CC REPEAT  
 CC I.  
 CC II.  
 CC III.  
 CC IV.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S1 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S2 OF REPEAT I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S3 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S4 OF REPEAT I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S5 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S2 OF REPEAT II (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S3 OF REPEAT II (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S4 OF REPEAT II (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S5 OF REPEAT II (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S6 OF REPEAT II (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S1 OF REPEAT III (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S2 OF REPEAT III (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S3 OF REPEAT III (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S4 OF REPEAT III (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S5 OF REPEAT III (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S6 OF REPEAT III (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S1 OF REPEAT IV (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S2 OF REPEAT IV (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S3 OF REPEAT IV (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S4 OF REPEAT IV (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S5 OF REPEAT IV (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S6 OF REPEAT IV (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC POLY-HIS.  
 CC BINDING TO THE BETA SUBUNIT.  
 CC ATP (POTENTIAL).  
 CC CALCIUM ION SELECTIVITY AND PERMEABILITY  
 CC (BY SIMILARITY).  
 CC CALCIUM ION SELECTIVITY AND PERMEABILITY  
 CC (BY SIMILARITY).  
 CC CALCIUM ION SELECTIVITY AND PERMEABILITY  
 CC (BY SIMILARITY).  
 CC SITE 664 664  
 CC SITE 1367 1367  
 CC SITE 1655 1655







FT TRANSMEM 1430 1448 S1 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1449 1463 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1464 1483 S2 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1484 1491 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1492 1510 S3 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1511 1519 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1520 1538 S4 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1539 1557 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1558 1577 S5 OF REPEAT IV (POTENTIAL).  
 FT TRANSMEM 1578 1638 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1639 1663 S6 OF REPEAT IV (POTENTIAL).  
 FT TRANSMEM 1664 2223 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 33 40 POLY-GLU.  
 FT DOMAIN 729 735 POLY-GLU.  
 FT DOMAIN 1064 1068 POLY-SER.  
 FT DOMAIN 386 403 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).  
 FT SITE 321 321 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 671 671 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1323 1323 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1611 1611 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT CA\_BIND 439 451 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RRS 1674 1674 BY SIMILARITY.  
 FT CA\_BIND 1692 1703 BY SIMILARITY.  
 FT CARBOHYD 287 287 POTENTIAL.  
 FT CARBOHYD 1300 1300 POTENTIAL.  
 FT CARBOHYD 1519 1519 POTENTIAL.  
 SQ SEQUENCE 2223 AA: 251827 MW; 27D453AE CRC32;

Query Match 13.5% Score 1678: DB 1: Length 2223:  
 Best Local Similarity 24.4%: Pred. No. 1.5e-77;  
 Matches 609; Conservative 387; Mismatches 830; Indels 666; Gaps 87;

QY 62 FYLSQDSRPRSMCLRTVCNPFERFVSMVLVILNCVIGMER--PCEDIACDSQCRITIA 119  
 DB 83 FLFEGEDNIVRSARVIEWPEFEYMLATIANCVVALQHLQHPNGD---KTPAKSLEQ 139  
 QY 120 FDDITFAFNAVENVKVALG-IFGKCYIGDTNRILDFVIAGMLEYSLDLDONVESA 178  
 DB 140 TEPYFICGFCEAGIKVALGFEVFNKSYLRNGVWDFVLSGLL--ATAATHFELRT 197  
 QY 179 VRTAVLRPLRAINRVPMSRLVTLTDLTPMLGNVLLCFEVEFIFGIVGYOLMGLLR 238  
 DB 198 LRAVRVLRPLKLVKSGISLQIVLKSIMKAVPRLQIGLLFPAILMFAITIGLEFYTGKLR 257  
 QY 239 NRCLPNEFLPSLVLEPYUQENEDESPFGISQPRENGMRSQSVPTLRGEGGGPPC 298  
 DB 258 RCTVTDAAAEELDLP-----PC 276  
 QY 299 SLDEIYNSSNTTCVWNNQYTNCSAGENHPKGAIPNINIGYAMIAIPQVITTEGWD 358  
 DB 277 GTQEPFLCNGVYCSW-----IGPDGIGTFQFNILFALLTYFOCTMGMTT 325  
 QY 359 IMFVMDA-HSFYNFYIFILLIIVGSEFMINCLVUATQFSETKORRESOLMREOVRFL 417  
 DB 326 ILVNTDGLAMNMWLYFPLIITIGSFVLNVLVGLSGFAERERV-----ENRSL 380  
 QY 418 SNASTLASFESQCYEELIKYUULIRKARLAOVRAI-GVAGLLSPYARSGQRP 476  
 DB 381 K-----LRQOQIERELNGLYRAMIDKAEVMLEEN 411  
 QY 477 QPAGSCTRSH--RRLSYNHLVNNHNNHNNHNGTLPVRSRPTIORDANGSRRLM 534  
 DB 412 KNGEKSALHVLRAITK-----KRMEN-----TQESSEDQ----- 445  
 QY 535 PPSSTPPSGPRGAEVSHSYFNADCHLEPVRCOAPRPPRSEASGRIVSGKYVPIVH 594  
 DB 445 ---YTEISSVGSPLARASIKS----- 463

QY 595 TSPPELTKOKALVEVAPSGPPTLTSFNIPGPFSSMKLLTOSTGACHSSCKRISPC 654  
 DB 463 -----TKLEGGSS----- 471  
 QY 655 SKADSGACGSDPCYCARTGAGPEASADHVPDSDSEAVYEFTQDAQSHDLDPHSRRQ 714  
 DB 471 -----YFRRE 476  
 QY 715 RSLGPAEBSVLAFLRLICDFRKIVDSKYFGRGIMAILVNTLSMGIEYHOPEBLTN 774  
 DB 477 RML-----RI-----STRHVKSHAFYIYLGVALNTCVAAVHIDQPLMSN 520  
 QY 775 ALFISNIFSLPALMLKLVLGYEGYIKNPYNIFDGVIVISWEIV-----GOOGG 829  
 DB 521 FLVYAEFTLGLFSSEMFKMYCGGRLYHSSFCDFGVIIISFDVWITIIPEPSF 580  
 QY 830 GLSVLPFRMLRKLKVRFLPALQRLQVLYMKTMDNVATFCMLMLTFIFISILGMHLFG 889  
 DB 581 GISVLAALRLIRFKITKYWASLRNLVLSMSKSTISLFLFLFVFPALQMLQFLG 640  
 QY 890 CKFASERDQTLPRKNDPSLMAIVYFQILTQEDMNVLYNGMAS-----TSSMALY 944  
 DB 641 GQNFEE--GTPP--TNEPTPAIITVQILTGEDMNEVMYNGIKSGGVNMGMSVY 696  
 QY 945 FIALMFGYVFNLLVALIVEGF-QAEFIGK-----REDASQSLSCIO-----LPVNSOG 994  
 DB 697 FIVLTFEGVYTLNVLALVANDLNAQELTKEDEEEEAINKHALQAKEVSPMSAPG 756  
 QY 995 GDAKSE-----SEDFSPSYDG-----DGD 1016  
 DB 757 PSTEREFRRHKMSIWEARTSOLARRMOSREALFDALQGLEGSRRYRRHSRIEPAE 816  
 QY 1017 KKKRLALVAGHAHL---RKSLLPPLIHTAATPMSLPRSSST---GVGALGSGS 1067  
 DB 817 SLRRLAQQAASHOLGVEGRFAFKSRLNSWQPAAPDRSSIKYNGOGALGSLV 876  
 QY 1068 RTSSSGSAEPAAHHEKSPSPSARSPPSASSTSRSSNSIGR-APSLKRRSP 1126  
 DB 877 EAGASPRMAEPFRARRRYS--LYEAKMGLEESFSLSRPRKNGRGLQOLCEQE 934  
 QY 1127 SG---ERRSLSGEQQES---ODEESEDPRASPAGSDRHGHSERKSSFEDLPDT 1179  
 DB 935 SGQLTQTEVMDAQOMAFQMOGPHSSMTRPDVTD-PSGNNLEKESGRY---PEN 990  
 QY 1180 LOVPGLHRTASGRSSASRHQD---CNGKSASGRLAFTLTDD-----POLDGD 1225  
 DB 991 ---GKEESANTSEQVNDOSWMLNLQOQATPGDRELTTGTROTKODKQOEOEIDVDC 1046  
 QY 1226 DNDE-----GNLSKGERLOAMVRSRLPACCREDBSMAYIF?POSRF-----R 1268  
 DB 1047 ENTETPMDSLVTPGN-----AYS-S---SVKEDEKSKALIPYTSMLFRKTPDIR 1095  
 QY 1269 LCHRIITHKMFHDVAVIIFLNCITIAMERKIDPISAERIFLTLSNYFTAVLAEMT 1328  
 DB 1096 RYCHETIVNLRFEKCIILVLAASSVALAEDP-IHKSARNOVLRKYDYFTGVTTEMY 1154  
 QY 1329 VKVVALGMCQGEQAYLSSNANVDGLVLSVIDI-LVSNVSDSGTKMLCLRYLRLLRT 1387  
 DB 1335 IKMDIGLVFEHGSYFRDWNILDFIIVSGALVAFATNLIGSGSGKDINTIKSLRVLRY 1214  
 QY 1388 LRLPLVISRAQGLKLYVETLMSLKPIGNIYVLOCAPFIIFGILGYOLFPGKFFVQGED 1447  
 DB 1215 LRLPLTKIRPLKLAIVDCVATSLKNVFNILYKLEMFIFAVALVQLFEGKFEYC--TD 1272  
 QY 1448 TRNITNNSDCAEASYSRWVRHK-----YNFDNLQOALMSLFLVASKRGWDIMY 1495  
 DB 1273 SSKMT-KODC-RGQFVLYLROTKLSINGNWTTFHYDNVWALLLFTVSTGSGWQVLD 1330  
 QY 1496 DGLDAVGVDQPIINHPNMLYFISLLVAFVFLVMEYGVVVENHFKROHOEEEAR 1555  
 DB 1331 HSYDVTEADGPIPGNMESIFIVYVFFPEFVNIIFVALIITF-----QOQDCK 1383



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FT TRANSMEM 478 497 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 498 510 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 511 530 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 531 539 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 540 558 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 559 568 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 569 587 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 588 606 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 607 626 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 627 679 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 680 704 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 705 750 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 751 811 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 812 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 831 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 832 841 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 842 851 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 852 861 S4 OF REPEAT III (POTENTIAL).
FT TRANSMEM 862 871 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 872 881 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 882 891 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 892 901 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 902 911 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 912 921 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 922 931 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 932 941 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 942 951 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 952 961 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 962 971 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 972 981 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 982 991 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1011 1020 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1021 1030 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1031 1040 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1051 1060 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1091 1100 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1101 1110 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1111 1120 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1231 1240 S6 OF REPEAT III (POTENTIAL).
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FT TRANSMEM 1261 1270 S6 OF REPEAT III (POTENTIAL).
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FT TRANSMEM 1281 1290 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1291 1300 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1301 1310 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1311 1320 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1321 1330 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1331 1340 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1351 1360 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1451 1460 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1631 1640 S6 OF REPEAT III (POTENTIAL).
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FT DOMAIN 1931 1940 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1941 1950 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1951 1960 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1961 1970 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1971 1980 S6 OF REPEAT III (POTENTIAL).
FT TRANSMEM 1981 1990 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1991 2000 S6 OF REPEAT III (POTENTIAL).

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Query Match 13.48; Score 1670.5; DB 1; Length 2272;
Best Local Similarity 23.88; Pred. No. 3.8e-77;
Matches 613; Conservative 398; Mismatches 850; Indels 717; Gaps 86;

QY 41 PGASDSEA-----EGLPALAPV-----FFY 63
DB 13 PGSGDSDSDSRNNGRGPVPAASGAAYKSKORANTALNYPYRONCTVNSLPI 72
QY 64 LQSDSRRSCLRTVCNPFERVSMLVILNCVTLGFR--PCEDIACDSQRCRIIQA 121
DB 73 FGEDNIVRYAKKLIDWPPEEYMLATIIANCIYLALEQLPEDDTPMSRR--LEKTE 129

122 DFTAFVAVMYKVALG-IGKKCYLGDWNRLDFFVIAGMEYSLDLON--VSFA 178
130 PYFGICFEAGIKIYALGFIHKGSYLRGNMNMDFIVLSGLTAFGHFTVDLRA 189
QY 179 VRTVVRVRLPRAINRVSMBILVTLDLPLMGVNLCCFPFFIFGIVGVLNAGLR 238
LB 190 LRAVRVRLPRLKLVGSLDQIVKSKAKAVPLDQGLLFAILFAITGLEFYSKJH 249
QY 239 NRCELPENFSLPVDLEPYQOTENEDSPFCSQPRENGMRCRSVPTLRGGGGPC 298
DB 250 RACFMNN-----SGILEGF-----DPRHPC-----GVQC 274
QY 299 SLDEYTNSSNTCYVMNMYTNCAGENHPKGAINDNIGYAIIFQVITLEGWD 358
DB 275 PAGE-----CKDW-----IGPNDGITOPDNILFAVLVFOCITMGWTT 314
QY 359 IMFVMDA-HSFYNYFIFILLIVSGFMINCLVYIATQFSETKORESQLRQVRFL 417
DB 315 VILNTDNLGATNMMLYFPLIITIGSFVNLVYLVSSEFAKEREV-----ENRRAF 369
QY 418 SNASTIASSEPOSCYEELKLVYTLKRAARLAQVSRAL-GVAGLSSPVARSQEP 476
DB 370-K-----LRQOQIERELNGYRAMIDKAEVMALEN 400
QY 477 QPSSGCTSRHRLSYHHLVHHHHHHHNGTLVPRASPEIODRDANGSRRLMPP 536
DB 401 KNSGTALVLRAT-----IKSRTEAMTRDSS----- 430
QY 537 PSTPTSGGPPRGAESVHSFYHADCHLEPRVQAPPRCPSPASRTPYVTVHTS 596
DB 430----- 430
QY 597 PPEPILKDALVEVAPSPBPPLTTFENIPGPFSSMHKLTQTGACHSCKISSPCSK 656
LB 430-----DEHCVDIS-----SVGTPLAR 445
QY 657 ADGAGCPSPCYCATGATGAPESADHWMPDSDSEAVYETDADHSLDRPHSRORS 716
DB 446 ASIKSKYDCAST-----FRHKE----- 464
QY 717 LGDABPSSVLAFWRLICDTEFRKYDSKYFGRGIMAILVNTLSGIVHDOPELTAL 776
DB 464-----RLRISIRHWKSOYFYWIVASVALNTACAIYHHNQPOLITLL 509
QY 777 EISNIVFTSLPEMLIKLVYGPYGIKNPNYIDGVIVISWEIVGQ-----QGGGL 831
DB 510 YTAELFELGLFLEMSLKAYGMPRLYFHSFNCDFGVGSIPEVYMAIFRPGTSPGI 569
QY 832 SVLRTFRLMKVLVRFPLALOROLVLMKTPMDNATFCMLMFIFFSTLGHNLGCK 891
DB 570 SVLRALRLIRIKIRKYANASRLNVLSSSKSTLSLFLFETVVALLGQLGEGR 629
QY 892 FASERDGLTPRKNFDSILMAIVTVFQILTOEDNNKLYLNGM-----ASTSSAALYFI 946
DB 630 F-NFNDG--TPSANFDFPAAIMTVFQILGEDMNEVMYNGISOGGVSSGMSAIYFI 685
QY 947 ALMTGNYVFLVLAIVLEGF-QAEELGK-----REDASGLSCITQLPVNSOGGDATKSE 1001
DB 686 VLTLLGNTLLNVLVAIVDLVLANAOELTKDOEEFEAFNOKHAL-----OKAKEVSPM 739
QY 1002 SEPDYFSPVDGDDGRKRLAL-----VALGHA 1031
DB 740 SAPNM--PSIEDRRRRHHMSMPERSSHLERRRRHMSWEDRTSOLRRHMQSSQEA 797
QY 1032 LKSLPLPLLIHTAATPV-----SLPKSSSTGVALGSGSRRTSSGSAEBGAA 1081
DB 798 LNKEPAPMNLPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLNPLN 857
QY 1082 HHEKSPSPASRSPHSPPSAS-----SW-----TSRR 1109
DB 858 KQDIGGLSALDNORSPLSLGKREPPMLPRSCHGNCODP10QOAGG3ETVYTFEDRARHRQ 917

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QY 1110 SSRNLSGAPSLKRRSPGERSLLSGEQSODEEESSEDRASPGSDHNRHSLERE 1169  
 DB 918 SORRHRHVRTEGKDSASASR--RSASQERSLDEGVSEBEKHEPHSHRSRSEPTIHE 976  
 QY 1170 AKSSFDL--PTLOVP---GL-----HRTASGRSSASPHODCNKASGR 1209  
 DB 977 ERTODLRTNLSMVPKSGSLGVALDEAETPLVDPQPLEYGVKDAALTEQAESSSOAL 1036  
 QY 1210 L-----ARTLRD-----DPQD-----GDDN 1227  
 DB 1037 LGDVLVDGRIISQSEPDLSMTANMDKATTESTSVTAIPDVPDLVDSTVAINSKTDG 1096  
 QY 1228 DEGNLSKE--RIQAMVNSRLPACCREDSMA-----YIFPQOSFRLCHRIITHK 1278  
 DB 1097 EASPLKEATKEEVEEVEKKKKKEKRETKAMVPHSSMLETSTNPIRACHITVNLK 1156  
 QY 1279 MEDHVLVFIIFNCITIAMERPKIDPHSAERIFLTLSNIFTAVELAMTVKVALGWC 1338  
 DB 1157 YEMCILVIAASSTALAEDEVLTNSENKYL--LAFDYVFTGVTFEMVIMKIDQGLIL 1215  
 QY 1339 GBOAYLRSSNVLDGLLVLSVIDI--LVSMSVDSCTKILGMLRVRLTLRLPLRVISRA 1397  
 DB 1216 QGGSYFRDLMTILDEFVYVYGALVAFALANALGTNKGROIKTIKSLRVLRVLRPLKTIKRL 1275  
 QY 1398 QGLKLVETLMSLRPIGNIVVICAFFIIEGLGVOLFKEGFEVC--QGEDTRN----- 1451  
 DB 1276 PKLKAIVDCVATSLKVNFFILVYKLFEMIFAVINOLFKGFEYCTDSKDETECIGN 1335  
 QY 1451 -ITNKSDCAEASRY--WVRKRYFNDLIGALMSLFVLASKDGWIMYDGLDAVGDQOPT 1508  
 DB 1336 YDHEKNKMEVGRKREKREHEFHNDLIMALLFTFVSTGEQWPOYLQHSVDEDRGPS 1395  
 QY 1509 MNHNPMLLYFISFLIYAFVPLNMGVGVNENHFKRHOHEEERAREERRLRLKX 1568  
 DB 1396 RSNRMEMSLFYVYVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFFVFF 1444  
 QY 1569 RRLMLDDVIASGSSASASEACRPY--YSDYSR--FRLLVHHLCTSHYLDLFTTGYIG 1624  
 DB 1445 NEACIDFAISA-----KPLTYKMQNRRHTFQRYWHVFWVSSEFYTIMAMIA 1492  
 QY 1625 LNVYVNAMEHYQOQILDEAKICNTIYVIVFESVEFKLVAFGRRRFODMNOLDLAI 1684  
 DB 1493 LNTVYLMKXYTAPCTEYELAKLNTAFMTAFVSELCVLIYAFGLNTRYRDWNJEDFT 1552  
 QY 1685 YLLSINGITLEEIVNASLPINPTIIRIMRVLIARVLKLVKAVGMRLDFTVQALPO 1744  
 DB 1553 VISITETILTDSKLVNTSGFNSTFKLTRA--ARLILKROGYITRILMTFVQSFR 1609  
 QY 1745 VGNLGLFLLFFIFALGVELFGDECD--ETHPCBGLGRHATFRNFGNAFTLFRVSTG 1803  
 DB 1610 LPYVCLLIAMLFITAIIGVQVGNKIDBESH--INRHNFRSFFGSLMLLFRSATG 1665  
 QY 1804 DNNNGIMKDTL--RDCDQESTC-----YNTVSPITYFVSFVLTAQVLYANVIANL 1852  
 DB 1666 EAAQOEIMLSCLGERGCEPTTAPSGONESERCGTDLAIVYSEIFGCSFLMNLNEAVAI 1725  
 QY 1853 MKHLEESNKEAK-----EEALEAELE-----LEMKTL--SPOPHSPLG-- 1890  
 DB 1726 MDNFEYITROSSILGPHHDEFPYVAWEYRAACGRHTHEMELTMSPLGIG 1781  
 QY 1890 ---SPLMGVGVNSP-----DSPKPAPTTAHIGAASG-----SLEHP 1928  
 DB 1782 KRCOSKVAKYRLVLMNPVADMTVHTSTIMALLIRTALDIKIAKGADROOLDSELOKE 1841  
 QY 1929 TMV--PHPEE-----VPVYLGDLTLVRSKSVSRHSPLPNDSYMCRNSTARSJGHG 1980  
 DB 1842 TLAIAPHLISOKMDLIVMKRASD--LTVGKIYAA--MMIMDYKOSKVKQKQOL-- 1894  
 QY 1981 WGLPKAOSGSLSVSOPADTSCILQPKDY-----HYLQPHGAPITGALPKLPPG 2033  
 DB 1994 ---EOKNAPMQRMEPS-----SLPQELIANAKALPLQOD---PVSGLSGRSGYTS 1940  
 QY 2034 RSLAQRPLRQAAIRTDSDLVQGLSREDLLEVSQSPCL-----TRSSFW--- 2083

DB 1941 MSPLSQELIFQACN--DPADGQFQEQSLY--VTDPSSMRRSFSTRIDRNSMSWLE 1996  
 QY 2083 ---GGSSIOVQORSIQS--KYSKHLRLPAPCGGLEPMSAKDPEPRSSLELDTLSW 2135  
 DB 1937 FSWERSENITYRSRRSYSHSLRLSAH--RL-----NDSGHSKSTHRS- 2039  
 QY 2136 ISGDLPLSSQEEP--LSPDLKCYSVETGSCRRRPGSMLEORRHSTAVSCLDGSGOPR 2193  
 DB 2039 -GGERGRSKERKHLSP--DYSCNSEE--RQIQAWESEPERQS----- 2080  
 QY 2194 LCPSPSLGQPLGPGSGRPPKRLSPSISID-----PPESQGSPPCSPGVCLR 2243  
 DB 2080 --RSPSEGRSQPPNRCGTSLSESSISIDSTPRRSRRQLPVPKPRLLSYSSLMR 2137  
 QY 2244 RRPAPDSKDPVY--SPLDSTASPSPKKDTLSLGSLSDDPDMOPVPLTPLPHLSPP 2300  
 DB 2138 HTGGLSPDPGSGGSPPL---ASQALBSNSACLTSSNSLHPQOGQHPSPQHYISEP 2191  
 RESULT 10  
 CCAE\_HUMAN STANDARD; PRT: 2312 AA.  
 ID CCAE\_HUMAN  
 AC Q15878; Q14581; Q14580;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL, ALPHA-1E SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM CHANNEL (1)) (BIT).  
 GN CACNA1E OR CACNL1A6 OR CACNB6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN.  
 RX MEDLINE: 95236033.  
 RA SCHNEIDER T., WEI X., OLCESE R., COSTANTIN J.L., NEELY A., PALADE P., PEREZ-REYES E., QIN N., ZHOU J., CRAWFORD G.D., SMITH R.G., APPEL S.H., STEFANI E., BIRNBAUMER M.;  
 RT "Molecular analysis and functional expression of the human type E neuronal Ca2+ channel alpha 1 subunit".  
 RL J. Biol. Chem. 269:22347-22357(1994).  
 RL J. Biol. Chem. 269:22347-22357(1994).  
 CC -FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPIRIDINES (DHP). OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA), CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.  
 CC -SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: ALPHA-1E-1 AND ALPHA-1E-3  
 CC (SHOWN HERE): ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURAL TISSUES AND IN KIDNEY.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L27745; AAA72125.1; -  
 CC DR EMBL: L29384; AAA59204.1; -  
 CC DR EMBL: L29385; AAA59205.1; -  
 CC DR MTM: 601013; -  
 CC PRAM: PF00520; Ion\_trans; 4.  
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 CC KM Calcium channel; Glycoprotein; Repeat; Multigene family;  
 CC KM Calcium-binding; Phosphorylation; Alternative splicing.  
 CC FT REPEAT 76 354  
 CC FT REPEAT 462 706  
 CC FT REPEAT 1139 1425  
 CC FT REPEAT 1462 1725  
 CC FT DOMAIN 1 89  
 CC FT TRANSMEM 90 108  
 CC FT DOMAIN 109 127  
 CC FT TRANSMEM 128 146  
 CC FT DOMAIN 147 158  
 CC FT TRANSMEM 159 173  
 CC FT DOMAIN 174 185  
 CC FT TRANSMEM 186 205  
 CC FT DOMAIN 206 223  
 CC FT TRANSMEM 224 244  
 CC FT DOMAIN 245 326  
 CC FT TRANSMEM 327 350  
 CC FT DOMAIN 351 476  
 CC FT TRANSMEM 477 496  
 CC FT DOMAIN 497 509  
 CC FT TRANSMEM 510 529  
 CC FT DOMAIN 530 538  
 CC FT TRANSMEM 539 557  
 CC FT DOMAIN 558 567  
 CC FT TRANSMEM 568 586  
 CC FT DOMAIN 587 605  
 CC FT TRANSMEM 606 625  
 CC FT DOMAIN 626 678  
 CC FT TRANSMEM 679 703  
 CC FT DOMAIN 704 1147  
 CC FT TRANSMEM 1148 1164  
 CC FT DOMAIN 1165 1188  
 CC FT TRANSMEM 1189 1208  
 CC FT DOMAIN 1209 1216  
 CC FT TRANSMEM 1217 1239  
 CC FT DOMAIN 1240 1253  
 CC FT TRANSMEM 1254 1271  
 CC FT DOMAIN 1272 1290  
 CC FT TRANSMEM 1291 1310  
 CC FT DOMAIN 1311 1397  
 CC FT TRANSMEM 1398 1421  
 CC FT DOMAIN 1422 1478  
 CC FT TRANSMEM 1479 1497  
 CC FT DOMAIN 1498 1512  
 CC FT TRANSMEM 1513 1532  
 CC FT DOMAIN 1533 1540

FT TRANSMEM 1541 1559 S3 OF REPEAT IV.  
 FT DOMAIN 1560 1570 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1571 1589 S4 OF REPEAT IV.  
 FT DOMAIN 1590 1608 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1609 1628 S5 OF REPEAT IV.  
 FT DOMAIN 1629 1697 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1698 1723 S6 OF REPEAT IV.  
 FT DOMAIN 1724 2312 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 2312 2312 POLY-ARG.  
 FT DOMAIN 716 721 POLY-GLU.  
 FT TRANSMEM 721 731 POLY-ARG.  
 FT DOMAIN 731 753 POLY-ARG.  
 FT TRANSMEM 753 772 POLY-VAL.  
 FT DOMAIN 1227 1230 POLY-ARG.  
 FT TRANSMEM 1230 1287 POLY-ARG.  
 FT DOMAIN 2283 2287 POLY-ARG.  
 FT TRANSMEM 374 391 BINDING TO THE BETA SUBUNIT (BY  
 FT SITE 309 309 SIMILARITY).  
 FT SITE 557 657 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 FT SITE 1371 1371 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 FT SITE 1662 1662 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 FT SITE 1662 1662 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 FT CA\_BIND 426 438 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RES 1733 1733 BY SIMILARITY.  
 FT CA\_BIND 1751 1762 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 FT CARBOHYD 254 254 BY SIMILARITY.  
 FT CARBOHYD 1565 1565 POTENTIAL.  
 FT CARBOHYD 1570 1570 POTENTIAL.  
 FT VARSPPLIC 748 766 MISSING (IN ISOFORM ALPHA-1E-1).  
 FT CONFLICT 648 648 I -> M (IN REF. 2).  
 FT CONFLICT 836 837 WP -> LAL (IN REF. 2).  
 FT CONFLICT 1854 1954 T -> A (IN REF. 2).  
 FT CONFLICT 1954 2008 MISSING (IN REF. 2).  
 FT CONFLICT 2076 2076 R -> P (IN REF. 2).  
 FT CONFLICT 2083 2083 G -> R (IN REF. 2).  
 FT CONFLICT 2205 2205 C -> W (IN REF. 2).  
 FT CONFLICT 2218 2218 S -> V (IN REF. 2).  
 FT CONFLICT 2244 2244 G -> R (IN REF. 2).  
 FT CONFLICT 2244 2244 G -> V (IN REF. 2).  
 FT SEQUENCE 2312 AA; 261727 MW; C04D476D CRC32;

Query Match 13.4% Score 1669.5; DB 1; Length 2312;  
 Best Local Similarity 23.6%; Pred. No. 4.3e-77;  
 Matches 616; Conservative 411; Mismatches 849; Indels 737; Gaps 91;

QY 41 PGADSEA-----EGLPYALA-----PV-----VEFY 63  
 DB 12 PGSGDGDSDQSRNQGIPVPASGQAAYKQTKQKARTMALYNPIPVQRCFTVNSLFT 71  
 QY 64 LSQSRPSPKCLRTVNCNPFERNVSMVLINCYTLGFR--PEEDIACDSQRCRIIAQFD 121  
 DB 72 FGEDNIVKRYKRLIDPPEPEYMIATIANCIYLALEQHLPEDDKTPMSRR--LEKTE 128  
 QY 122 DEIFAFAVENVAVMVLG--IFGKKCYLGDVNRDLDFEYIAGMLEVSLDLO--VSFSA 178  
 DB 129 PYFGICFCFEGAGITVALGFLFRKSGTLRNGWNVMDIVLSGLATAGTHTVADLRT 188  
 QY 179 VRTVRLVRLPAINRVDSMRILVTLDTLPMGLNVLLCFEFTFFGIYGVOLMAGLAR 238  
 DB 189 LRAVRVLPKLVGIGISLQIVLKSIMKAVPPLQIGLLFFAIFALIGLEFGSKLH 248  
 QY 239 NRCLPENSFLPLSVLDPEPYQTEDESEFICSQPRENMSRCSVPYLRGGGGGPPC 298  
 DB 249 RACPMNV-----SGLIEG-----DPPHC-----GVQC 273  
 QY 299 SLDEYIYSSNTQVWVWNYTNCSGAENPKGAINFNIGYAMIAFOYTLLEGWD 358  
 DB 274 PAGE-----CKW-----IGPDDGTLQDNLIFAVLIYFOCLTMEGWT 313  
 QY 359 IMYIVMDA-HSFNFYIFILLIIVGSEFMINCLVVIATQSEFTRQESQMLRQVRFL 417  
 DB 314 VLYNTDNLGATNWLWYFIPLIIIGSFFVLNLVLGLVISEFAKERRV-----ENRRAM 368



QY 418 SNASTLASFSEPGSCYEELKLYVILRKARLAQVSRAL-GVRAGLLSSPYARSGOEP 476  
Db 369 K-----LRRQOIERELNGYRAMIDAEVMALEEN 399  
QY 477 QPSGCTSRSHRLSVHHLVHHHHHHHNLGCTLVPRAPSPIDORDANGSRRLMFP 536  
Db 400 KNACTSALEVLRRAAT-----IKRSRTKMTDRSS----- 429  
QY 537 PSTTPSGGPRGAEVSHFYHADCHLEPYRCQAPPRCPSEAGRTVSGKVPYVHTS 596  
Db 429 ----- 429  
QY 597 PPPILLKDALVEVAPSPGPTLTLSNIPGPFSSMKLLETOSTGACHSSCKTSSPCSK 656  
Db 429 -----DEHCVDIS-----SVGTPLAR 444  
QY 657 ADSGACGSDSCPYCARFCAGEPESADHYMPDSDSEAYEFTQAOHSDLRDPHSRRQRS 716  
Db 445 ASIKSAKVDSVY-----FRHKE----- 463  
QY 717 LGPDAEPSSVLAFLRICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEOPELTNAL 776  
Db 463 -----RLKLSIRHWKSGQFYWIVLSLVALNTACVALVHNOQWMLTHL 508  
QY 777 EISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGYIVVISWELVGO-----QGGGL 831  
Db 509 YAAEFLFGLFLEMLSMYGMGPRLYPHSSFNCFEGVTGSIJEVWMAJFRPGTSFGI 568  
QY 832 SVLFRFRMRVLYKIVRPLALOROLVVMKTMNVATFCMLLFIFFISLIGHLGCCK 891  
Db 568 SVLRRLRLRIFKIKYVNASRLNVLSMSKSTISLFLFLFYVAFALGQMLRGR 628  
QY 892 FASERDQGLTPDRKNFDSILNAIVTFQILQEDMNKLYNGM-----ASTSSMALYFI 946  
Db 629 F-NFNDG--FPSANFDFPAAITIVFOILGEDMNEVYMGISOGGSGMWSAIYFI 684  
QY 947 ALMTGCVYVFLVAILVEGF-QAEIGK--REDASGGLSCIQLVYNSOGGDATKSE 1001  
Db 685 VLTLEGTNTLLNVLALAVLANAOELTKDOEEBAFNOKHAL-----QKAKEVSPM 738  
QY 1002 SEPDEFSVDDGDRKKRLAL-----VALGHE--AEIKSL----- 1037  
Db 739 SAPNM--PSIEDRRRRHHMSWEPSSHLRRRRHHMSWEOQTSQLRHHMOSSQEA 796  
QY 1037 -----LPLIHTAATPMSL-----PKSSSTGVEALGSSSKRTSSGSAEP 1078  
Db 797 LNREAPTNPLNPLNPLSLNPLNAPSLYKRPRAIEGWPLALEKFEERISNGSLK 856  
QY 1079 G-----AAHHEKSPPSAASSPHSPMSA-----ASSWTS 1107  
Db 857 GGGGDRSSALDQRTPLSGOREPMLARPCGNCDDPTQOEAEGGEAVVTFEDRARHQS 916  
QY 1108 RRSRNSLGR-----APSLKRRSPGERSL--LSGEOESOD-----EESSEEDR 1152  
Db 917 QRSRRRVRTEGKESSASRSRSASQERSLDEAMPTEGKDELHNGHGAKEPTIOER 976  
QY 1153 ASBAGDHHRRGSLREAKSSF-----DLPDTLOVPLHTAAGRSASASHOCCNKS 1205  
Db 977 A-----ODLRTNSLWVSRSGSLAGLDEADTPLVLPHELE--VGKHAVLLEOPEBSS 1029  
QY 1206 ASGRLAR-----TLRTD-----POLDG----- 1224  
Db 1030 EQALLGNVOLDMGRIVISOEPDLSCITANTDKATTESTSVTAIDVPLVDVSTVHSHN 1089  
QY 1224 -----DDNDEGNLSKGERIOAWVRSLPACCRERDSKATIFPPQSRF 1267  
Db 1090 KTDGEASPLKEAERREDEEVEKKQKKEKRETC-KAMPHS-----SMFISTPIPI 1141  
QY 1268 RLCHHIIHKMDHVVVYIIFINCTITAMERPKIDPHAEKIFLITLSYIFTAVFLAM 1327  
Db 1142 RRACHYIVNLFEMCILLVIAASTALAEDEVLTNSERNKV-LKYPDYVETGVTFTEM 1200

QY 1328 TVKYVALGMCGEQAYLRSSNNVLDGLVILSVTDI-LVSWSDSGTIKGLMLRFLRL 1386  
Db 1201 YIKMIDQGLILOSDFEYDLMNILDFFVVVVGALVAPLANLGNKRDKITIKSLRVL 1260  
QY 1387 TLRLPVRISRAOGLKLVYETLMSLKPIGNIVICAFIIFIGILVOLKFKGFVNC--Q 1444  
Db 1261 VLRPLKTIKRLPKLKAVDCVTSLSKNVFNLIYKLFEMFIFAVIAVOLKFKGFYCTDS 1320  
QY 1445 GEDTRN-----TINKSCAASR--WVRKYNNDNIGQALMSIFVLASDGMVDIWDG 1497  
Db 1321 SKDTEKECIGNVDEKEMKMEYKGMKRHEFYDNIIWALLTFTVSTGEMPOVLQHS 1380  
QY 1498 IDAVGDOOPINNPNMLLYFISFLIVAFVNMFEVGVVENEHROHOEEEARRR 1557  
Db 1381 VVTEEDNPSNMSNMEISIFYVYVFPFFYNIPALIIIF-----QGGQKMM 1433  
QY 1558 EKRRLRREKRRNMLDVIASGSSASASEAOCKP--YSDYSR--FRLVHHLTSH 1613  
Db 1434 EECSL-----EKNERACIDFAISA-----KPLTRYMPONRHTFOYRVHFPVSP 1477  
QY 1614 YIDLFTGYIGLVNTYAMMEHQOQPOLIDEALKICNTLFTVIFEVESYFKLVAGFRRF 1673  
Db 1478 SPEYTIMAIALNTVLMKKYISAPCTELALKIYLAFTVFSLECYLKIAGFLNIF 1537  
QY 1674 ODRMOLDIAYILSINGITLIEIEVNASLPINPTIIRIMVRLIARYLKLKNAVGMRA 1733  
Db 1538 RDTWNIFFPITYIGSITEILLDSKLVNTSGFMSFLKLFRA--ARLIKLRGGYIRI 1594  
QY 1734 LDDTYMQLPQVNGUGLFLMFLFIFFAALGYELGDECD--ETHPCEBGLHAFNRNGM 1792  
Db 1595 LMTFVOSFKALPYCLLILAMLEFYAIIIGMVFENIKLDESH--INHNHNRSPFG 1650  
QY 1793 APLTFRSTGNNWNGIMKDTL--RDCDOESTC-----YNTVISPIYFVFLTAQ 1841  
Db 1651 SMLLFRSTAGMOMIOLMSICEKGCEPDTTAPSGOMENRCIGDLAYVVFSTIFPCS 1720  
QY 1842 FVLVNVVIAVLKHLSESKKAK-----EAELEALE-----LEMKTL- 1881  
Db 1711 FLMLNLFVAVINDFEYLRDSSILGPHHLDFFVYMAEYRAACGRITYTEMEMTLTM 1770  
QY 1881 SPQHPPLG-----SPFLMPGEBGVNSP-----DSPRGAHPHTAHGAASG-- 1923  
Db 1771 SP-----PILGKRCBQKVAVKRLVLMNPEVADMTVHTSTLMALIRALDIKAKGAD 1826  
QY 1923 -----FSLHPYVY--PHBE-----VVPPLGDLTVKSGVSRHSLPDSYMRNG 1969  
Db 1827 RQDLSELQKETALIMPHLSQKMDLVMPKASD-LVYGKITYA--MMINDYKQSKV 1882  
QY 1970 STARSIGHRGWLCPAOSGSLISVHSOPADTSCILQPKVY-----HYLDQHGAPT 2022  
Db 1883 KROQOL-----EEOKNAPMFORMEPS-----SLPOELIANAKALPYLOO--PV 1925  
QY 2023 WGAIPKLPREGSRPLAORBLRQALIRTDSLDVOGLSREDLSEVSGPCLTRSSSFM 2082  
Db 1926 SGLSGSGIFSMSPJSPQIFOLACM--DPTDDGQFOEQSLSEPEVSELKSQVPSNHGTY 1983  
QY 2083 GSGSIOVQOSGSIQSVKSHIRLPAPCPGLEPSMAKDPETRSF--ELDTLELWSIG 2138  
Db 1984 LPDQTOEHAGSGRASM-----PRLTVDPQVYVTPFSMRSPSTIRDKRSNSGSLLE 2035  
QY 2139 DLLPSSOEPLSRDLKCYSVETQSCRRRPGSLDQORRHIANSCUDSGOPRLCSP 2198  
Db 2036 FMSERSSENYKSR--RSHVSLRLSABRLNS-----DSGKSDTHNS- 2078  
QY 2199 SSLGQPLGGPGSRPKKLSPPSIS-----IDPESOGSRPPCSGVOLRRRA 2246  
Db 2078 --GGRERG--RSKERKHLSPVSCNSEKRTQADWSPERRQSRSP-SFG--RQGT 2128  
QY 2247 P-----ASDSKDPVSVSPSLDSTAASPPKKDTLSLSGLSDPTDMVPLTLP--HL 2297  
Db 2129 PNRGTSLSLESSIPVSD-----TSTPRRSRQLPVPKPKRLLSYSSLIRHAGSI 2181  
QY 2298 SPP--GADPSSASMAAFKSPFA--ASSHEAPH 2226



Db 2182 SPPADSGEGLTSCALENNACLTSSNSPH 2214

RESULT 11  
CCAB-RABIT STANDARD; PRT; 2339 AA.  
AC 005152;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL II) (BII).  
GN CACNA1B OR CACNA1AS OR CACNS.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA MEDLINE; 93236885.  
RA FUJITA Y., MYNLEIFF M., DIRKSEN R.T., KIM M.-S., NIDOME T., NAKAI J., FRIEDRICH T., IWABE N., MIYATA T., FURUTACHI T., FURUTADA D., MIKOSHIBA K., MORI Y., BEAM K.G.;  
RA "Primary structure and functional expression of the omega-conotoxin-sensitive N-type calcium channel from rabbit brain."  
RT Neuron 10:585-598(1993).  
RL -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-IIA (OMEGA-AGA-IIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.  
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.  
CC -1- HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.  
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAK, PKC AND CGK (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.  
CC -----  
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CC -----  
CC EMBL: D14157; BAA03202.1; -  
DR PFAM: PF00520; IAO3-trans. 4;  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family;  
KW Calcium-binding; Phosphorylation; ATP-binding.

|    |          |          |            |   |
|----|----------|----------|------------|---|
| FT | REPEAT   | 82       | 359        | I.  |
| FT | REPEAT   | 469      | 713        | II.   |
| FT | REPEAT   | 1142     | 1424       | III.  |
| FT | REPEAT   | 1461     | 1714       | IV.   |
| FT | DOMAIN   | 1        | 95         | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 96       | 114        | S1 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 115      | 132        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 133      | 152        | S2 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 153      | 163        | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 164      | 183        | S3 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 184      | 187        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 188      | 206        | S4 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 207      | 225        | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 226      | 245        | S5 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 246      | 331        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 332      | 356        | S6 OF REPEAT I (POTENTIAL).                               |
| FT | DOMAIN   | 357      | 483        | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 484      | 502        | S1 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 503      | 517        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 518      | 537        | S2 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 538      | 545        | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 546      | 563        | S3 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 564      | 574        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 575      | 593        | S4 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 594      | 612        | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 613      | 632        | S5 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 633      | 685        | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 686      | 710        | S6 OF REPEAT II (POTENTIAL).                              |
| FT | DOMAIN   | 711      | 1156       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1157     | 1174       | S1 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1175     | 1190       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1191     | 1210       | S2 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1211     | 1222       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1223     | 1241       | S3 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1242     | 1251       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1252     | 1270       | S4 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1271     | 1289       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1290     | 1309       | S5 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1310     | 1396       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1397     | 1421       | S6 OF REPEAT III (POTENTIAL).                             |
| FT | DOMAIN   | 1422     | 1476       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1477     | 1495       | S1 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1496     | 1510       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1511     | 1530       | S2 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1531     | 1538       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1539     | 1557       | S3 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1558     | 1566       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1567     | 1585       | S4 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1586     | 1604       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 1605     | 1624       | S5 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1625     | 1686       | EXTRACELLULAR (POTENTIAL).                                |
| FT | TRANSMEM | 1687     | 1711       | S6 OF REPEAT IV (POTENTIAL).                              |
| FT | DOMAIN   | 1712     | 2339       | CYTOPLASMIC (POTENTIAL).                                  |
| FT | TRANSMEM | 2051     | 2055       | POLY-HIS.   |
| FT | DOMAIN   | 2119     | 2123       | POLY-SER.   |
| FT | TRANSMEM | 2319     | 2324       | POLY-GLY.   |
| FT | DOMAIN   | 379      | 396        | BINDING TO THE BETA SUBUNIT (BY SIMILARITY).              |
| FT | NP BIND  | 452      | 459        | ATP (POTENTIAL).  |
| FT | SITE     | 314      | 314        | CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). |
| FT | SITE     | 663      | 663        | CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). |
| FT | SITE     | 1370     | 1370       | CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). |
| FT | SITE     | 1658     | 1658       | CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). |
| FT | MOD_RES  | 1722     | 1722       | PHOSPHORYLATION (BY CAPK) (POTENTIAL).                    |
| FT | CA_BIND  | 1740     | 1751       | BY SIMILARITY.  |
| FT | CARBOHYD | 256      | 256        | POTENTIAL.  |
| FT | CARBOHYD | 1566     | 1566       | POTENTIAL.  |
| FT | CARBOHYD | 1678     | 1678       | POTENTIAL.  |
| SO | SEQUENCE | 2339 AA; | 261178 MW; | DC58C56D CRC32;   |



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QY 1875 -----LEW-KTLPSPHSPG-----SPLPWGVGVNSPDSPKPGAPHTAH 1917
DQ 1743 AGRISYSDMEMLKHMSP-----PLGJGKKCPARAVAKRLVRNMPISSEMTHTFSTL 1798
QY 1918 GA-----AGFSLEHTWPHREVEV-----PLGPDLLTVRKS 1952
DQ 1799 MALIRTALDIKLAPAGTQKQOCDAELREKISCWANLPQKTLDLLVPHKDEMTGVKY 1858
QY 1953 VSRTHSLPNDSCYRNGSTARSISGHWGLPKAOSGSLSVHSQAPDTSIILPVDH 2012
DQ 1859 AA-----LMIFDY--KONKTSDDQOQABGL--SOLGPNLSFH----- 1895
QY 2013 YLLOPHGAPWGAIPKLEPP--GRSPLAOR--PLRQAAIRTSLDVQ-----GLGSR 2061
DQ 1895 -----PLKATLEQTOPALRGARAFLRQKSASLSNGAVQOESGIESVWGQRT 1946
QY 2062 EDLSEVSGPCPLTRSSSF--GSSIQYOQNS-----GIOS--KVSK 2101
DQ 1947 QDVJCEA--RAPLERGSHAEIPVGQPTLAVDQOMQNTLGSFPDABOPGLESGRAAS 2003
QY 2102 HIRLPA--PCPGLEP-----SMAKDP----- 2122
DQ 2004 MPRLAETQAPADSPKRSISTLAPRPHARLSTALDRPAPSOAPHHHHCHRRDR 2063
QY 2122 -----EIRSSLELDELTSWIS--GDLLPSSQEPPLSPDKKCYVETQSCRRRPGSMD 2174
DQ 2064 KQSLKLEGPSTLADTDAPSTVGPLTGTGPGCRERERQERQSGRRQPSSSS 2123
QY 2175 EQRHSHAVSCIDSGSPRLCPSPS-----SLGGQL----- 2207
DQ 2124 EKHF--YSCDRGGRPEPPQPKSLSSHTSPTAGOEPHPHOGSGSVHGLSTGA 2180
QY 2207 --GGPGSR--PKKULSP-PSISIDPPESQ-----GSRPPCSPG-----VCLRR 2244
DQ 2181 STPGRGRHQLPQPLTPRPSVTYKTANSPPVHAGAPSGLPAPSPGLSLGSLSENHALDQ 2240
QY 2245 RAPS-----DSKDPVSPPSPLDS-----TAASPCKKDTLS--LSGL 2279
DQ 2241 RDLSPRLAPGSRIGSDPYLQRLDSEAPARALPDAPEFETAANSVGRSRTSYVSSL 2300
QY 2280 SSDPTMDPVLPTLPH 2295
DQ 2301 TSQP-----PPLRRVFN 2312

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CC CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC CC BY NICKEL, AND PARTIALLY BY OMEGA-AAGATOXIN- IIA (OMEGA-AGA-IIIA).
CC CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
CC CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
CC CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
CC CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
CC CC IMPORTANT FOR INFORMATION PROCESSING.
CC CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -I- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
CC CC INSULINOMA.
CC CC -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC CC -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC CC FAMILY.
CC CC -----
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CC CC -----
DR DR AMBL, L15453; AAA40855.1; -
DR DR PFM; PF00520; Ion_trans; 4.
KW KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW KW Calcium-binding; Phosphorylation.
FT FT 27 305 1.
FT FT REPEAT 413 657 II.
FT FT REPEAT 1092 1378 III.
FT FT REPEAT 1415 1678 IV.
FT FT DOMAIN 1 40
FT FT TRANSSEM 41 59
FT FT DOMAIN 60 78
FT FT TRANSSEM 79 97
FT FT DOMAIN 98 109
FT FT TRANSSEM 110 124
FT FT DOMAIN 125 136
FT FT TRANSSEM 137 156
FT FT DOMAIN 157 174
FT FT TRANSSEM 175 195
FT FT DOMAIN 196 277
FT FT TRANSSEM 278 301
FT FT DOMAIN 302 427
FT FT TRANSSEM 428 447
FT FT DOMAIN 448 480
FT FT TRANSSEM 481 489
FT FT DOMAIN 490 508
FT FT TRANSSEM 509 518
FT FT DOMAIN 519 537
FT FT TRANSSEM 538 556
FT FT DOMAIN 557 576
FT FT TRANSSEM 577 629
FT FT DOMAIN 630 654
FT FT TRANSSEM 655 1100
FT FT DOMAIN 1101 1117
FT FT TRANSSEM 1118 1141
FT FT DOMAIN 1142 1161
FT FT TRANSSEM 1162 1166
FT FT DOMAIN 1167 1170
FT FT TRANSSEM 1170 1192

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FT DOMAIN 1193 1206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1207 1224 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1225 1243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1244 1263 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1264 1350 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1351 1374 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1375 1431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1432 1450 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1451 1467 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1468 1485 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1486 1493 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1494 1512 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1513 1523 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1524 1542 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1543 1561 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1562 1581 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1582 1650 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1651 1676 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1677 2232 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1677 2232 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 667 672 POLY-ARG.
FT TRANSMEM 699 704 POLY-ARG.
FT DOMAIN 718 723 POLY-ARG.
FT TRANSMEM 1058 1064 POLY-GLU.
FT DOMAIN 1180 1183 POLY-GLU.
FT TRANSMEM 2193 2196 POLY-ARG.
FT DOMAIN 325 342 BINDING TO THE BETA SUBUNIT (BY
SIMILARITY).
FT SITE 260 260 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 608 608 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 1324 1324 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 1615 1615 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT CA_BIND 377 389 BY SIMILARITY.
FT MOD_RES 1686 1686 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CA_BIND 1704 1715 BY SIMILARITY.
FT CARBOHYD 205 205 POTENTIAL.
FT CARBOHYD 1518 1518 POTENTIAL.
FT CARBOHYD 1523 1523 POTENTIAL.
FT CARBOHYD 1641 1641 POTENTIAL.
FT SEQUENCE 2222 AA; 252114 MW; 9CCABB68 CRC32;
```

Query Match 13.2%; Score 1649.5; DB 1; Length 2222;  
Best Local Similarity 24.0%; Pred. No. 4,3e-76;  
Matches 607; Conservative 393; Mismatches 835; Indels 689; Gaps 85;

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QY 62 FYLSODSRPSCMLRTVCNPMFEERVSMLVILLNCVTILGMR--PCEDLACDSQRCRILOA 119
DB 21 FIFGEINIRKAKYAKKIDMPPEFYMLATIANCIYLAEOHLPDDDKTPMR--LEK 77
QY 120 FDDIFAFRAVENVMKVALG-IFGKKCYLGDTWNRIDFFIYIAGMLEYSLDLO--VSF 176
DB 78 TBYFIFGICFEAGIKIVAGLGFIFHGSLYLRNGMNMDFIVLSGLIATAGHTHTHDL 137
QY 177 SAVRTAVRLRLAIRNVRSMRTVLLDLPMLGNVLLLOCFEYFIFGIYQVLMAGL 236
DB 138 RILRAVRRLPLKLVGIPSLQIVLSIMKAMPILQIGLLFFALIFALIIIGLEYISGK 197
QY 237 LRNRCELPENFSLPLVDLEPYQOTENEDSPFICSPRENGMRCRSVPTLRGEGGAP 296
DB 198 LHRACCMNN-----SGILEGF-----DPRHC-----GVQ 222
QY 297 PCGLDIETYNSSNTTCVANNQIYTCNSAGEHNPFGAINDFNIGYAMAIQVITLBSM 356
DB 223 GCPAGE-----CKDW-----IGPNDGIOTFDNIIFAVLTVFOCITMEGW 262
QY 357 VDIIMYVMDA-HSFNYFIIFILLIIVGSPFMILCLVIAIOTSETKORESQLMREOVR 415
DB 263 TTVLYNTNDALGATWMLYFIPLIIGSFVVLNVLGVISGEAFKEREY-----ENRRA 317
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QY 416 FLNASTLASFSPGSCYEELIKLVYLILKRAARLAQVSRAI-GVRAGLLSSPVARSQ 474
DB 318 FVK-----LRQOQIEELINGYRWIDKAEVMAIE 348
QY 475 EPOPSGSCSTRHRLSLVHHVHHHHHHHHYHLGNGTLVRPASDEIODRANGSRRLML 534
DB 349 ENKNSGTSALVLRAT-----IKRSRTREATRDS----- 380
QY 535 PPSPITPFGGPPRAEASHVSHYHADCHLEPVRQAPPPRCPSEASGTVSGKYPTVH 594
DB 380 ----- 380
QY 595 TSPPEILDKALVEAPSPPTLTSFNIPGPPSMKLELTOSTGACHSCKISSPC 654
DB 380 -----DENICVIDS-----SVGPPL 393
QY 655 SKADSGACGPDSCPYCARTGAGEPPESADHVMPDSEAVYEFTQDAQSDLRDPSRRQ 714
DB 394 ARASIKSTVDGASY-----FRKE----- 414
QY 715 RSLGPPAESSVLAFWRLICDIFRKIVDSKYRGIMIALVNTLSMGIEYHEQPEELTN 774
DB 414 -----RLRISIRHAKVSOVPTWYLVLSVALNTACVALVHHNDPOMLTH 457
QY 775 ALEISNIVFTSLFALEMLKLIVYGPFGYIKNPYNIFDGVIVISWEIVQO-----OGG 829
DB 458 LUYAFAFLGLGLELLEMSLKMVGMPRLTFHSSFCFEGVYGSIFEVVAIFRGTSE 517
QY 830 GUSVLTFRMLRYKLVRRLPALQOLVYLMKTMNVATFCMLMLFIFISILGMHLFG 889
DB 518 GISVLAALRLRLRFTKTKWASIRLVLSMSSKISLFLFLFVLRVLAQMOLFG 577
QY 890 CKFASREDGDTLPDRKNPDSLLMAIVTVOILOEDMKNVLYNGM-----ASTSSMALY 944
DB 578 GRF-NENDG---TPSANFTFPRAIMTYFOILTEGDMNVGMNGIRSGOVSSGMSAIY 633
QY 945 FIALMFGNVYLFNLLVAIVLGEF-QAEIIGK---REDASQSLCIQLPVNSQGGDATK 999
DB 634 FIVLTLEGNVTLNVLVAIVNLAQELTKDEDEEFAFNOKHAL-----QRAKVS 687
QY 1000 SESEPFESVSDGDDRRKKRLAL-----VALGEH 1029
DB 688 PMSAPNM--PSIERDRRRRHHSWMEPRSSHRLRERRRHHSWMDQRTSOLRRHQMSQ 745
QY 1030 AELRKSILPLIHTATPM-----SLPKSSSTGCVGALSG-----SRRTSSSG 1074
DB 746 EALNKEAPRPNLNLNPLNLPLNANPSLYRRRPTEGALIGLEKCEERISRG 805
QY 1075 SAERG-----AAHHEKSPPS--ARSSPHSPMSA-----ASS 1104
DB 806 SLKGDIGLTSVLDNCRSPSLGKREPMLPRCHGNCDPTOETGGGETVVFEDRAH 865
QY 1105 WTSRRSRNLSGRAPSLKRRSPSGERRSLLSGGGODESESSSEEDRSPAGSDRHNG 1164
DB 866 ROSORRRHRNRVTEGKESASASR--SASQESLDEGYSIDCKEKEHQSSHRSE 921
QY 1165 SLEREAKSSFDL--PDLQVP--GL-----HRTASGRSSASEHODCNK 1204
DB 922 PTIHEERTQDLRTNSLWMPRGSLVGLADEATPLVQPOPELEVGKDAALTEQAEGS 981
QY 1205 SASGRLA-----RLKIDDPOL----- 1222
DB 982 SEQALLADVOLDVGRGISOSEPDLSCMTNMDKATTESTSVTAIPVDPLVDSTVNIS 1041
QY 1222 ---DG-----DDNDGNTLSKGERIOAWRSRLPACCRDSDMSAYIFPPQSR 1266
DB 1042 NKIDGESPLKEKETKEEVEVKKKQKREKTEG-KAWVPHS-----SMFISTTNP 1093
QY 1267 FRLCHRIITHKMDHVVVLIIFLNCITIAMERPKIDPASHERIFLLTNSYFTAVFLAE 1326
DB 1094 IRKACHYIVMLRFEMOILIVIAASSIALAEDPVLNBSRNKV-LRYPDYVFTGVTFPE 1152
QY 1327 MTVAIVVALGCMFGEOAYILRSSNVLDGLVLIVIDI-LVSNVSDSGTILGLRLVRL 1385
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|    |      |   |      |
|----|------|---|------|
| Db | 1153 | NYTKMDGOLLJODGSPFRDLMLNIDPFVVVYVGVALFALNALMGTCMKGDITIKISLRYL  | 1212 |
| Qy | 1386 | FTLRLPLVYISRAQGLKLVETLWMSLKPIGNIVYICAFITIFGILGOLFEGKFFVC--    | 1444 |
| Db | 1213 | RYLRLPKITIKRLPKAKAVDFCVTSLKNVNNIILVKLFEFIFAVIAYOLFEGKFFCYCD   | 1272 |
| Qy | 1444 | OEDEFRN-----LYNKSDCAEASYSR-VWRHKYNFDLQAGALMSVLVASKQGWINDYD    | 1496 |
| Db | 1273 | SKDKTEKEBIGVYDHEKNKNEVAGREKMKHEFHIDNITALLTLTYSYTGGMQVLOH      | 1332 |
| Qy | 1497 | GIDAVGVQOPLMHNHPMLLYTISLLIYAEVLNKGVVVENFKRCROHEEAKR           | 1556 |
| Db | 1333 | SYDVTEEDRGSRSSRKMESIFYVYVYVVPFFEFVIFALLITTF-----QEGDGM        | 1385 |
| Qy | 1557 | REERLRLREKRRRLMDVDVIVAGSSASASAQCKPY--VSDYSR--FRLVNHCTS        | 1612 |
| Db | 1386 | MEECSL-----EKNERACIDPAISA-----KPLRTYPOKRTFYRVNHFVYS           | 1429 |
| Qy | 1613 | HYLDLFTVIGLVNVTWAMEHHYQOPLDEALKICNYITFYVFEVSFKLVAFGRFR        | 1672 |
| Db | 1430 | PSEFTIYAMALNTVYLMKYYAPWTYELAKYLNTIAFTWFSLECYLVANGFLNTY        | 1489 |
| Qy | 1673 | FODRNOQDLNIVLISMGITLIEVNABSLPNPTIKMYRLARARLYKLKMGAMR          | 1732 |
| Db | 1490 | FRDTNINIDFTVIGISTEITLIDSKLVNTSGFMSFFLKFRA--ARILKILRGYTYR      | 1546 |
| Qy | 1733 | ALDDTMOALPOVONLGLLEMLJFETFAALGVELFEDLSCD--ETHPCBGLGHAFGRFG    | 1791 |
| Db | 1547 | ILMTWFOQSFYALPYVCLLJAMLEFIYAIIGMVFPCNITLDESH--INRHNRFEF       | 1602 |
| Qy | 1792 | MAFLTFPVSQGDWNNIMDYL--KCDQESTC-----YNTYSPIFYVSEVTLA           | 1840 |
| Db | 1603 | GSMLTFESATGEAMQIMCISGKQCEPDDTAPSGNSESRCGTDLAYVFSFIFFC         | 1662 |
| Qy | 1841 | QFVLNVNVIYAMLHBEESKNEAK-----BEALEBALE-----LEKMTL              | 1880 |
| Db | 1663 | SFLMLNLFVANITMNFYLIIRDSSILGPHHIDFVYVMAEYRAACGRHNTTEMETLTL     | 1722 |
| Qy | 1881 | -SPQPHSLG-----SPFLMPEVEGVNSP-----DSBKPAPHHTAHGAASG--          | 1923 |
| Db | 1723 | MSP-----PLGIGKRCPSKVAYKRYLVLMNHPVAEDMTVHFTSTLMLITRDLIKANGA    | 1778 |
| Qy | 1923 | -----FSLHPRTWV--PHDEE-----VPVPLGDLTLVRKSGVSRKHSUPNOSYKRN      | 1968 |
| Db | 1779 | DROQLDELOKETIATIPRLISQMLDLVMPKASD-LTVGKIYVA--MMIMDYQOSK       | 1834 |
| Qy | 1969 | GSTRSLGHRGWLCPAOSGSILSVHSOPAD-TSCILDLPDVHYLLQHPAGATWGAIP      | 2027 |
| Db | 1835 | VKKROOUL-----EECKNAMFQRMPESSIPGEIISMAKALPYLOQD--FVSLGSG       | 1883 |
| Qy | 2028 | KLPPRGSPILAOPRLRQOALIRTDISLDVQGLSREDLSEVSGPCLP-----TRSS       | 2079 |
| Db | 1884 | RSGTFSMSPISPOEIRQLAOM--DPADDOQFOEQOSIV--YTPDSMRKRSFTYRDRSN    | 1939 |
| Qy | 2080 | SFW-----GSSSIOVQARSIGDS-FVSKHIRLPAAPCLSEPSMAKDEPPTRSLEL       | 2129 |
| Db | 1940 | SSWLEFSSMERSESNYTKSRBSYHSLSLNHH-RL-----NDSCHKS                | 1982 |
| Qy | 2130 | DTELSTWISGLLSSOEER--LSRPLKLCYIVETQSCRRRPGSWLDEORHSTAVSCLD     | 2187 |
| Db | 1983 | DTHRS--GGREGRSKRKHLISP-DVSCNDEE-----RGTOADESPERROS-----       | 2029 |
| Qy | 2188 | SGSOPRLCPSSLLGQPLAGPSPSRKRLTSPSITD-----PPESQOSRPPCS           | 2237 |
| Db | 2029 | -----RSPSGRQOTPRQCTGSLSSSTIPSTIDSTRPKSRQOLPVPKPKRLLS          | 2080 |
| Qy | 2238 | PQVCLRRRPAASQKDPV--SPLDSTAASPPKPKDTLSLGLSDPTDMVPLTPLPH        | 2296 |
| Db | 2081 | YSSLMRHTGIGISPPDGESEGSPL-----ASQALESNSACTRESSNLSLHPQGGHPSPQHY | 2136 |
| Qy | 2297 | LSPP  | 2300 |

Db 2137 ISEP 2140

RESULT 13  
C.S. LABIT

| ID | CCAS RABIT  | STANDARD; | PRT; 1873 AA. |
|----|---|-----------|---------------|
| AC | P07293;   |           |               |
| DT | 01-APR-1988 (Rel. 07, Created)  |           |               |
| DT | 01-APR-1988 (Rel. 07, Last sequence update)                             |           |               |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update)                           |           |               |
| DE | VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL                                |           |               |
| DE | CHANNEL, L TYPE. ALPHA-1 POLYPEPTIDE, ISOFORM 3, SKELETAL MUSCLE.       |           |               |
| GN | CACNA1L3 OR CACNA13 OR CACNA1   |           |               |
| OS | crystallagmus cuniculus (Rabbit).                                       |           |               |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;           |           |               |
| PN | Eutheria; Lagomorpha; Leporidae; Orcytolagus.                           |           |               |
| PC | [1]   |           |               |
| PC | SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.                               |           |               |
| PC | TISSUE-SKELETAL MUSCLE;   |           |               |
| RX | MEDLINE; 87258269.  |           |               |
| RA | TANABE T., TAKEISHIMA H., MIKAMI A., FLOCKERZI V., TAKAHASHI H.,        |           |               |
| RA | KANGAWA K., KOJIMA M., MATSUD H., HIROSE T., NODA S.;                   |           |               |
| RT | "Primary structure of the receptor for calcium channel blockers from    |           |               |
| RT | skeletal muscle."   |           |               |
| RL | Nature 328:313-318(1987).   |           |               |
| RL | [2]   |           |               |
| RP | SEQUENCE FROM N.A.,   |           |               |
| RC | TISSUE-SKELETAL MUSCLE;   |           |               |
| RX | MEDLINE; 88336904.  |           |               |
| RA | ELLIS S.B., WILLIAMS M.E., WAYS N.R., BRENNER R., SHARP A.H.,           |           |               |
| RA | LEUNG A.T., CAMPBELL K.P., MCKENNA E., KOCH W.J., HUI A., SCHWARTZ A.,  |           |               |
| RA | HARPOD M.M.;  |           |               |
| RT | "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2      |           |               |
| RT | subunits of a DHP-sensitive calcium channel."                           |           |               |
| RL | Nature 241:1661-1664(1988).   |           |               |
| RL | [3]   |           |               |
| RN | BETA-SUBUNIT BINDING DOMAIN.  |           |               |
| RX | MEDLINE; 94150724.  |           |               |
| RA | PRAGNELL M., DE WAARD M., MORI Y., TANABE T., SNUITCH T.P.,             |           |               |
| RA | CAMPBELL K.P.;  |           |               |
| RT | "Calcium channel beta-subunit binds to a conserved motif in the I-II    |           |               |
| RT | cytoplasmic linker of the alpha 1-subunit."                             |           |               |
| RL | Nature 368:67-70(1994).   |           |               |
| RL | [4]   |           |               |
| RN | PHENYLALKYLAMINE-BINDING SITE.  |           |               |
| RX | MEDLINE; 91067656.  |           |               |
| RA | STRIESSNIG J., GLOSSMANN H., CATTERALL W.A.;                            |           |               |
| RT | "Identification of a phenylalkylamine binding region within the alpha 1 |           |               |
| RT | subunit of skeletal muscle Ca2+ channels."                              |           |               |
| RL | Proc. Natl. Acad. Sci. U.S.A. 87:9108-9112(1990).                       |           |               |
| RL | [5]   |           |               |
| RN | DIHYDROPYRIDINE-BINDING SITE.   |           |               |
| RX | MEDLINE; 92021019.  |           |               |
| RA | NAKAYAMA H., TAKI M., STRIESSNIG J., GLOSSMANN H., CATTERALL W.A.,      |           |               |
| RA | KINAKA Y.;  |           |               |
| RT | "Identification of 1,4-dihydropyridine binding regions within the       |           |               |
| RT | alpha 1 subunit of skeletal muscle Ca2+ channels by photoaffinity       |           |               |
| RT | labeling with diazepam."  |           |               |
| RL | Proc. Natl. Acad. Sci. U.S.A. 88:9203-9207(1991).                       |           |               |
| RL | [6]   |           |               |
| RN | DIHYDROPYRIDINE-BINDING SITE.   |           |               |
| RX | MEDLINE; 92073369.  |           |               |
| RA | STRIESSNIG J., MORPHY B.J., CATTERALL W.A.;                             |           |               |
| RT | "Dihydropyridine receptor of L-type Ca2+ channels: Identification of    |           |               |
| RT | binding domains for [3H](+)-PN200-110 and [3H]azidopine within the      |           |               |
| RT | alpha 1 subunit."   |           |               |
| RL | Proc. Natl. Acad. Sci. U.S.A. 88:10769-10773(1991).                     |           |               |
| RL | [7]   |           |               |
| RP | PHOSPHORYLATION OF SER-687 AND SER-1617.                                |           |               |
| RX | MEDLINE; 89008428.  |           |               |
| RA | KOHRRASTEN A., MEER H.E., NASTAJNCZYK W., SIEBER M., HOFMANN F.;        |           |               |
| RT | "Camp-dependent protein kinase rapidly phosphorylates serine-687 of     |           |               |
| RT | the skeletal muscle receptor for calcium channel blockers."             |           |               |

[illegible]

Db 117 YRSQNNVLDLIVLIFVGFALLEGVNVNQSNTAPMSKSGAGLDVYALAFVLRRLRV 176  
QY 192 NRPSPRILVTLTLLDLPMLGNVLLCFVFFFGIVGQVANGLLRNCPENFSLPL 251  
Db 177 SGVPSQVAVLNSLFKAMLPFLHALLVLFMVILYALIGLELFGKHKHKTUY- 229  
QY 252 SVDLBYOTENEDESPFCISOPRENGMRSRCSVPFLNREGGGGPPCSLDITYNSSMT 311  
Db 229 -IGTDIVAVENKPS-CAET- -GSGRBC- -TINGS- 260  
QY 312 TCVMNQVYTNCSAGEHNFKGALINDNIGYAMIAFOVLTLEGVNDIMYFMDA-HSEY 370  
Db 260 -ECRGWPGPNHGITHFDNFGFSLVYQCTIMEGMDVLYVNDALIGNM 309  
QY 371 NFIFYLLIYGSFEMINCLVIAVAFQSEYQKQESQMLREORVFLSNASTLASFSEPG 430  
Db 310 PMIFYVTLILGSEFLLNVLVGLSEF--TKEREKAKR- -GTFOKLREKO 357  
QY 431 SCYEELLYVYILKKAARLAQVSRALGVAGLLSPVARSQGPPOPSGSTRSHRLS 490  
Db 358 QLEEDLRGMSMTQ- -GEVMDVEDLRGKLS- 388  
QY 491 VHHLYHHHHHHHLYLNGTLRVPRASPEIQDRANGSRRLMLPPSTPPSGPPRGA 550  
Db 388 - -LEEG- 393  
QY 551 ESHVSPHADCHLEPVRCQAPPPRCPSEASRTVSGKVPYVHTSPPELLKALVEY 610  
Db 393 - 393  
QY 611 APSGPPILTSFNIPPGPSSMHKLLTQSTGACHSCKISSPCKADSGAGPDPSPYC 670  
Db 393 - 393  
QY 671 ARTGAGEPESADHVPDSSEAVE- -FTQAOHSDLDPRSRKROSLGDAEPS 724  
Db 393 - -SDTESLYEIEGLNKTIQPIR- 414  
QY 725 SVLAFWRLLICTFR- -KIYDSKYFGRGIMAILVNTLSMGIEYHDEPDELTALEISN 780  
Db 414 - -WRQNNRFRKCKHDVYSRFFVWLYLIVALTNLSTLASEHNOPLMLTHLQDIAN 468  
QY 761 IYFTSLFLMLKLLVYGPFGYINPYNIDGVIVISWEIYQOGG- -GLSVLR 835  
Db 469 RVLSTLEIEMLLKMYGLGRQYFMSIFNRFDCFYVCSGILELLEVESGAMTPIGISVLR 528  
QY 836 TERLRAVLKLVFALPACROLVLMKTMNDVATCMILMFIFFSTILGMLFCGRASE 895  
Db 529 CIRLRLKRIKRYWTSLSNLVASTLSRSTASLTLLELFTILFALGMLFGGRYDFE 588  
QY 896 RDGDTLPDRKNFDSLMLAVTVFQILTQEDWNKVLVNGMASTSS- -WALYFTALM 949  
Db 589 - -DTEVRSRNEDNEPQALLISVFOVLTEGDMNSWYNIMAYGSPYGVLYCYITIFL 645  
QY 950 TFGNVYLFNLVAILIYEF- -QAEELGKREDAAGOLSCIOLEPVNSOGDARKSESEDPFS 1008  
Db 646 VCGNITILNVLAIVDLAEASL- -TSAQAKAE- 680  
QY 1009 PSVDGDRKRLALVALGEHAELRSLPLPLHTAATPMSLKSSSTGVGELSGSR 1068  
Db 680 - -ERRKRMKSRGLPDKTEEKSV- 702  
QY 1069 RTSSGSAEPGAHHEMKSPSARSSPHSPWASAASWTSRSSRNSLGRAPSLKRRSPG 1128  
Db 702 - -AKKLEOK-PKG 711  
QY 1129 ERRSLSGEGESODESSSEEDRASPAGSDHRRGSIERAKSSFLPDTLOYPGIART 1188  
Db 712 EG- -IPTTAKLKYDEESNVNEVKP- -YPSADFP- 743  
QY 1189 ASGRSSASEHODCKSASGRILARTLRTDDPOLDDGDDNDEGNLSKGERIOAWRSRLPA 1248

Db 743 - -GDEDEDEPEI PVSPPRPLAEQL- 767  
QY 1249 CCKER- -DSWASYIFPPOSRPRLLCHRIITHKMEHDVAVLIYFNCTIAMERPKID 1303  
Db 767 - -KEKAVIPBASSEFIFSPTNKRVLRCHRIYAVATNTNILLFILLSALAE- -D 820  
QY 1304 PHASERIFLLISNTI- -FPAVLAEMTVKVALGWCFGEOAYLRSSWNLGLLVLISY 1360  
Db 621 PIRAESVANOILGYFDIAFTSVFVEIVLKMITYGAFHLHGKSCFRNFILDLVAVS- 880  
QY 1361 IDILVSWSDGKTIILGMVLRLLRPLRLPRLYISRAOQKLVAVELMSSLRKIGNIVY 1420  
Db 880 - -LISMGLESST- -ISVVAIKVLRPLRLPRLRKRGKLVHVOCVFVAIRITGIVAV 934  
QY 1421 CCAFFIIFGLIGVOLFNGKFFVOCGEDTRNTKSDCAEASV- -RMV 1465  
Db 935 TTLQFMFACIGVOLFNGKFFSC- -NDLSKMT- -EEBCRGYIYYKDGDPLOMERPRQMI 991  
QY 1466 KIKYNEPNLGOALMSLFLVLAASKGWDIMYGDVAVDQOPIAHNPMMLYFISLLI 1525  
Db 992 HNDHFEDNVLSAMMSLEFVSTFEGWOLLYRAIDSNEEDGPPYNNRVEMALFEIYIIL 1051  
QY 1526 VAEFVLMFVGVVENEHRCROHEEAEARREKRLRLEKKRRMLMDVYIAGSSAS 1585  
Db 1052 IAFPMNIIFGVYIYF- -QOGETEYKNC- -LDKQRCV- -QYAL 1093  
QY 1586 AASEAQCKPYSDYSRRLVHLLCTSHYLDLFTIGVIGLVNTYAMERYOQPOLIDEAL 1645  
Db 1094 KARPLRC- -YIPKNPYOYOVWVYTSYFEYLMFALIMLNTICGMQYHOGSEEMNHS 1150  
QY 1646 KICNYIYFVFESEYFKVAFEGFRFODRMNODLAVLISIMGITELEV- 1700  
Db 1151 DIINAVFTIIFTEMILKLAERKARQYFQDPWNEFELVISIIDVILSEIDFLASSG 1210  
QY 1700 - -NASLPINPTIIRIMVLRILARVILKLLKAAVGRALLDVTM- -OAL 1742  
Db 1211 GLYCLGGGCGNVDPSARISSAFRFLPRVML- -IKLSAEGVFTLMLFISFOAL 1267  
QY 1743 POGVNGLGFMLFFIIFALVGLVLEGDLE- -CETHPCBSLGHAFFRNGMAELTFRVS 1801  
Db 1268 PYY- -ALLIVMLFFIYAVIGMQEMFKIALVDGTO- -INNHNFOFPQAVLFLFRA 1320  
QY 1802 TGDNMNGIMKMDL- -RDCOES- -TCYNYIYSPYVSVLVLAQVYLVAV 1851  
Db 1321 TGRAMOBILLACGYKLCRPSBESDYABGEYTC- -GYNFAIYFISYMCALFIINLEFVAV 1379  
QY 1852 LM- -KHLESNKEAKEAELEAE- -TELEMTLSPOHSPILGSPFL 1893  
Db 1380 IMDNFDYLTRDMSIILGPHLDEF- -KAIMAEYDPEAKGRKHLADVTLRLRLOPPLGPKF 1438  
QY 1894 WP- -GVEGVNSP- -DSKPGAPHTTAHIGAAGSGLBHP- 1929  
Db 1439 CBRVACKRLVKNMPLNSDGTVTFNALLFALVRLALIKIEGNEFOANEELAIKKIW 1498  
QY 1929 - -TMVPHPEVEVVPGLDILTVRKSGVSRTHSLPNDYSWCRNGSAEBSLHRRGGLPKA 1966  
Db 1499 KRYSKMLDQVAPRIQDDDEVYKGFATFLIOENHRKRWKRO- -EYIGR- -PKK 1550  
QY 1987 QS- -GSLVSHSOPA- -DTSCILQRPKDVHYLLOPHGAPTWGAIBKLPPPG 2033  
Db 1551 DTVLOAGLRTIEEBAEIRRTISGDLTAEBELERAM- -V 1589  
QY 2034 RSPLAQRLPRLQAAI- -RTDSL- -DYQGLSREDLISVSGP- 2072  
Db 1590 EAMAEERIRRTIGGLFGOVDTFLERTISLPYMANQRLPQAEIEMELEBPVLEDFPQ 1649  
QY 2072 - -SCPLRASSFWGSSIOV- -QORSGIOKVSXHIPLPAPCGLEPSWAKDPPETRSS 2126  
Db 1650 DARTNPLAANTNANANAVAGNSHNSNMOMFSVH- -CERNEPGEAETRAAGRA 1703  
QY 2127 LEDDTLSWISDILLPSSQOEBLSRDLKCYSVETOSCRRRPQSWITDEORRHSIAVSL 2186  
Db 1704 J- -SSHRALGPHS- -KPC- -AGKLNQOLVOPGMITWO- 1736



|    |      |   |                 |      |
|----|------|---|-----------------|------|
| OY | 2187 | DSSGQPLCPSPSSLSGGQPLGCGSGRPKKKS-PPSISIDPDE---       | SOGSSAPPCSPCVCL | 2244 |
| DB | 1736 | ---APPAPCCQPT-----DPEEGGQRRTLTGSLDDEAPRRSSGSPT----- |                 | 1778 |
| OY | 2243 | RRRAPAD--SKDPVSVPDSTAAASPSRKDTLSLGSSPDDMDP          | 2288            |      |
| DB | 1778 | RRRPAFALLIGELVIRGSLDTLAADAG---EVTATSQLADACQMEE      | 1822            |      |

  

|           |  |           |      |          |
|-----------|--|-----------|------|----------|
| RESULT 14 |  |           |      |          |
| ID        | CCAF_HUMAN   | STANDARD: | PRT: | 1966 AA. |
| AC        | 060840: C43901:  |           |      |          |
| BT        | 15-JUL-1999 (Rel. 38, Created)   |           |      |          |
| DT        | 15-JUL-1999 (Rel. 38, Last sequence update)                            |           |      |          |
| DR        | 15-JUL-1999 (Rel. 38, Last annotation update)                          |           |      |          |
| DE        | VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL, ALPHA-1F SUBUNIT.            |           |      |          |
| GN        | CACNA1F OR CACNA1F1.   |           |      |          |
| OS        | Homo sapiens (Human).  |           |      |          |
| OC        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;          |           |      |          |
| NC        | Eutheria; Primates; Catarrhini; Hominoidea; Homo.                      |           |      |          |
| RN        | [1]  |           |      |          |
| RP        | SEQUENCE FROM N.A., AND VARIANTS CSNB2 D-369; Q-508; W-1049 & H-1364.  |           |      |          |
| RX        | TISSUE-RETINA:   |           |      |          |
| RA        | MEDLINE: 98324776.   |           |      |          |
| RA        | STROM T.M., NYAKATURA G., APPELSTEDT-STYLA E., HELLEBRAND H.,          |           |      |          |
| RA        | LORENZ B., WEBER B.H.F., WUTZ K., GUPTILLINGER N., RUTHER K.,          |           |      |          |
| RA        | FORSCHER B., SAUER C., ZENNER E., METTINGER T., ROSENTHAL A.,          |           |      |          |
| RA        | MEINDL A.;   |           |      |          |
| RT        | "An L-type calcium-channel gene mutated in incomplete X-linked         |           |      |          |
| RT        | congenital stationary night blindness.";                               |           |      |          |
| RL        | Nat. genet. 19:260-263(1998).  |           |      |          |
| RN        | [2]  |           |      |          |
| RP        | SEQUENCE OF 1200-1966 FROM N.A.  |           |      |          |
| RX        | MEDLINE: 98008923.   |           |      |          |
| RA        | FISHER S.E., CICCODICOLA A., TANAKA K., CURCI A., DESICATO S.,         |           |      |          |
| RA        | D'URSO M., CRAIG I.W.;   |           |      |          |
| RT        | "Sequence-based exon prediction around the synaptophysin locus reveals |           |      |          |
| RT        | a gene-rich area containing novel genes in human proximal xp.";        |           |      |          |
| RL        | Genomics 45:340-347(1997).   |           |      |          |
| CC        | -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE     |           |      |          |
| CC        | ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED       |           |      |          |
| CC        | IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE          |           |      |          |
| CC        | CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,     |           |      |          |
| CC        | CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F      |           |      |          |
| CC        | GIVES RISE TO L-TYPE CALCIUM CURRENTS, LONG-LASTING (L-TYPE)           |           |      |          |
| CC        | CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)          |           |      |          |
| CC        | GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),                     |           |      |          |
| CC        | PHENYALKYLAMINES, BENZOHAZEPINES, AND BY OMEGA-AGATOXIN-IIIA           |           |      |          |
| CC        | (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-     |           |      |          |
| CC        | GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).          |           |      |          |
| CC        | -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT       |           |      |          |
| CC        | COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS     |           |      |          |
| CC        | IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-      |           |      |          |
| CC        | FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS     |           |      |          |
| CC        | SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM            |           |      |          |
| CC        | CHANNEL ACTIVITY. THE AUXILIARY SUBUNTS BETA AND ALPHA-2/DELTA         |           |      |          |
| CC        | LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.            |           |      |          |
| CC        | -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.                   |           |      |          |
| CC        | -I- TISSUE SPECIFICITY: EXPRESSION IN SKELETAL MUSCLE AND RETINA.      |           |      |          |
| CC        | -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE            |           |      |          |
| CC        | HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE        |           |      |          |
| CC        | POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS             |           |      |          |
| CC        | PARTIALLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A      |           |      |          |
| CC        | SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.      |           |      |          |
| CC        | -I- DISEASE: DEFECTS IN CACNA1F ARE THE CAUSE OF INCOMPLETE X-LINKED   |           |      |          |
| CC        | CONGENITAL STATIONARY NIGHT BLINDNESS (CSNB2), A NONPROGRESSIVE        |           |      |          |
| CC        | RETINAL DISORDER CHARACTERIZED BY DECREASED VISUAL ACTIVITY AND LOSS   |           |      |          |
| CC        | OF NIGHT VISION.   |           |      |          |
| CC        | -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL, ALPHA-1 SUBUNTS        |           |      |          |
| CC        | FAMILY.  |           |      |          |

[illegible]



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FT DOMAIN 1110 1113 POLY-TIDE.
FT DOMAIN 1629 1634 BINDING TO THE BETA SUBUNIT (BY
FT DOMAIN 395 412 SIMILARITY).
FT SITE 330 330 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 700 700 (BY SIMILARITY).
FT SITE 1075 1075 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1372 1372 (BY SIMILARITY).
FT SITE 1372 1372 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT BINDING 1049 1139 TO DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1386 1452 TO DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1398 1441 TO PHENYLALKYLAMINES (BY SIMILARITY).
FT MOD_RES 1441 1441 PHOSPHORYLATION (BY CARK) (POTENTIAL).
FT CA_BIND 1459 1470 BY SIMILARITY.
FT CARBOHYD 295 295 POTENTIAL.
FT VARIANT 369 369 G -> D (IN CSNB2).
FT VARIANT 508 508 R -> Q (IN CSNB2).
FT VARIANT 1049 1049 R -> Q (IN CSNB2).
FT VARIANT 1049 1049 R -> W (IN CSNB2).
FT VARIANT 1364 1364 L -> H (IN CSNB2).
FT CONFLICT 1225 1225 E -> V (IN REF. 2).
FT CONFLICT 1265 1271 MISSING (IN REF. 2).
FT CONFLICT 1652 1767 MISSING (IN REF. 2).
FT CONFLICT 1849 1849 A -> G (IN REF. 2).
SQ SEQUENCE 1966 AA; 219494 MW; A04DE750 CRC32;

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Query Match 12.9%; Score 1608; DB 1; Length 1966;  
 Best Local Similarity 23.5%; Pred No. 4,7e-74;  
 Matches 581; Conservative 331; Mismatches 749; Indels 816; Gaps 78;

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QY 1 MDEEDGAGAEESGQPRSTQTLNDLSGAG-GRQ-----GPGSTKDPGSADSEAEGLPY 54
D 1 MSEEKGKDTTPPEPSP-----ANGAGGPEMGLCPPEPAVEGE-----SSGASLGLTP 48
QY 55 -----ALAPVFFYLLSQDSRPSMCLRTVCNP-----W--FERYSMLV 90
D 49 KRNQSHKRTVAVA-----SAQSPRALFCLTLANPLARSCISIVMKCFDILLT 101
QY 91 ILLNCYTLGFRPCEDLACDSQRCRILOAFDEIF-AFAVENVVWVVLG-IFGKKYL 148
D 102 IFANCVALGYIIFPEDDSTANHNLEQV--EYFLVITFETVLYKIVAGLVLPDSAT 159
QY 149 GDTWNLDFEIVYAGMLETSLD-----ONVSFAVTVRVLRPLRAIR 193
D 160 RNMWNLDFEIVYAGMLETSLD-----ONVSFAVTVRVLRPLRAIR 219
QY 194 VPSMRILVTLTDLTLMGLNVLLCFEVEFIRIGVQVOMAGLRKRCLEPENSISLPSV 253
D 220 VPSLHVLSIMKALPLHLIALVLFVITITAIIGLEFLGRMHTCYF-----LGS 272
QY 254 DLEPYQTEENEDSPFICOSPRENMRSCRSVPTLREGEGGPPCLDYEYTNSSNTIC 313
D 273 DME-----AEDEPSP-----CAS-----SGSGRACL 295
QY 314 VMNNOYVYTCASGEHPFGAINFGIATGAMIAFOVITLLEGWMDIMFVMDAHSE-YNF 372
D 295 ---NQ--TECRGRWPGPNNGITNEDFFAMLVFOCVTMEGWTVLYLMQDAMGEYELPW 349
QY 373 IYFILLIIVGSEFMILNCLVATIQPSE-----TKRESOLMEQVRRLSNAS 421
D 350 VYFVSLVIGSEFVNLVYLGIVSGESKREKAKARGDQOKREKQNE----- 399
QY 422 TLASSEPGSCYEELIKYVILRKARLAQVRAIGVRAGLISSPVARSQGEPPSGS 481
D 399 -----EDLRGYLDWITQ--AEELD-----MDPSADNLDLQGLAEL 432

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QY 482 CTRSHRRUS-VHHLVHHHHHHHHHVLNGTLVRPASPEIQDRDANGSRRLMPPSTP 540
D 433 TNRNRKRLWFESHSTSTSHSTSHSL-----PASD 463
QY 541 TPSSGPPRGAESVSHFADCHLEPVRQAPPPRPSASGRVSGKYPTVHTSPPE 600
D 464 TSMETQGDDEEGALASC-----TRC----- 488
QY 601 ILKDALVEAPSPPTLTSFNIPPGPSSMKLLETOSTGACHSCKISSPSKADSG 660
D 488 -----LNKMKR----- 496
QY 661 ACPPDSCPCARTGAGEPSADHWPDSDSEAYEFTQAOHSDLRDPSRRORSLEPD 720
D 496 -----VCRRL-----RRARVL----- 508
QY 721 AEPSSVLAFWRLICDTPRKIVSKYFGRGIMATLVNTLSMGIEYHQPPELLTALEISN 780
D 508 -----RARC-----RAVKSNACTYAVLVLLVNTLITASHHQPWLTQIQETAN 554
QY 781 IVTSLFALLEMLKLKLVYGPFGYIKNPYNID-----GVIVISWETVGGQGGSLVLR 835
D 555 KVLCLFTEVEMLLKLYGLGSAVYSPFNRFDCFVCGGLETTLVVGANQPLGISVLR 614
QY 836 TPLLRVLRKIVREFALOROLVLMKTMDNATCMMLMFLFISLGHMLGCKFRASE 895
D 615 CVRLIRIKVTRHWASLSNLVASLSNKSJASLLLFELFIIFSLGQLEFGCKFNFD 674
QY 896 RDGDTLPDRKNEDSLIMATVTFQILTOEDWNKVLVNGMAS-----TSSMAALYFTALM 949
D 675 Q---THTKRSFDFEPQALLVTLVFOILGEDMNVMYGIMAYGGPFPGMLVCYFIILF 731
QY 950 TPQNVLENLVALIVEGFOAEIEGKREDASGLQCLPVNSOGDAPKSESEPPFPSP 1009
D 732 ICGNYILNLVFLAIVADNLASGDAGTAKDKGEKS-----NEKD----- 771
QY 1010 SVDDGDKRRLVALVALGEHAELEKRLSLPLIHTATPMSLPKSSSTGVGEALGSGSR 1069
D 771 -----LPQNE----- 777
QY 1070 TSSGSAPGAHHHMKSPSPASRSPSPWSAASMTSRSSRSNLSLRAPSLKRSPGE 1129
D 777 -----GLVGEKEEPEG 790
QY 1130 RRLSLSGGQSQDEEESSEEDRASPGSDHRRGSLERAKSSFDPDLOVPGGLHRTA 1189
D 791 RREGADMEEEEEEDEEEDEEAGAGVE-----LLOEV-----VPKRYVP----- 834
QY 1190 SGRSSASPHQDNCNGKSASGRLATLFTDDPDQDDDDNDGNSLKGRIQAWRSRLPAC 1249
D 834 -----IFEGSAFCLQSOTNP-----LRKG----- 853
QY 1250 CREBDSMSAYIFPQSRFRLCHRITTHKMFHDVIVLIIIFLNCITIAMERKIDPHSAER 1309
D 853 -----CHTLIHNVFTNLIVFILLSSVSLAEDP-IRASIFRN 890
QY 1310 IFLLSNVITFAVLAEMTKYVALGWCFOEAYLSSSNWVLDGLVLVLSIDILVSNVS 1369
D 891 HILQYFAFISITVYELLKMTVFGAFLHRGSEFCRSWEMMLDLVAVSVLSIFGIH--- 948
QY 1370 DSGTKILGMLRVLRILTRTPPLRVISPAQGLKLVLEWMSLSPIDNIGVYICAFILIFG 1429
D 948 ---SSAISVYKILRVLRVLRPLRAIRNAKRLKIVQOCVFAITGIMIMVTLTLOFMRA 1004
QY 1430 ILGVLTKGKFFVYQGGEDTEN-----ITNKSQCAEASVY--VWRHKYNFMDLGOA 1477
D 1005 CIGVQLFKGFEYCTDEAKHTPOCKGSEFLVYDPGVSPRYERLRWNSDFNFQVLSA 1064
QY 1478 LMSLFVASKDWDIMYDLDVAGVDQOPIMNHNWMLLIFSLIYAFVLANKEFV 1537
D 1065 MMALFTVSTFEGNPALYKALDAVADHGTIVYREIVSEIFVYIIITIAFPMNIFVGF 1124
QY 1538 VVENFHRCROHDEEENARRREERLRLREKKRRNMLDVIASGSSASAASAOCKPYVS 1597

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FT TRANSMEM 539 557 S4 OF REPEAT II.  
 FT DOMAIN 558 576 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 577 596 S5 OF REPEAT II.  
 FT DOMAIN 597 651 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 652 675 S6 OF REPEAT II.  
 FT DOMAIN 676 815 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 816 834 S1 OF REPEAT III.  
 FT DOMAIN 835 850 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 851 870 S2 OF REPEAT III.  
 FT DOMAIN 871 882 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 883 901 S3 OF REPEAT III.  
 FT DOMAIN 902 908 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 909 927 S4 OF REPEAT III.  
 FT DOMAIN 928 946 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 947 966 S5 OF REPEAT III.  
 FT DOMAIN 967 1056 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1057 1081 S6 OF REPEAT III.  
 FT DOMAIN 1082 1134 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1135 1153 S1 OF REPEAT IV.  
 FT DOMAIN 1154 1168 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1169 1188 S2 OF REPEAT IV.  
 FT DOMAIN 1189 1196 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1197 1215 S3 OF REPEAT IV.  
 FT DOMAIN 1216 1252 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1253 1271 S4 OF REPEAT IV.  
 FT DOMAIN 1272 1290 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1291 1310 S5 OF REPEAT IV.  
 FT DOMAIN 1311 1377 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1378 1402 S6 OF REPEAT IV.  
 FT DOMAIN 1403 1852 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 4 12 POLY-GLY.  
 FT DOMAIN 400 403 POLY-LEU.  
 FT DOMAIN 577 583 POLY-LEU.  
 FT DOMAIN 1062 1068 POLY-ILE.  
 FT DOMAIN 374 391 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).  
 FT SITE 309 309 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 628 628 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1030 1030 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1344 1344 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT BINDING 1004 1093 TO DIHYDROPYRIDINES (BY SIMILARITY).  
 FT BINDING 1358 1424 TO DIHYDROPYRIDINES (BY SIMILARITY).  
 FT BINDING 1370 1413 TO PHENYLALKYLAMINES (BY SIMILARITY).  
 FT CA BIND 1431 1442 BY SIMILARITY.  
 FT MOD\_RES 1407 1407 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RES 1413 1413 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RES 1471 1471 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RES 1523 1523 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT MOD\_RES 1738 1738 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT CARBOHYD 99 99 POTENTIAL.  
 FT CARBOHYD 102 102 POTENTIAL.  
 FT CARBOHYD 274 274 POTENTIAL.  
 FT CARBOHYD 470 470 POTENTIAL.  
 FT CARBOHYD 1157 1157 POTENTIAL.  
 SO SEQUENCE 1852 AA; 210096 MW; 46513952 CRC32;

Query Match 12.9%; Score 1604.5; DB 1; Length 1852;  
 Best Local Similarity 24.0%; Pred. No. 6.5e-74;  
 Matches 479; Conservative 323; Mismatches 523; Indels 667; Gaps 55;

CY 128 FAVENVVAVKVALG-TEGKCTYIGTWANLDFEVIAGMLEYSLDLQNV----- 175  
 DB 116 FLTBOELIVAVGLFHBGAVLRNOMNTLDFIVFMGLTIVDTINTIAGVPTREKGGF 175  
 CY 175 SFSAVRTVAVLPRLAIRVPSMRLVTLTLDTLPMIGNVLLLEFFEFIFGIYGVQDMA 234  
 DB 176 DMKALRARVRLPRLVGVPSLOVMSILKSMPLFHALLVFVWHYAIAGLFLK 235  
 CY 235 GLLRRCFLPENFSLPLSVLEPYQTEEN-----EDSPICSPRENGMRSQSVPTL 288  
 DB 236 CMHKTCT-----YVQGINIIVAREGNKRPSCAQ----- 265  
 CY 269 REGGGGPPCSIDETTYNSSNTTCVANNQYVTCSGAENHPFGAINEFDNIGTAMIAIF 348  
 DB 265 --AGHGRCTIN-----GTECRAGWPQPNIGTHFNSCFMPLTF 303  
 CY 349 QVITLEGWVDIMYFVMDA-HSFYNYFILLIIVGSPFMILCLVATATQSEKRESEQ 407  
 DB 304 QCITTESVTDVLYMTNDAMGDMWITFILLITLVGSEFILLVYGAISGEF--TKREES 361  
 CY 408 LMR--EQVRELNAASTLASESEPGCYEELKLYVILRKARRLAQVRAIGVRAGL 465  
 DB 362 RSRGEYQKLR-----ERQODEDELEGYMEW----- 388  
 CY 466 SSPVARSQGEQPGSGCTSRSHRLSVHHVHHHHHHHNGTLRVPRASPEIODRD 525  
 DB 388 -----THAEVWDG 396  
 CY 526 ANGSRRLMLPPSTPTPSGPPRGAEVSHSFYHADCHLEPVCQAPPPRCPSEASGRTVG 585  
 DB 397 --SEALL----- 403  
 CY 586 SGKYYPIVYHSPPPELLKDALVEVAPSPGPPTLTSTNPDPGFFSMKLLTQSTGACH 645  
 DB 403 -----LRKD----- 407  
 CY 646 SSCAKISSPCSKADSGAGGDPSCPCYARTGAGPEPSADHVVPDSDSEAVYEFITDQASHDL 705  
 DB 407 -----TDSOSDLQMD----- 420  
 CY 706 RDPHKKRORSIGDAPSSVLAFWRLI-----CDTFPKIYDSKYGFGIMATIL 755  
 DB 420 -----QGVIVFYRLARRWNVLRKCHVM---VKSFFNMWVLLVVL 458  
 CY 756 VNTLSKGIETHQDEEELTNALNLSIVTSFLALMLKLLVYGPYIKNPINFDGYI 815  
 DB 459 LNTLVIMAEHNNQTEGLTSFODTANVILLACFTIEMVMKAYAFGPRAVPSIFNRPDCV 518  
 CY 816 VVISWEIVGQGG-----GLSVLRTPRLMRVLKIVRFLPALQROLVLMKTMDNVATFC 870  
 DB 519 VTILELEILLVNSIMPLGLISVWRCTRLRLFKLRYWTSLNVLVASLIVSKSIASTL 578  
 CY 871 MLMLFFIFISILGMILFGCKFASERDGTLPD-----RNFDLSLMAIVYFOILQEDM 926  
 DB 579 LLELFIVIFAILGMQVFGKF-----NFPDRVIGRSNEDNFPALLSVQVLGEEM 631  
 CY 927 NKVLYNKM-----ASTSSMAALYFALMTFGVYVFNLIIVALEGF-QADEIGKREDA 979  
 DB 932 DSIWYNGIMAHGPPQSGILVSYFILLVYCCGNFVLNVLAVDNLEAESTLRA----- 688  
 CY 980 SGOLSCIQLPVNSGGDPTKSESEDPFFSPSYVDGDRKKRLALVALGHAELKRSILDP 1039  
 DB 688 -----AQEKRAE-----EKARKKIMRTLPKSEBERALVMK 718  
 CY 1040 LIHTHTATPMSLPKSSSTGVGALGSGSRTSSGSAEBAAHHEKSPSPASPSHFW 1099  
 DB 719 RLMESSKKEGAGHTAKIKIDEFSN-----VNEVKDPFPADP----- 759  
 CY 1100 SAASWTSRRSSSNNSUGRAPSLKRRSPSGERSLSLGEQESQDEESSEEDERASPSGD 1159  
 DB 759 -----GDHEVEPEIPISP----- 773  
 CY 1160 HRRHGLEREAKSSFDLPDTLQVGLHRTASGRSSASEHODCNKGSASQRLARTLRTDDP 1219

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Db 773 -RPRMADLQJLKEV-----VP----- 789
QY 1220 QLDGDDNDNDESNLKGRIQAWVRSLPACCREDNSAYIFPQSHRLLCHRIITHKM 1279
Db 789 -----TAEASSFFIFGQHKFRKLRHYNHT 816
QY 1280 FDHVVYIIFLNCITTIAMERKIDPHSAERITLNSVIFTAVFLAEMTVKVALGWCFCG 1339
Db 817 FTNILLFILLSSISLAEDP-IDPRSFNKKVLAYADIVFTVFTIEIVLKMVYGAFH 875
QY 1340 EQAIIRSSNNVLDLVLVLIISYIDLVGNSVSDSGFKIIGMLRVLRLLRPLRVISPAOG 1399
Db 876 TGSFCRNSFNLLDLIVGVS---LISGMESST--ISVAILRVLRVLRRAINRAK 929
QY 1400 LKLVEITLMSLKPIGNIVIVICCAFFIIFGILVQLFKGKFFV-----CQGEDT 1448
Db 930 LKHVQCMFAVAKTIGNIVLVTMLDMEFACIGVQLFKGKLYCTDPLQKTAECQGTFL 989
QY 1449 RNITKSDCAEASIR-WVRHKYNFDNLGQALMSLFVLASKDGVDMYDGLDANGVQOP 1507
Db 990 KHPNSLHDIEVHQRMWNSDFNEDNVLNGLALFTISTEGMPEILYKAIDSNVDTGP 1049
QY 1508 IMNHMPMLLVEFISFLVAFVLMFVGVVNFHKOHOEEEAARRREKRLRLER 1567
Db 1050 LYNNVVGISIFFIYIITIAFFMANIFGVYIVTFOK---QGEQYKDC-----LDK 1099
QY 1568 KRNIMLDDVYASGSASASEAOCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLV 1627
Db 1100 NQOCV-----QYALKARPLKC---YIPKNPHQYRWYFVTSCEYELMFLMINT 1148
QY 1628 YTMAMEHQQOQIIDEALKICNYIFTYVFESEVKLVAFGFRFQODRMQDLATVLL 1687
Db 1149 ICLGIQHCNOSDHTIKLSDTJNLFTVLEFTGEMIVKLIARAKGFGDPWNVDFIIVG 1208
QY 1688 SIMGITLEIE-----VNASLEPIN-----TIRIRVLRIRARVLLKL 1725
Db 1209 STVDVVLSEVDALFARGIMCLHGCACAEVNMQAIABENRVSTIFRRLFRVLRLLKL 1268
QY 1726 KVAAGMALDLTVMQALPOVGNLGLLFMLLFFIFALGVELFGDLE-CDETHPCGGLGRH 1784
Db 1269 NRSEGI RNILMTFIRKSFQALPHVGLLIYMLFEIYAVIGMOMFGKVALVDGTE---INRN 1324
QY 1785 AFRFNGMAFLLEFVSTGDMNNGIMKDL--ROCD-----QESTCYTVISPIYFV 1834
Db 1325 NNFQTFPOAVLLEFRVATGEOMPKVILASMGKLCDAKSDIGPGEYITC-GSSIAVETFL 1383
QY 1835 SFVLTAQFVLVNVVIAVLM-----KHLESNK-EAKEEAELEAELE-LEM 1877
Db 1384 SFYIIICAFIILNLFVAIINDVNYLTDWMSILGPHHDEFKIYAEYDPEATGRKIHLDV 1443
QY 1878 KTLSPQPHSPLG 1889
Db 1444 VTLRLRIOPPIG 1455
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Search completed: January 15, 2000, 18:40:02  
Job time: 4565 sec

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2000, 21:28:25 ; Search time 46.51 seconds  
(without alignments)  
2407.653 Million cell updates/sec

Title: PCT-US99-19675-2

Percent score: 12469  
Sequence: 1 MDEEDGAGAESGQPSRFT.....LREKGKGPVMPRLPTPGA 2374

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database: PIR.62.\*

Word size: 0

Number of hits that pass the threshold: 142080

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID    | Description           |
|------------|--------|-------------|--------|----------|-----------------------|
| 1          | 11719  | 94.0        | 2254   | 2 T09053 | low voltage-activated |
| 2          | 3546.5 | 28.4        | 1657   | 2 T15838 | hypothetical prote    |
| 3          | 1714.5 | 13.8        | 2339   | 2 A42566 | omega-conotoxin-se    |
| 4          | 1688.5 | 13.5        | 2259   | 2 S29236 | calcium channel pr    |
| 5          | 1688   | 13.5        | 2288   | 2 S41080 | calcium channel al    |
| 6          | 1678   | 13.5        | 2336   | 2 A45386 | omega-conotoxin-se    |
| 7          | 1678   | 13.5        | 2223   | 2 A47447 | calcium channel pr    |
| 8          | 1670.5 | 13.4        | 2272   | 2 C54972 | voltage-dependent     |
| 9          | 1664   | 13.3        | 2178   | 2 S29237 | calcium channel pr    |
| 10         | 1653.5 | 13.3        | 2251   | 2 B54972 | voltage-dependent     |
| 11         | 1653   | 13.3        | 2270   | 2 A54972 | voltage-dependent     |
| 12         | 1649.5 | 13.2        | 2222   | 2 A37490 | voltage-dependent     |
| 13         | 1608.5 | 12.9        | 1873   | 2 A30063 | dihydropyridine re    |
| 14         | 1606.5 | 12.9        | 2166   | 2 S11339 | calcium channel pr    |
| 15         | 1598   | 12.8        | 2143   | 2 JH0427 | voltage-dependent     |
| 16         | 1596.5 | 12.8        | 2140   | 2 JH0426 | voltage-dependent     |
| 17         | 1589.5 | 12.7        | 1977   | 2 S54771 | sodium channel alp    |
| 18         | 1587   | 12.7        | 2139   | 2 A44467 | voltage-dependent     |
| 19         | 1586.5 | 12.7        | 2016   | 2 A38195 | sodium channel pro    |
| 20         | 1586   | 12.7        | 2208   | 2 A37860 | calcium channel pr    |
| 21         | 1585   | 12.7        | 2181   | 2 A38198 | calcium channel al    |
| 22         | 1583   | 12.7        | 2171   | 2 S05054 | calcium channel al    |
| 23         | 1576   | 12.6        | 2161   | 2 JH0564 | calcium channel al    |
| 24         | 1572.5 | 12.6        | 2108   | 2 S72458 | sodium channel pro    |
| 25         | 1568   | 12.6        | 2019   | 2 A33996 | sodium channel pro    |
| 26         | 1568   | 12.6        | 1873   | 2 A35645 | calcium channel, v    |
| 27         | 1563.5 | 12.5        | 1957   | 2 S68453 | calcium channel al    |
| 28         | 1561.5 | 12.5        | 1957   | 2 JCS280 | sodium channel pro    |
| 29         | 1559   | 12.5        | 2206   | 2 A46227 | voltage-dependent     |
| 30         | 1558.5 | 12.5        | 1610   | 2 JH0422 | voltage-dependent     |
| 31         | 1545   | 12.4        | 1646   | 2 JH0422 | sodium channel pro    |
| 32         | 1535.5 | 12.3        | 1963   | 2 A60054 | calcium channel pr    |
| 33         | 1535   | 12.3        | 2326   | 2 B47447 | calcium channel pr    |
| 34         | 1533.5 | 12.3        | 1951   | 2 S00320 | sodium channel pro    |
| 35         | 1532.5 | 12.3        | 2005   | 2 A46269 | sodium channel alp    |

|    |        |      |      |          |                    |
|----|--------|------|------|----------|--------------------|
| 36 | 1532.5 | 12.3 | 2220 | 2 A45290 | calcium channel pr |
| 37 | 1531   | 12.3 | 2005 | 2 B25019 | sodium channel pro |
| 38 | 1530.5 | 12.3 | 1820 | 2 A33299 | sodium channel pro |
| 39 | 1530   | 12.3 | 1976 | 2 S65555 | sodium channel pro |
| 40 | 1527   | 12.2 | 1689 | 2 S72467 | sodium channel pro |
| 41 | 1527   | 12.2 | 1840 | 1 CHERM1 | sodium channel pro |
| 42 | 1514.5 | 12.1 | 2273 | 2 I46477 | calcium channel BI |
| 43 | 1511.5 | 12.1 | 2009 | 2 A25019 | sodium channel pro |
| 44 | 1511.5 | 12.1 | 2273 | 2 I46478 | calcium channel BI |
| 45 | 1511.5 | 12.1 | 2424 | 2 I46479 | calcium channel BI |

## ALIGNMENTS

## RESULT 1

109053  
low voltage-activated, T-type calcium channel alpha chain - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 11-Jun-1999 #sequence #revision 11-Jun-1999 #text-change 11-Jun-1999  
C:Accession: T09053  
R:Pelez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.;  
Nature 391, 896, 1998  
A:Title: Molecular characterization of a neuronal low voltage-activated, T-type, calc  
A:Reference number: 216538  
A:Accession: T09053  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2254 <P>  
A:Cross-references: EMBL:AF027984; NID:g3786350; PID:g3786351  
A:Experimental source: strain Sprague-Dawley; brain  
C:Genetics:  
A:Map position: 17  
A:Note: CACNAG  
C:Keywords: calcium channel; voltage-gated ion channel

| Query Match                | Score                                | DB 2   | Length | 2254 |
|----------------------------|--------------------------------------|--|--------|------|
| Best Local Similarity      | 97.98                                | Pred. No. 0  |        |      |
| Matches 2241; Conservative | 1; Mismatches 12; Indels 34; Gaps 2; |  |        |      |
| QV                         | 1                                    | MDEEDGAGAESGQPSRFTQNDLSGAGRGQPGSTKDGSDSEAGLPYPALAPV      | 60     |      |
| DB                         | 1                                    | MDEEDGAGAESGQPSRFTQNDLSGAGRGQPGSTKDGSDSEAGLPYPALAPV      | 60     |      |
| QV                         | 61                                   | FFYLSQDSRPSWCLRTVCNPFERVSMLVILLNCVTLGMRPCEDTACDSQRCLIQAF | 120    |      |
| DB                         | 61                                   | FFYLSQDSRPSWCLRTVCNPFERVSMLVILLNCVTLGMRPCEDTACDSQRCLIQAF | 120    |      |
| QV                         | 121                                  | DDFPAFAVENVMVALGFGKCYLGDWNRDLDFIVTAGMLEYSIDLQNVSESAVR    | 180    |      |
| DB                         | 121                                  | DDFPAFAVENVMVALGFGKCYLGDWNRDLDFIVTAGMLEYSIDLQNVSESAVR    | 180    |      |
| QV                         | 181                                  | TVKVLRFRAINRVPSMKRLVTLTLLDTPMLGNVLLCFEYFFIGVIGVQWAGLRRN  | 240    |      |
| DB                         | 181                                  | TVKVLRFRAINRVPSMKRLVTLTLLDTPMLGNVLLCFEYFFIGVIGVQWAGLRRN  | 240    |      |
| QV                         | 241                                  | CELQNFLEPLSVLEPYQTEENDESPTCSOPRENGMRSRVPTLRKGGGPPCSL     | 300    |      |
| DB                         | 241                                  | CELQNFLEPLSVLEPYQTEENDESPTCSOPRENGMRSRVPTLRKGGGPPCSL     | 300    |      |
| QV                         | 301                                  | DIETNNSNTTCVNMNQYVNCAGSENPCKAINDNIGVMAIAFOVITTEGVWDIM    | 360    |      |
| DB                         | 301                                  | DIETNNSNTTCVNMNQYVNCAGSENPCKAINDNIGVMAIAFOVITTEGVWDIM    | 360    |      |
| QV                         | 361                                  | YFVMDASHFYNFIFILLIIVGSFFMINCLVATATFSETKQRESQLMREQVRFLSNA | 420    |      |
| DB                         | 361                                  | YFVMDASHFYNFIFILLIIVGSFFMINCLVATATFSETKQRESQLMREQVRFLSNA | 420    |      |
| QV                         | 421                                  | STLASFSPGSCYELLKYVITIRKARLAQVSAIGVAGILSSPVARSQEPQPSG     | 480    |      |
| DB                         | 421                                  | STLASFSPGSCYELLKYVITIRKARLAQVSAIGVAGILSSPVARSQEPQPSG     | 480    |      |

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QY 481 SCTSRRLSVNHLVHHHHHHHHLGNGTLVPRASPEIQDNDANGSRRLMPPSTP 540
Db 481 SCTSRRLSVNHLVHHHHHHHHLGNGTLVPRASPEIQDNDANGSRRLMPPSTP 540
QY 541 TPSSGPPGASVHSFYADCHLEPRVCOAPPPOCPSPASGRTGSGVYTVITSPPE 600
Db 541 TPSSGPPGASVHSFYADCHLEPRVCOAPPPOCPSPASGRTGSGVYTVITSPPE 600
QY 601 ILKDALVAVAPSPGPPLTSTFNPFPSSMHKLLTQSTGACHSSCKISSPCKADSG 660
Db 601 ILKDALVAVAPSPGPPLTSTFNPFPSSMHKLLTQSTGACHSSCKISSPCKADSG 660
QY 661 ACPGSPCYCARTGAGBPESADHVPDSDSEAVYFTQDADHSDLRDHSRRRQSLGPD 720
Db 661 ACPGSPCYCARTGAGBPESADHVPDSDSEAVYFTQDADHSDLRDHSRRRQSLGPD 720
QY 721 AEPSSVLAFWRLICTDFRIYDSKFGGIMAILVNTLSMGIEYHEQPEELTNALEISN 780
Db 721 AEPSSVLAFWRLICTDFRIYDSKFGGIMAILVNTLSMGIEYHEQPEELTNALEISN 780
QY 781 IVFTSLFALEMLLKLVTGPEGYIKNPINIEDGVTVISWEIYGQGGGIVLRTFRLM 840
Db 781 IVFTSLFALEMLLKLVTGPEGYIKNPINIEDGVTVISWEIYGQGGGIVLRTFRLM 840
QY 841 RVLKLVRELPALOROLVYMKTMNVAFQMLMFIIFSTILGMHLFGCKFASRQDGT 900
Db 841 RVLKLVRELPALOROLVYMKTMNVAFQMLMFIIFSTILGMHLFGCKFASRQDGT 900
QY 901 LPRKRFSDLMAIYVFOILTOEDMNKVLVNGMASTSMALYFIALMTEGNYVLEML 960
Db 901 LPRKRFSDLMAIYVFOILTOEDMNKVLVNGMASTSMALYFIALMTEGNYVLEML 960
QY 961 VALIVEGFOAEIIGKREDSGQLSCLQLPVNSQGDATKSESEPPFPSPVDGDDRRKR 1020
Db 961 VALIVEGFOAEIIGKREDSGQLSCLQLPVNSQGDATKSESEPPFPSPVDGDDRRKR 1020
QY 1021 LALVALGEAEELRKSLPLLIHTAATPMSLPKSSSTGEGALGSGSRTSSGSAEAGA 1080
Db 998 LALVALGEAEELRKSLPLLIHTAATPMSLPKSSSTGEGALGSGSRTSSGSAEAGA 1057
QY 1081 AHHEMKSPSARSPSPSAAASWTSRRSSRNSLGRAPSLKRSBPSGERRSLSGEOE 1140
Db 1058 AHHEMKSPSARSPSPSAAASWTSRRSSRNSLGRAPSLKRSBPSGERRSLSGEOE 1117
QY 1141 SODEESSSEDRASPAGSOHRHRSLEERAKSFDLPDLOVPGIHRASGSSASEHD 1200
Db 1118 SODEESSSEDRASPAGSOHRHRSLEERAKSFDLPDLOVPGIHRASGSSASEHD 1177
QY 1201 CNGKSASGLARTLRTPDDQOLDGDDNDGNTLSKGERIQAWYRSRLPACCRERDSMAVI 1260
Db 1178 CNGKSASGLARTLRTPDDQOLDGDDNDGNTLSKGERIQAWYRSRLPACCRERDSMAVI 1237
QY 1261 FPPQSPRLCHRIITTHKMFDAVYVYIFLNCITTIMERPKIDPHSAEKLFTLSNYFT 1320
Db 1238 FPPQSPRLCHRIITTHKMFDAVYVYIFLNCITTIMERPKIDPHSAEKLFTLSNYFT 1297
QY 1321 AVFLAETVYVVALGMOFGFOAYLRSSMWVLDGLVLIVISIDIVSMVSDSGTKILGMR 1380
Db 1298 AVFLAETVYVVALGMOFGFOAYLRSSMWVLDGLVLIVISIDIVSMVSDSGTKILGMR 1357
QY 1381 VLRLRLRLRLRLVISAQGLKLVETLMSLKPIGNIVYICCAFIIIFGILQVLFKGF 1440
Db 1358 VLRLRLRLRLRLVISAQGLKLVETLMSLKPIGNIVYICCAFIIIFGILQVLFKGF 1417
QY 1441 FVCGGEBTNRITKSDCAEASYSRWYRKXNFDMGLMSLFLVASKDQWMDIMDGLDA 1500
Db 1418 FVCGGEBTNRITKSDCAEASYSRWYRKXNFDMGLMSLFLVASKDQWMDIMDGLDA 1477
QY 1501 VGVDOOPIMHNMPLMLYFISFLIYAFVLNMFVGVVVENFKRCQHOEEBARRREK 1560
Db 1478 VGVDOOPIMHNMPLMLYFISFLIYAFVLNMFVGVVVENFKRCQHOEEBARRREK 1537
QY 1561 RLRLERKRRLMLDVIASGSSASASEAQCKPYISDYSRFLVHLHCTSHYLDLFTT 1620

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Db 1538 RLRLERKR-----SKEMAEAQCKPYISDYSRFLVHLHCTSHYLDLFTT 1586
QY 1621 GYIGLVNVTMAEHYQOQOILDEALKICNYIFTYVFESEYFKLVAEFGFRFODRNQOL 1680
Db 1587 GYIGLVNVTMAEHYQOQOILDEALKICNYIFTYVFESEYFKLVAEFGFRFODRNQOL 1646
QY 1681 DLATVLSMGITLIEIEVNASLPINPTIIRIMRVLRLARVLKLLKMAVGARALDVTMQ 1740
Db 1647 DLATVLSMGITLIEIEVNASLPINPTIIRIMRVLRLARVLKLLKMAVGARALDVTMQ 1706
QY 1741 ALPOVGNLILFMLELFFIFALGVELFDLECDETHPCGELGRNATERFNGMAFLTFRV 1800
Db 1707 ALPOVGNLILFMLELFFIFALGVELFDLECDETHPCGELGRNATERFNGMAFLTFRV 1766
QY 1801 STGDNNNGIMKTOTLRDCODESICNTVISPITYFVSFVLTAQFVLVNVYIAYMKHLESN 1860
Db 1767 STGDNNNGIMKTOTLRDCODESICNTVISPITYFVSFVLTAQFVLVNVYIAYMKHLESN 1826
QY 1861 KEAKEAELEAELEEMKTLSPQPHSPLSGPFLMPGVEGVNSPDSKPGAPHTTAHIGAA 1920
Db 1827 KEAKEAELEAELEEMKTLSPQPHSPLSGPFLMPGVEGVNSPDSKPGAPHTTAHIGAA 1886
QY 1921 SGFSLHPTWVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSTYCRNGSTAERSLGHRG 1980
Db 1887 SGFSLHPTWVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSTYCRNGSTAERSLGHRG 1946
QY 1981 WGLPKAOSGILSVHSOPADTSCIIOLPKDVHYLLQPHCAPWGAIPKLPFGSPFLAOR 2040
Db 1947 WGLPKAOSGILSVHSOPADTSCIIOLPKDVHYLLQPHCAPWGAIPKLPFGSPFLAOR 2006
QY 2041 PLRQOAIKRTSDLDVGLSREDLSEVSGPCPLTRSSSFGGSSIOVQORSIGIOSKYS 2100
Db 2007 PLRQOAIKRTSDLDVGLSREDLSEVSGPCPLTRSSSFGGSSIOVQORSIGIOSKYS 2066
QY 2101 KHIRLPPCGELPSPNAKDPETRRSLLEDTLSMTSGULPSSGEBPLSPDKKCYSV 2160
Db 2067 KHIRLPPCGELPSPNAKDPETRRSLLEDTLSMTSGULPSSGEBPLSPDKKCYSV 2126
QY 2161 ETQSCRRRPPFWLDEORRHSHIVASCDSGQPLCSPSLGGQPLGGRGSPKKLSP 2220
Db 2127 ETQSCRRRPPFWLDEORRHSHIVASCDSGQPLCSPSLGGQPLGGRGSPKKLSP 2186
QY 2221 SISIDPESSGSRPPSPGVCLRRRAPASDSKDPVSSPLDSTAASPEKKTLSLGLS 2280
Db 2187 SISIDPESSGSRPPSPGVCLRRRAPASDSKDPVSSPLDSTAASPEKKTLSLGLS 2246
QY 2281 SDPTDMDP 2288
Db 2247 SDPTDMDP 2254

RES:LT 2
115638
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C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: 115838
R:Minx, P.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C54D2.
A:Reference number: Z18415
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A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1657 <MIN>
A:Cross-references: EMBL:U07548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C5
A:Gene: CESP:C54D2.5
A:Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3;

Query Match 28.4%; Score 3546.5; DB 2; Length 1657;

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Best Local Similarity 41.8%; Pred. No. 3e-201;  
Matches 810; Conservative 240; Mismatches 450; Indels 439; Gaps 45

[illegible]

Db 924 -----KRLQEDAPKQANVEEDERKRELELT-----IAATTS- 957

QY 1042 IHTAATPMSPKSSSTGVGALGSGSRRTSSGSAED--GAAHENKSPSARSSPHSP 1098

Db 957 -----AFNNGVAPAECTCORPSSPEESPRLLSANYH----- 990

QY 1099 WSAASWTSRRSSRNSLGRAPSLKRRSPSG-----RRSLSGEGESQDEESSSEEDRA 1153

Db 990 -----PSPERKHSANLDAIITDKRLVL-----RNSAPFDR- 1019

QY 1154 SPAGSDHRRHSGSLEREAKSSFDLPDTLOVPGLHRTASGRSSASEHODCNKASGLIART 1213

Db 1019 SPV-SEGRRDSSRLNRHA--SLVLPVANGV-----YRRQRVHSWKASQGLKQA 1063

QY 1214 LTRDDQGLQDDDDNDGSGNLSKGERIQAWYRSRL-PACCPRRDSWSAIIYPPQSRFLLCH 1272

Db 1064 LAEEKRNEKQKQ-----TFWRKLKTKTCLNHRFEESFLMGPKPKRLIKCL 1110

QY 1273 RIITHMFDPHVLLVLIIFLNCITIAMERPPIIDPASAERIFLTSSNYFTFAVFAETMVKV 1332

Db 1111 OTQOKKGEVDYVLFEGINCITILAMERSPLPDSFERQGLHISGILFTYIIFGEMAK-- 1169

QY 1333 ALGMCGEQAYLRSSNNVLDGLLVLIISVIDLVSWSDSGTIKLGMRLVRLFLRLPLR 1392

Db 1169 ----- 1169

QY 1393 VISRAQGLVLETTLMSSLPKIGNIVICAFPIIFGILGYOLFKEFPVCGEDIRNT 1452

Db 1169 -----VSHRIPTLPKIGNIVLTICTFTPIIFGILGYOLFKEGMATHCIGPEGNVT 1217

QY 1453 NMSDCASIR--VWRHKTNPDLGOALMSLFVLASKDGVMDIMTDLDAVGVDQOPIIN 1510

Db 1218 TADICIE-DYRKWVNHRRYFNPNLGOALMSLFVLSKDGWASIMYGIDAVGVQPIEN 1276

QY 1511 HNFPMILYFISFLIYAFVLMFVGVVYVENHFKRQHOHEEERAKREKRLR----- 1565

Db 1277 YNEMRIYITSELLVGFVLMFVGVVYVENHFKRKEALEKMREREKRLRLKLRK 1336

QY 1565 -----LEKRRNLMLDDVYASGSASAEAOCKPEYSDYSRFLVHLNLCSTHLDPT 1619

Db 1337 FEESMAGKKRRKRI--VWAGSAIKSIFSEVENYPIYHYGTRFLFHLIIVYSKFDLAI 1393

QY 1620 TGVIGINVTYAMEMHYQOPIIDLEALKICNTFTYIYVFESYFKLVAFGRFFEDRMO 1679

Db 1394 AAVTIGINVTSMEMHYQMPMGKLYVKALNFVTLFLEAMKLIALGFRKFFIEKMR 1453

QY 1680 IDLAVVLISIMGITLEEIEVNASLFINPTIIRIMAVLRARVLRKLKMAVGRALLDVM 1739

Db 1454 LDMFVILLISAGIIFEEPEA-DELPINPTIIRYMYVLRARVLRKLKMAKAGIRSLDVG 1512

QY 1740 QALPOYGNLGLLMLLFFLIFALGVLEFGDECDETHPCBGLGRHATFRNFGMAFLTFR 1799

Db 1513 EALPOYGNLGSLEFLFFLIFALGVLEFGKLECSDEHPCDGLGEHAHFKNFGMAFLTFR 1572

QY 1800 VSTGNMNGIMKDTLR-QCD-----QESTQNTVYISPIFYFSVLTAAQVLYVNYIVLM 1853

Db 1573 IATGNMNGIMKDALRDCDSDSHCETNCVDPILAPCFVIFVLISQFVLNVVAVLM 1632

QY 1854 KHLSESNKEAEAELEAE 1872

Db 1633 KHLSESN--KRDAEPAE 1648

RESULT 3

A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively sp

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Sep-1998

C:Accession: A42566

R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patchi, S.; Smirson, S.; Maroufi, A.;

Science 257, 389-395, 1992

A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-

A:Reference number: A42566; MUID:92335886

A:Accession: A42566  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-2339 <NTL>  
 A:Experimental source: IMR32, hippocampus  
 A>Note: sequence extracted from NCBI backbone (NCBIP:109168)  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.8%; Score 1714.5; DB 2; Length 2339;  
 Best Local Similarity 24.1%; Pred. No. 5.9e-93;  
 Matches 644; Conservative 379; Mismatches 833; Indels 811; Gaps 91;

QY 27 GAGGAGGCGSTGKDPGADSEAEGLPYPALAPVF-----FYLSQSSRP 70  
 DB 25 GAGGAGGCGPGGIGPGRVLYKQSIQARATMALNPVKNCFYVNSLFESEDDVV 84  
 QY 71 RSMCLRTVCNPFEEVSMVLVLLNCVTLMFPCEDICDSQRCRIQAQD---FTFAF 127  
 DB 85 KRYAKRTIEMPFEEYMLATITIANCIYAL---EQHLDPDGKTMSERLDTEPFYIGI 140  
 QY 128 FAVENVYKVALG-IFGKCYLGDITWNRIDEFTIAGMLETS--LDLQNSFSKATVR 183  
 DB 141 FEFEGIKITIALGFVFKHSYLRNGMNWMEFYVLTGILATAGTDFDLR-----TLRAVR 195  
 QY 184 VLRPLAIRVPSMRLITVLLDITLPMIGNVLLCFEVEFFIGIVGQVLMAGLLRNCFEL 243  
 DB 196 VLRPLKLVSGIPSLQVLYKSIKRAVAPLQIGLLFFAILMFAITGLTEFGKRRKACF- 255  
 QY 244 PENFSLPLSVLDEPYQOTENEDESPPICQPRENGMRSQSVPTLRGEGGGPCSLDYE 303  
 DB 255 -----PNSTDAEPV-----GDFPCQKRAP 273  
 QY 304 TYNSSNTTCVNMNOYITNCSAGENHPFGAINFENIGYAMAIQVTTISGNDIMFV 363  
 DB 274 ARLCBEGTEC---REYWP-----GPNFGITNFNILLFALTIVQCITMEGMDILYNT 323  
 QY 364 MD-AHSFYNFYIFILLIIVGSEFMILCLVATIGFOSFETKQRES-----QLMRQORAF 416  
 DB 324 NDAGNTMMLVFTIILIGSFFMLNLVIGVSGEFAKREVENRRAFKLRQOQIE- 383  
 QY 417 LSNASTIASFSEPGSCYEELLYLYYLKKAARLAQVSRALGVAGLLSPFVARSQGP 476  
 DB 383 -----RELNGYLEWIFKAEMEVLAEED-----RNAEEK 410  
 QY 477 QPBGCTRGHRLSVHNLVHHHHHHHNLGTLRVASPELQDRDANGSRRLMP 536  
 DB 411 SPLDLVLRATKRSNDLH-----AEEGDRPAD----- 441  
 QY 537 PSTPTSGGPPRGAEVSHSFYHADCHLEPRVQAPPPRCPSEASGRTVSGKVPYVHTS 596  
 DB 441 ----- 441  
 QY 597 PPELLIKALVEADSPGPPTLTSNIPPGPPSMKLLFTQSGACHSKKISSPCK 656  
 DB 441 -----LCVGSPPAR 450  
 QY 657 ADGAGGPPSCPCARTGAGEPESADHVMPDSEAVYFTQDAQSDLRDPSRRORS 716  
 DB 451 AS-----LKSGETSSSTF-----RRKEK- 470  
 QY 717 LGPDAESSVLAFWRLICDFFRKIVDSKYFGINGIMAILVNTLSMGIYHEQPEELTNAL 776  
 DB 470 -----MFRFF-----IRRWAKQSFYVWVLCVVALNLTLCVAMVAYNOPRLTTL 514  
 QY 777 EISNIYFTSLFALMLKLIVGPGYIKNPYIEFGVIVISYWTIVG---QGGG--GL 831  
 DB 515 YFAEFVFLGFLTEMSLKMGLGRSRFSRSSFCEGVIYGVSEFVWMAIKPGGSFGI 574  
 QY 832 SVLRTEPLMVLVLRPLRLQLOQLVLMKTQNVNATFECMLMLFFIISILGMLFGCK 891  
 DB 575 SVLRALRLKRIEYVTYKWSLRLVYSLNSMKSITSLFLFLFIVFVALLQMLQFGQ 634

QY 892 FASERDGTLPDRKNFDSLMAIVTFQILTOEDMNKVLNGM-----ASTSSMAALYFI 946  
 DB 635 YNFODETP-----TFDFPRAILLVFOILIGEDMNAMVYIGISQGVSKGMSSEFYFI 690  
 QY 947 ALMTGNYVLFNLVAILVEGF-QAEITGK---REDASGO-----LSCI 986  
 DB 691 VTLFGNTYLLNVFLAIVANDLANAOELTKDEEEMEAANOKLALOKAKEVAEYSPMSAA 750  
 QY 987 QLPVNSQGDARKSESDPEFSPSVGDGDRKRRLALVALGEHAELEKSLPPLIHPTAA 1046  
 DB 751 NISIAHQNSAKASVWE-----QASQRLNLNLASCEALYSEMDPEERLFA 800  
 QY 1047 TPLSLPKSSSTGVGE---ALGSGSRRTSSSGSAPPGA-----HH---EKMS 1087  
 DB 801 TTRHLRPDKTLHDLRLVYELRGDARGVGGKARPEAAEAPGVDPRRHRRHDKDT 860  
 QY 1088 P-----PSANS---PASPMSAASMTSRSSNSIGRAPSLKRSPS 1127  
 DB 861 PAAGDODRAEAFAKAESEGEAREERPRRSHSKAA--GPPAASERGRG---GPE 913  
 QY 1128 GERSSLLSGEGODEE-----ESSEDRASPAGSDHRHRSGLS---REAKSSF 1174  
 DB 914 GGRHRRRSPPEAAREPRRRRAHRHQPSKECAGANGERARRHRRGPPRAGPREAEG- 973  
 QY 1175 LEPDTLQVPG-LHRTASGRSSASE--HODCNKSASGLA-----RTLRTDDPOLDG 1223  
 DB 973 -----EPPARRRRARHKAQPAHEAVEKETTEKAEIYEADEKKELELNHQPREDH 1026  
 QY 1224 DDNDGNSLKSERIOAWRSRLPACRRER-----DSW----- 1257  
 DB 1027 CDELTGTYVGP-----MHTLPSTCLQKEQEPEDADNORNTRMGSQPPDPYTHI 1080  
 QY 1257 -----SAYTFPQSRFR 1268  
 DB 1081 PVMLTGPBLGATVPSGNVDLSQAQKEVEADVWMSGRPIYPSMFCPLSTNLLR 1140  
 QY 1269 LICHRIITRKEDVVLVYIFLNCITIAMERKIDBSAEKIFLLSNITFNAVLAEMT 1328  
 DB 1141 RCHYIATMYFEVVLVIALVIALSSIALAEDP--VRTDSPRNALVLYDITFPGVTFEYV 1199  
 QY 1329 VKVYALGWCGBQAYLRSSSNVYDGLVLYISYDILYSVW--SDSGTKILGMLRVRLRT 1387  
 DB 1200 IKMIDGLLHPGAYFRDLNLIID---FIVSGALVAFAFGSKGKQINTKSLRLRV 1255  
 QY 1388 LRPLRVISRAQGLKLVETLMSLRPGINIVYICCAFIIIFIGLYOLEKGFYVQGE- 1447  
 DB 1256 LRPLKTIKRLPKIKAVFDCVNSLKNVLMILLYUMFIFAVIAVQLRGKFFCYTDES 1315  
 QY 1447 -----DTRN--TINKSDCAEASTR--VVRHKYFNEDNLGQALMSLFVYASDQGVNDIMYDL 1498  
 DB 1316 KELEPRDGRGYLDYEKEEYVAQPRQWKYDFHDVNLMLTLFTVSTEGMPVRLKHSV 1375  
 QY 1499 DAVGVDDQPIAMNHPMLLIFSLITLVAFFVLMFVGVVENFHKROHEEARRE 1558  
 DB 1376 DAYTEEGPSPGRMELSTIYVYFVFFFYFNIAIILLITF-----QGGQKVMS 1429  
 QY 1559 EKRLRLERKRRRLMDDVVIASGSSASAASEAQCKPY--YSDSYR--PRLVHHILCTSHY 1614  
 DB 1430 -----CSLEKNER-ACIDFALSA-----KPLTRYMPNROSFOYKWTFFVSP 1472  
 QY 1615 LDLFITGVITGLNVTAMMEHYQOPILDEALKICNTIFVIYFESVFLVAFGFRFPQ 1674  
 DB 1473 FEYFIMAMIALNTVYLMKKYDAPYEYELMLKCLNTVFTSMSECVLTIKFAGVLYNTR 1532  
 QY 1675 DRMNQDLAIVLISMGITLEET-EVNASLPIPTIIRIVRILARVILKLMAYGMA 1733  
 DB 1533 DAWNVPDPVYVLSGITDILVTEIAETN-----NFIMLSFLRLRARARILKLRQGTIRI 1587  
 QY 1734 LLDFTVQALPQVGNLGLFMLEFFIFAPALGVELFGDECEDETHPCGLGHATFRFGNA 1793  
 DB 1588 LMTFVQSFKALPYVCLLIMLFEIYAIIGQVFGNIALDDD--TSINRHNHFRTELOA 1644  
 QY 1794 FLTLFRVSTGDNMNGIMKDLRD--CDQE--STCYNVIVISPIYFVSLTAQVVLNVVI 1849



Db 1645 LMLFSAATGEANHEIMLSLSSNACDEQANMAEDCGSDFAFFVFSITFLCSLMLNFV 1704  
QY 1850 AVLMKHLSEENKAK-----EEALEALE-----LEM-KTSLSPQHSPL 1888  
Db 1705 AVIMDNFEYLTROSSILGPHHLDEFIRVMAEYDPAACGRISYNDMEFLKHMSP---PL 1760  
QY 1889 G-----SPLMGVEGVNSPPDSPKPGARPTTHAHIGAAFSLE-----HPLMPV 1932  
Db 1761 GLCKKCPARVAAYRLVRMKNPISNEDTTHFTSLMALRTALEIKLAPQATKOHODAE 1820  
QY 1933 HPEEVPV-----PLGPDLLTVRKSGVSRTHSLNDNSYMCNNGSTARSAG 1977  
Db 1821 LRKEISVYMANLPQKTLDDLVPYHKPDEMTYGVYAA--LMLFDY--KONKTTDQHQ 1875  
QY 1978 HRGWGLPKAOSGSLSVH-----SQPA-----DTSCILQ-----L 2007  
Db 1876 QAPGGL--SQMGVSLFHPFLKATLEQTPAVLNGARVFLRKSTSLNSGATQNESGI 1933  
QY 2008 PKVYHLLQ-----PLGAPTWGAIPKLPYRPGSRPLAQRLRQAALRTDSLDVQ----- 2057  
Db 1934 KESVSMOTQRTODAPRHA-----RPLERHGSTIEIPVGRGAL--AVDQOMOSITR 1982  
QY 2057 -----GLGSRBDLS--EWSGRCPLTRSSFSWGSGSIQVOORSGIQSVSKHIL 2105  
Db 1983 RQDPQEPQGLSEQQAASMPRLAETQPYTDASPMKRISITLQAPRG-----THLS 2036  
QY 2106 PAPCPGLEFSMAKDPPEITS-----SLEDTELSTWISGDL 2140  
Db 2037 TTP-----DRPPSQASHHHHHRRDRKORSLKPGSLSDMDGAPSSAVGPG 2088  
QY 2141 LPSQOEPLSPDLKKCYEVETQSCRRRPGSNLDEGRHSIAVSCLDSSQPLCPSPS- 2200  
Db 2089 LPPGEQPTQCRKRERKQERKSGQERKQPSSSSEKQRP--YSCDRFGGREPKPKPSL 2145  
QY 2200 -----SLGQGPL-----GPGGSR---PKKTLSP-PSIS- 2224  
Db 2146 SSMPTSPTAGQEPGRPHQSGSVNSPFLSTGSASTPGGQGRQLPQTLLTPRPSITTYT 2205  
QY 2224 -----IDPESQSGSRPCSPG-----VCLRRAPASD-----SKDPSSVSPLD 2261  
Db 2206 ANSSPIHFQAQOTSIPAFSPGRLSRGLSEHNALLQDPLSLQPLAPSRIGSPYIQGRAD 2265  
QY 2262 STAASPSKKDTLSL-----SGLSS 2281  
Db 2266 SEASVHALPEDTLTEEAAYVNSGRSS 2292

RESULT 4  
S29236  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 13-Jan-1993 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
C:Accession: S29236  
R:Ridome, T.; Kim, M.S.; Friedlich, T.; Morl, Y.  
FEBS Lett. 308, 7-13, 1992  
A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit  
A:Reference number: S29236, MUID:92354772  
A:Accession: S29236  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2259 <NT>  
C:Cross-references: EMBL:X67855, NID:q1472, PID:CAA8040.1, PID:q1473  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C:Keywords: transmembrane protein

[illegible]

QY 1065 SGRSRTSSGSAEPGAHHEKSPPS--ARSSPHSPWSA-----ASSMT--- 1107  
 DB 842 KCEBHSVRSGSLGALDCQ--RSPSLSGRREP--PWLARCHGNCBPALQETGGEIVVT 898  
 QY 1107 -----SRRSRNLSGRAPSLKRRSPGERSLLSGGQESQDDEESSEDRASPAGSDH 1160  
 DB 899 FEDARRHOSORRSHRRVTRTEAKESSASRS-----RSVQSERLDEGASTEGGRDH 951  
 QY 1161 RHRGS-----LEREAKSSFDLPDTLOYV-----GLHRTAS-----GRSSA 1195  
 DB 952 EARGSHGKEPTIHEEERAOQLRRTDSLMVPGKSLAGLDEAGTPLYLSPEGVKEEA 1011  
 QY 1196 SEHODCKSKASGR-----ARTLRDTPOL-----DQDDD 1226  
 DB 1012 PTEGHADSGEPALGHVOLDVGRALISQSEPDLSCTATDTKVTTESTDVTVAIPDEPL 1071  
 QY 1227 NDE-----GNLSKGE-----RIQAWVRSLPACCREDSWSA--YIFPQSR 1266  
 DB 1072 VDSIVVHIGNKTDESPFOEAEMKEAQETEKOKKRRAPASGKAMPHSMSIFSTSNP 1131  
 QY 1267 FRLCHRIITHKMDHVVLIIIFLNCITIAMERKIDPDSERIFLISNYITFAVLA 1326  
 DB 1132 IRRACHYVNLRYFEMCILLVYASSIALAEDPVLINSENRV--LRFYDYVETGVTFE 1190  
 QY 1327 MIVKVALGCEGEQAYLRSSNNVLDGLLVLSVDI--LVSMVSDSGTKILGMLRVLRL 1385  
 DB 1191 MVIKMIIDGLLIDSGSYFRDLMNIIIDFVVVGVVAVGALAFALNALGTNGKRDITKISRLV 1250  
 QY 1386 FRLRLPVRISRAQGLKLVETELMSLKPIGNIVVICAFFIIFGILGVOLEKGFVC-- 1444  
 DB 1251 RVLRLKTKIKRPAKAVPCDVITSLKNVFNLLIYKLFMFIVAVIOLFKGFEFCTD 1310  
 QY 1444 OGEDTRN-----ITNKSDCAEASTR--VWRKYNFNDICGLMSLFVYASGDVNDIMYD 1496  
 DB 1311 SSKDEKEKIGNYVDHEKMKMEVKEGKREKRFHFHNDIMALLTLFTVSTEGEPVYLOH 1370  
 QY 1497 GIDAVGDOOPRLMNNHNPWMLLFISFLILVAFVNMVGVVVEFHCKRQHOEEER 1556  
 DB 1371 SYDVTEEDGSPRSNKMENSTIYVYVFVFFEFYVNIITVALIITF-----OEGDKM 1423  
 QY 1557 REEKLRLLEKRRRLMDLVIVASSSASASEAOCKPY--YSDYSR--FRLVHLHLCST 1612  
 DB 1424 MECSL-----EKNERACIDFALISA-----KPLTRYMPQNRHTFYRWHEFVS 1467  
 QY 1613 HTLDLFTIGVIGLVNTYAMMEHYQOPLIDELKATCNITFYIVFVESVFLVAFGRFR 1672  
 DB 1468 PSEFYTIMAMIALNTVLMKXYSACTYELAKYLNTIAFTWVSECVLVIAEGFVNY 1527  
 QY 1673 FODRNNQDLALVLLSIMGITLEEIEVNASLPINPTIIRIMRLVRIAVLKLKMAVGM 1732  
 DB 1528 FROTNWIFPITVIGSITITVITLDSKIVNTTFPNMSFLKFLPA--ALLIKILRGYIR 1584  
 QY 1733 ALLDTYMAQLPOVNGILGFLMLFFLFAALGVELFGDECD--ETHPCBGLGHATERNFG 1791  
 DB 1585 ILLMTFVQSKALPYVCLITIAMFLFYAIIAGVGNIRLDESH-----INRHNFRSFF 1640  
 QY 1792 MAFLIFRSTGDNNGIMKDTL--RDCC-----QESCTYNTVSPITFYVSFVLA 1840  
 DB 1641 GSIIMLFRSATGEAWOELMISCLGKCEPDTTASGQESERCGTDLAIVYFSIFTC 1700  
 QY 1841 OFVLVAVVAVLAKMLHEENKEAK-----EEALEAELE-----LEMRTL 1880  
 DB 1701 SFMLMLFAVAVIMDNFEYILROSSILGRHIDEFVAVMAEYRAACGRHYHEMMLTL 1760  
 QY 1881 -SPQHPSPUG-----SPLMPGVEGVNSP-----DSPKPAHTTAHTGAASG-- 1923  
 DB 1761 MSP-----PLGLGRKSPSKAAYKRYLVLMNPVADMTVHTSTLMALIRIATLIDIKIAKGA 1816  
 QY 1923 -----FSLHPTMV--PHPEE-----VPVPLGPDLLVRRKSGVSRHSPLSNDSYMCRN 1968  
 DB 1817 DRQQLDSELOKETLAIWPHLSQKMDLLVMPRASD--LTVGKIYAA--MMIMDIYKOSK 1872

QY 1969 GSTAERSLGHGWGLPKAOSGSLSVHSOPADTSCILIPKDYVILLQPHGAPTGAIPK 2028  
 DB 1873 YAKORROL-----EQKNAPMFQRMPEPS-----SLPGEI--INAKALP--CLPQ 1913  
 QY 2029 LPP-----PGRSLPAQRLPRLROAIIPTD-----SLDVQGLGSRDLISLEVSG 2070  
 DB 1914 GPAPLGRSGCPAPMSPLSQIFOLTCMDPADDDGOFQEOBRSVLVTPDSRRRSFTIR 1973  
 QY 2071 PSCPILTRSSFW-----GGSSIOVQORSIGOS--KVSKHILPAPCPGLEBSMAKDP 2120  
 DB 1974 -----KRRSSSWLEEFSEKRSNDNTYKRRKSYSLSLSAH--RL----- 2013  
 QY 2121 PETRSLDELTELSWISGDLPLSSQOEPLSPRDLKCYVETQSCRRRPGSWLDEQRHS 2180  
 DB 2013 -NSDGHKSDTHRSQ--GREGRSKREHLLASADYSRCSEE-----RGAQADM--DSPERH- 2065  
 QY 2181 IAVSCIDSGSOPRLCPSPSSSLGOLGPGSPRPKKLSPLSISIDPESQSRPCPGV 2240  
 DB 2065 -----PSRPSGSRGSPSPROGTGSLSESLSPSVSDISTPRHSRQLPVPV-- 2112  
 QY 2241 CLRRAP-----ASDKDPS--VSSPLD-----STASPSPKKDTLSGLSSDPTMDPVL 2290  
 DB 2112 ---KRPPLISTSLKQPSNFSPPADSGGSLAPLESNOYGL-----PESSD--- 2160  
 QY 2291 PTLPHLSPGADPSSASWAFLKSPTAASSHEAPLPSVAAGDDEONF 2340  
 DB 2160 -----SPRRAQSHASPORIYSEPYLA--LHEDSH--ASDCGEETLTF 2199

RESULT 5  
 S41080  
 calcium channel alpha-1 chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
 C:Accession: S41080  
 R:Copolia, T.; Waldegg, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; La  
 FERS Lett. 338, 1-5, 1994  
 A:Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Eviden  
 A:Reference number: S41080; MUID:94139884  
 A:Accession: S41080  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-228 <COP>  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match: 13.5%; Score 1688; DB 2; Length 2288;  
 Best Local Similarity 24.3%; Pred. No. 2,1e-91;  
 Matches 648; Conservative 368; Mismatches 793; Indels 854; Gaps 99;

QY 27 GAGRGPGSTKEDPGSADSEAGLPPYALAPVF-----FYLSQDSRP 70  
 DB 25 GAGGAGPGGGGLPGQRLVYKOSIAQARATMALNPIPVKNCFTVNRSLVFSEDNV 84  
 QY 71 RSMCLRTVCNPMFERYSMVLVILNCVTLGMRPCEDDIADSORCILQAQFD--FIFAF 127  
 DB 85 RYKAKRITTEWPPREYMIATIIANCIVLAL---DQHLPDGDKTPMSERLDTDEYFIGI 140  
 QY 128 FAVENVYKWAIG--IFGKACYLGDITNRLDPTVLAGMLEYs---LDLONVSFAVPTVR 183  
 DB 141 FCEBAGKITIALGFVHKSKSYLRNGMNVDEYVVLGLIATAGTDEDLR-----TLRAVR 195  
 QY 184 VLRLAIRINVPSEMLIVLLDITLPMGLNVLLCFEVEFIFGIVGVLAMGLNNRCFL 243  
 DB 196 VLRPIKVSGLPISLOVYVLSIMKAMVPLIIGLLEFALIMGIIIGLEBYMKFKACF- 255  
 QY 244 PENFSLPLSDLEPPYQOTENEDSPITCSQPRENGKRSRSPVTLRGEAGGCPSPSLDYE 303  
 DB 255 -----PNSDTDEPV-----GDFPGKDP 273  
 QY 304 TYNSSNTCTVNNNOYVNTNCSAGEHNPFGAIFNDIGYAMIAFOVITLGEAMVIMFV 363  
 DB 274 AROCDGDTCC--REIWP-----GPNFGITNFDNLLFAILLVFOCITMEWTDLIVNT 323



Db 2099 TSPAALEPAPHPQSGSVNGLMSTSGAITPGRGKROLQPLPRPSITITKANS 2158  
 Oy 2224 -IDPESGSRPPSPG-----VCLRRAPASD-----SKDPVSPIDSTAA 2265  
 Db 2159 PVHFEQSGSLPAPSPGRLSGLSEHNLKKEPLSQPLAPGSRGSDPYGLQDSEAS 2218  
 Oy 2266 SPSPKKDTLST-----SGLSS 2281  
 Db 2219 AHTLEPDLTTEEAVALNSGRSS 2241

RESULT 6  
 A45386  
 omega-conotoxin-sensitive calcium channel alpha-1 subunit rdb-1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Sep-1998  
 C:Accession: A45386  
 R:Dubel, S.J.; Starr, T.V.; Hell, J.; Ahlthjan, M.K.; Enyeart, J.J.; Catterall, W.A.;  
 Proc. Natl. Acad. Sci. U.S.A. 89, 5058-5062, 1992  
 A:Title: Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calcit  
 A:Reference number: A45386; MUID:92279265  
 A:Accession: A45386  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-2336 <DUB>  
 A:Experimental source: brain  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:104355)  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.5% Score 1678; DB 2; Length 2336;  
 Best Local Similarity 24.0%; Pred. No. 8.3e-91;  
 Matches 645; Conservative 364; Mismatches 826; Indels 846; Gaps 96;

Oy 27 GAGGROGPSTKEDPGSADSEAGLPPALAPVF-----FYLSQDSRP 70  
 Db 25 GAGGAGGPGGGLPQGRVLYKOSINQARMAVLPVKNQCFVRSLEFSEDMV 84  
 Oy 71 RSKCLRTVCNPFERYSMLVILNCVTLGMPEDDIACDSQKILQAFD--FIRAF 127  
 Db 85 RKYAKRTKMPPEEYMIITAIIVLAL---EQHLPDGDKTMSERLDTDEYFTGI 140  
 Oy 128 FAVEMVKKVVALG-IPGKCYLGDITWRNRLDFFIVAGMLEYS---LDLQNSFSAVRT 183  
 Db 141 FCEAGIKITIALGTFVHKSYLRNGNNVDFVVLLEIATAGTPEDLR---ILRAVR 195  
 Oy 184 VLRLPRAINRVSMLVTLTLLDTPMLGNVLLCFEYFIFGIVGVLMAGLRNCEL 243  
 Db 196 VLRLPLKVGISPLQVVLKSIKMAVPLQIGILLFFAILMFAITGLERYMKFRAQCF- 255  
 Oy 244 PEFNLSPLVLDLEPYVOTENEDSPFICQPRNGMRSCRSVPTLRGEGGGPCLDYE 303  
 Db 255 -----PNSTDAEPV-----GDFPGCKEAP 273  
 Oy 304 TYNSSNFTCVNNQYITNCSAGEHNPFGKAINFDNIGYAMIAIQVITLLEGVDMITFV 363  
 Db 274 ARLCDSDTEC---REYWP-----GPNFGITNEDMILFALLITVRCIMEMWTILYNT 323  
 Oy 364 MD-AHSFYNEFYILLIIVGSEFMNLCVIVATOFSETKORES-----QIMREQVRF 416  
 Db 324 NDAAGNTMNLWLYPIPLIISFEMNLIVGLVSGEFAKEREVENRRARLANRROOOLE- 383  
 Oy 417 LSNASTLASSEPGSCYEELTKYLVILKRAARLAQVRAIGVRAGLSSPVASGQEP 476  
 Db 383 -----RELNGYLEMTFKAEVYMAED-----KNAEEK 410  
 Oy 477 QP-SGCTSRHRLSVNHLVNNHHNNHHYLNGLTLRVPRASPELODRDANGSRRLMLP 535  
 Db 411 SPLDAVLAKRAATKSKRNDLH-----AEEGEDR----- 439  
 Oy 536 PSTPTPSPGPRGAEVSHFYADCHLEPVRCQAPPPRCPSASRTVGSQKVPYTVHT 595

Db 439 ----- 439  
 Oy 596 SPPPELTKDALVEYAPSPGPPTLTSFNIPPGPFSSMHKLETOSTGACHSKISSPCS 655  
 Db 439 -----FVLD-----CAAGSFA 450  
 Oy 656 KADSGAGCPDSCPYCARIGAGEPEESADHMPDSDSEAYEFTODAOHSDLRDPHSRROR 715  
 Db 451 RAS-----LKSQTESSSYF-----RRERK 470  
 Oy 716 SLGPDAPSSVLAEMRLICDTRFKYVDSYGRGIMIAIIVNTLSMGTEYHOPEBELTNA 775  
 Db 471 -----MREFL---IRRMVKAQSFYWVVLGVYALNTLCVAHVHYNQPLRTTA 514  
 Oy 776 LEISNFTSLALEMLTKLVYGEFYTKNPNYFIDGVIIVISWEIVGO-----QGGG 830  
 Db 515 LTFAEVFLGLLETKSLKMYGLGRSFRSSFCNCFDGVIGSIFEVYMAAIKPGTSFG 574  
 Oy 831 LSVLRTFRMLRYKLVRFLPALORQVLYMLKTMVNAVIFCMILMFIIFISILGMHFGC 890  
 Db 575 ISVLRALRLIRFKYTKYWNLSRLNVLVSLNSMKSIISLFLFLFVYFALLGQWLFGG 634  
 Oy 891 KRASEDQDTLPDRKNFDSLMAIVYQIITQEDMNKVLVNGM-----ASTSSMAIYF 945  
 Db 635 QFNFODEPT-----TNFDTPAAILTVQIITGEDMNAVMTHGISQGVSKGMFSFYF 690  
 Oy 946 IALMFGNYVFLNLAIVLVEGF-QAEIIGK---REDASQGLSCIQ----- 988  
 Db 691 IVTLTGNTLLNVLALAVDNLNARQELTKREEMEEANAKLQAKEVAEVSPMSA 750  
 Oy 988 -----LFPVNSQGG-----DATKSESEP----- 1006  
 Db 751 ANTSIAAROONSAKARSWEQARASQRLQNLRAQCEALYSEMDPEERLYASTRHVRDM 810  
 Oy 1006 -----FSPSVYD---DDRRKRLALVALGEAELEKSLPLPLIH-----TA 1045  
 Db 811 KTHMDPLVPEGRDGLRQPAQKSK-----PEGTETECADPPRRHHRDRDKTSA 863  
 Oy 1046 ATP-----MSLPKSSGTCVGEALGSGSRRTSSGSAPPGA-----AHHEMKSP 1088  
 Db 864 STPAGGRDQTDGPKAESIETGARERARPRRSHSKEA-PGADTOVRCBSRRHHRGSP 922  
 Oy 1089 PSA-----RSSPHSPMSAASWTSRRSSRSLSGRASLKRSPSGRRSLGEGE 1140  
 Db 923 EEAETERPRRRHRAHQDS-----SKQKETAVAL---VFKGRRARRHGRPTG 970  
 Oy 1141 SQDEEESSEDRASPGSDHRHRSLSREAKSGFDLPDTLOVPGLR-----RTASGRSS 1194  
 Db 971 PRETENSEPTR-----RHR-----AKHYPTLLEPPERVAEKESGVYEGDKE 1014  
 Oy 1195 ASEHOD---CN-----GKSAAGRLARTL--RTDDPOLGDDND----- 1229  
 Db 1015 TRNQKREPRCDLEAIATVGLVSLHMLPSTCLOKVDQBPADADQNRVTRMGQSOPDPSTT 1074  
 Oy 1229 -----EGNLKGERIQV-WRSRLPACCRERDSMSAVI--F 1261  
 Db 1075 VHYVVTLTGPPGEATVPSANTDLGQAEQKKEAEDVLRQP---RPIVPSYFEGCL 1131  
 Oy 1262 POSRFRLLRHRIITHKMPGHVVVLIIFLNCITIAERPKIDPESARFILTLSNYIFA 1321  
 Db 1132 SPVTLRFRCHYIYIMRYFEMVILVIALSSILAEDP-VRIDSFRNNALAKYMDITFG 1190  
 Oy 1322 VFLAEMTVKVALGWCGEQAYLRSSNNVLDGLVILISYDI-LYSMSVDSGKILGMIR 1380  
 Db 1191 VFTEFEMVKMIDGLLHPGAYFRDLNIIIDFIVSGALVAFAFSSFMGSKDKDINTIK 1250  
 Oy 1381 VLRLTLRLPLRVISRAQGLKIVETLMSLRKIGNIVYCCAFIIFGLIGVQLFKGF 1440  
 Db 1251 SLRLVRLRPLKTKRLPKRAVDCVNSLKNVLLIYLYMLEFIFAVIAQLKGF 1310  
 Oy 1441 FVCOGE-----DTRN---ITNKSQCAEASR-VWRHRYNFDNLGQALMSFLVASKDGV 1491  
 Db 1311 FYCTDESKELERDCRGYLDYEKEVEYDAPRQKKKDFHDVNLMLLTLFTVSTGEGMP 1370



QY 890 CFEASERDDTLPRKKNFDSLMLATVYFOLLQEDMKNVLYNGMAS-----TSSMALY 944  
 Db 641 GGFNFEE--GTPP--TNFTFPAITIVFOILGEDMNEVMNGIKSGGVNGMSVY 696  
 QY 945 FIALMTFGVYVFNLLVALVLEGF-QAETIGK-----REASGOLSCIO-----LTVNSG 994  
 Db 697 FYLLTFGVTLLNVLALVADNLAANOELTKEECEEALINOKHALAKAKVSPMSAG 756  
 QY 995 GDAATKE-----SEPDEFSPVDG-----DGD 1016  
 Db 757 FPETEFERRHKMSTWEARTSOLRRRMSSREALFTALGLBSRRYRRHRSILFEAE 816  
 QY 1017 RKRRLALVALGEHAEL---RKSLLPILIIHTAAPMSLPKSSST-----GYGELSGGS 1067  
 Db 817 SLRRLAEQQAESHQGEVGRREAFKRSRLRNWOPAGPKRSSIKVNGEOGRALGRSV 876  
 QY 1068 RRTSSGSAEPGAHHHEMSPPSARSSPHSPMSAASWTSRSSRSNLSGR-APSLKRSP 1126  
 Db 877 EAGASFRMAEPITARRRYS--LYEAKMGLSEASTLSRRPKKKEGRLLQOLCEOE 934  
 QY 1127 SG---ERRSLSGESES---ODEESESSEDRASPAGSDHRRHSGSLEREASSFDPDPT 1179  
 Db 935 SGGLTQTEPMVMDQGMKAFSWQGEPHSSMTPTPDVTD-PSGGLKESEGT---PEN 990  
 QY 1180 LQVPLGHLRTASGRSSASEHOD---CNGKSASGRLARILRTDD-----POLDGD 1225  
 Db 991 ---GKEESANTSEOVNEOSNMNLNLQINQATPGDRELTTGTTRDKODTQOEOTEIDVDC 1046  
 QY 1226 DNDP-----GNLSKGERIQAWVSRPLPACCRSDSMTAVIFPPQSRF-----R 1268  
 Db 1047 ENETTPMDSLVTON-----AYSS---SVKDEKSKRAIIPYTSMPLEFKTNPIR 1095  
 QY 1269 LILCHRIITRHKMFHYVLIIFLNCITIAMERPKIDPHASERILFLSNYIFTAFLAEXT 1328  
 Db 1096 RVCFIYINLTFEWCILLYIAASSVALAEDP-IHKDSANQVLYRYDFVTFGEFFEMV 1154  
 QY 1329 VKVVALGWCGEQAYILSSNNVLDGLLYLSVDI-LYSVWSGSKILGMLRVRLMT 1387  
 Db 1155 IKMIDIGLVHEGSYDFDVNNILDFIVSGALVAFATNIGSSSKDINTIKSLVLAIV 1214  
 QY 1388 LRLPRVIRSRAGKILVETVETMSLKPIGNIVYICAFIIFGLIGVQLFKGKFEVCOGED 1447  
 Db 1215 LRLPKTILKRLKAVFDVYSLKAVFNLLIYKLEMFIFANVIAQLFKGKFEYC--TD 1272  
 QY 1448 TRNITNKSDCAEASRYVRHK-----YNEDNLGQALMSLFVYASKGWDVMT 1495  
 Db 1273 SSKMT-KQDC-RGQFVLYRQRTKLSENGVNTTFHYDNVVALLLTFVSTGGMPOVLO 1330  
 QY 1496 DGLDVAVGDOOPTMNNHNPMLLYFISFLVAFVLMFVGVVNFHKCRQGESEEAR 1555  
 Db 1331 HSYVVTADQOPTPGNKMENSIFLYVVFPEFFVITFALIIITF-----QDQDK 1383  
 QY 1556 RREKRRLRLEKRRNMLDVLVJASGSASASEAOCKPY--YSDYSR--FRLLVHLCT 1611  
 Db 1384 MLEESSL---EKNERACIDPAISA-----KPLTRMPQRKQFQRYVWQFVY 1427  
 QY 1612 SHYDLITGYIGLVNVTYMAHEHQOQOLIDEALKICNTFYTYVYESFKVYAGFRR 1671  
 Db 1428 SPSEFYILTMIALNTVYLMKHHSPPGFASVYKMNIAFTITFTECLIKTIAGFELN 1487  
 QY 1672 FEODRMNOLDIAIYLLISMGITLEEIE---VNASLPINPIIRIMRVLRVARYKLKMA 1728  
 Db 1488 YFRSMNVDFVYVGSISEIYTECNKFEVNS-----FLKFRARLKLRLROG 1538  
 QY 1729 VGMRLDITVQAALPOVGNIGLFLMFLIFALGVELFGDLECDETHPEGLGRATFR 1788  
 Db 1539 ITRILMTFVQSPKALPYVLLIAMLFEIYALIGMQLFGNIGDHTP---INRHNFH 1595  
 QY 1789 NFGNAFLTFEVSTGDNWNGIMKDTL--ROCD--QESTCYNTVSPYFVSFLTAQFV 1844  
 Db 1596 TFFNALMLFRSATGESWQEIIMACTSGKECEGTREPC--GTDVAIFYFVSFIFLSCFLM 1654

QY 1845 VNVYVIAVMKHLSESNKAE-----BEAELEAELE-----LEMKTL-SPQ 1883  
 Db 1655 LNFVAVIMDNFEYLLTRDSSILGPHHLDEFVRYWAFIDYAAACGRHYHYDMYMLTMSF 1714  
 QY 1884 PHSPLG-----SPLMPGEGVNSP-----DSPKGAHPHTAHIGAAGSFLEHP 1928  
 Db 1714 ---PLIGKCKCPKVAVKRLVLMNMPVEDKTVHFTSLMGLIRALQIKLARGA---- 1767  
 QY 1929 TWPDPHEVYVPLGPDLLYKRSKVSRTSL--PNDSTYCNCRGNTAERSLGRNGLPKA 1986  
 Db 1767 ---DKQQLDAELRKEIMTWPLSQKTLDLLVPMHTY-----SDLTVG-----KI 1808  
 QY 1987 QSGSILSVHSGPADTSCITLQPKDVHYLLQPHGAPWGAIPKLPGRSPLAQR-----PL 2042  
 Db 1809 YAAIMNDYKOSKNNKYKQLQE-----QSRTPMQRREASGL 1847  
 QY 2043 RQQAIRTDILDY--QOLGREDLSEVSGPSCPLTRSSFWGGSIOYQOASGQSKVS 2100  
 Db 1848 PQLIISTKGLPYLQGTGTGPDVDSREFT-PLVPLPVMFOQGRSSQGEELHKQPKEL 1906  
 QY 2101 KHTLPAP-----CPGLEPSMAKDEPPTRSSLEL-----DTLSLWISGDL 2140  
 Db 1907 KTKLEYPHYGHYLIEMOGRAYSMPLLETESAEDTSPKRSISTTAHNSSTWLNES 1966  
 QY 2141 LPSQEEPLSPDLKCYSVETOSCRRPQSWLDEQRHRSIAVCLDSGQPRLCPSPS 2200  
 Db 1967 L-----ERAGPELTKRMS-----RRP-----LSPRS 1991  
 QY 2201 LGGQPLGPGSPRPKKLSPSISIT-----DPSESOG-----SRPPCSQVCLRRARA 2248  
 Db 1992 NAGSRENG-RSREKHLISERSYCSGQCAHPSQHRHLDQRLSRSP-SFGSHRREGV 2049  
 QY 2249 SDSKDPVSSPLDSTASPPPKDITLSGLSDPDMDVPLT-----LPHLSP--- 2301  
 Db 2050 NSSVS---ESPVSSTGSPKQGOLOPOTPSKPRPLVSYVAQRGVSGHCSMKCE 2106  
 QY 2301 ---GADPSASMAAFKSPTAASSHEAPH 2326  
 Db 2107 TRYQSLRQPSKALMS---ESPGRSRESEQH 2135

## RESULT 8

C54972 voltage-dependent calcium channel alpha 1E - mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #ext\_change 24-Sep-1999

C:Accession: C54972

C:Accession: M.E.; Matubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;

J. Biol. Chem. 269, 22347-22357, 1994

A:Title: Structure and functional characterization of neuronal alpha-1E calcium chan

A:Reference number: A54972; MUID:94350992

A:Accession: C54972

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-2272 <MIL>

A:Cross-references: GB:129346; NID:9522330; PIDN:AAA59206.1; PID:9522331

A:Notes: authors translated the codon AGG for residue 788 as Lys, and CCT for residue

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.4% Score 1670.5; DB 2; Length 2272;

Best Local Similarity 23.8%; Pred. No. 2.2e-90;

Matches 613; Conservative 398; Mismatches 850; Indels 717; Gaps 86;

QY 41 POSADSEA-----EGLPYALAPV-----FEY 63

Db 13 PSSGGDSDSRNKGCTVTPASGPAAYKOSKAORARTALYNIPYRONCFYVNSLFT 72

QY 64 ISQDSRPSWCILRTVCFNPFERVSMLVILNCVTLGMR--PCEDIACDSQRCRIQAFD 121

Db 73 FGEDNIVKRYAKKLIDWPFEYMIATITANCIVLALEQHLPEDDKTPMSR--LEKTE 129

QY 122 DFIAPFAVENYKVALG-IFGKKCYIGDTWRNLDFEYIAGMLEYSLDLQN--VSFSA 178









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Db 1251 RVLRLPLKIKRLPKLKAAYDCVATSLKVNPNLLIYKLFMFIFANVIAQLKGFNFYCTD 1310
QY 1444 QGEDIRN-----ITNKDCAEASR-WVRKRYNDNGIALMSIFVLASDGVNDIMYD 1496
Db 1311 SSKDTEKCEKIGNYVYDHEKKNKVEKREKREKREKREKREKREKREKREKREKREKREK 1370
QY 1497 GIDAAGVDOQPIIMNPNMMLYFISFLTIVAFVLMGVVNVENFHCRQHOEEERR 1556
Db 1371 SYDVTEEDRGSRNRMKMSIFVYVYFVFPFVFNITVALITTF-----OEGDKM 1423
QY 1557 REEKLRLREKRRNMLDVIASGSSASAASEAQCKPY--YSDYSR--FRLLVHLCTS 1612
Db 1424 MECSL-----EKNERACIDFAISA-----KPLRYMQRNRTFQRYVWHFVYS 1467
QY 1613 HYLDLFIINGVGLNVYVMAHGYOQPOLLDALKICNIFIVIVFESVFLVAFGRRF 1672
Db 1468 PSFETTMAMTALNTVLMKTYSAPTYELATYLMIAFTVFSLECVLVIAFGEVNY 1527
QY 1673 FODRNNQDLAIVLSTINGITLLEEVNASLPINPTIRIRVRIARVRLKLMAYGMR 1732
Db 1528 FRDMNIDFIVIGTIEIYLTDSKLVNTGFMNSFLKLR-----ARLLKMQGTIR 1584
QY 1733 ALDVTVALQVGNLGLLMLFFIFPALDVELFGDIED-ETHPCEGLGRATFENFG 1791
Db 1585 ILLMTFVOSFALPVCYLLIMLFFIYALIGMVFGNIRLDEESH-----INRHNPSRF 1640
QY 1792 MAFLTFVSTGDMWNGIMKDTL--ROCD-----QESTCNVYISPIYFSEVLA 1840
Db 1641 GSIMLTFSAIGEMAOELMISLCEKCEPDTLPASGOSEKCGTDLAVYFVSFIFFC 1700
QY 1841 QFVLNVVIAVLMKHLSESNKAR-----EAELEAELE-----LEMKTL 1880
Db 1701 SFLMLNLFVAIMNFEYLTRDSILGPHLDEVVAEYRAACGRINHTYEMTLTL 1760
QY 1881 -SPQPHSLG-----SPFLMPVEGVNSP-----DSPKGAHTTAHGAASG-- 1923
Db 1761 MSP-----PLGGRKCPSPVAKRLVLMNMPYAEADMTVHTSTLMALIRLALDIKAGGA 1816
QY 1923 -FSLHPRTV--PHPE-----VPYPLGRLTLVRKSGVSRTHSLPNDSYCRN 1968
Db 1817 DRQDLDSLOKETLAIMPHLSQKMLDLVPRKASD-LTVGKIYAA--KMLNDYKQSK 1872
QY 1869 GSTIERSLGHRGWLPRAGQSGSLIVSHOPADTSCILQPKDVYLLQPHGATWGAIPK 2028
Db 1873 VKKOROL-----EOKNAPMFORMERS-----SLQOEI--IANKALP--CLPQ 1913
QY 2029 LPP-----PGRSPLAQRLPRLQAIRTD-----SLDVGLSGREDLLSEVSG 2070
Db 1914 GPRAGLGRSGCPAMSPSLSPQIFOLTCMDPADDDGOFQEOGRSLVYTDPGSMRRSFTIRD 1973
QY 2071 PSCPLTRSSSFV-----GGSSIOVOORSGIOS-KVSKHIRLPAPCGLSPMAKDP 2120
Db 1974 -KSSSSWMLSEFEMERSSDMTYKSRRSYHSLRLAH-RL----- 2013
QY 2121 PETHSSLELTSLWISGDLPLPSQEBPLSPRDLKCYVETOSCRRRPGSWLDEORRH 2180
Db 2013 -NSDSGHSKSDTHRSQ--GREGKRSKREHLLSADYVSRSSSE-----ROADMDMSPERHPS 2066
QY 2181 IAVSCIDSGOPRLCPSPSLGOGPLGPGSPRKKKLSPPSISIDPPESGSGSPRC----- 2237
Db 2067 RSPBEGSGSPSKOGTGSLSSESTLPSVSDTSTPQOQMGPEBEGVLLHPHCGGMPCDRR 2126
QY 2237 -SPGVCILRRAPASDKPSVSSPLDSTAAS 2266
Db 2127 WMPG---RRGMSEKSHSLPLPHGGRDSTGA 2154

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RESULT 10

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C:Species: Homo sapiens (man)

C:date: 12-Apr-1995 #sequence\_ revision 12-Apr-1995 #text\_change 24-Sep-1999

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C:Accession: B54972;
R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;
  Biol. Chem. 269, 22347-22357, 1994
A:Title: Structure and functional characterization of neuronal alpha-1E calcium chan
A:Reference number: A54972; MUID:94350992
A:Accession: B54972
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-2251 <WILL>
A:Cross-references: GB:U29384; NID:9495867; PIDN:AA59204.1; PID:9495868
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match      13.3%; Score 1653.5; DB 2; Length 2251;
Best Local Similarity 24.0%; Pred. No. 2.2e-89;
Matches 625; Conservative 396; Mismatches 835; Indels 751; Gaps 94;

QY 41 PGADSEAE-----EGLPYALA-----PV-----VFFY 63
Db 12 PGSGDDSDSQSRKRGSTPYPASGOAAKQTAQARATMALYNPIPVHONCFYVNRSLFT 71
QY 64 LSGDSRPSWCLRTVCNPFERVSMLVILNCVTLGMR--PCEDIACDSQRCRILQAFD 121
Db 72 FGEDNIVRKAKKLIDWPFEYMLATIANCIVALDQHLPEDKTMSR--LEKTE 128
QY 122 DFFAFPAEMVKKVALG-IGKKCYIGDTNRLDFTIVAGMLEYLDLN--VSFSA 178
Db 129 PFYIGFCEAGIKIVAGLGFIFHKGSYLRNGWNVDFIVLSGIATAGTHFNHVDLRT 188
QY 179 VETVRVLRPLRANRVPMSRILVTLDTLPLMGVLLCFVFIFGIVQVQAGLRL 238
Db 189 LRAVRLRLKLVSGSPISQIVKSKIMAMPDLQIGLFFALIMFALIGLEFSGALH 248
QY 239 NRCFLPENFSLPVDLEPYOTENEDSPFICSPRENGKRSQSVPTLREGGCGGPC 298
Db 249 RACFMNN-----SGILBGF-----DPPHPC-----GVQGC 273
QY 299 SLDEYFNSSNTQVNNQYTYNCSAGEHNPFGALINFDNIGYAMIAIPQVITLEGVD 358
Db 274 PAGYE-----CKDW-----IGNDQITQEDNILEAVLVFOCIMEGWTT 313
QY 359 IMYFWADA-HSFYNEIYFILLIVGSPFMINCLVAVIATOPSETKORESQLMRQVRL 417
Db 314 VLYNNDALGATWMLLYLPIILLISFVLNLYGVLSGEFAKERER-----ENRAFM 368
QY 418 NASTLASSEPGSCYEBLLKYLYILRKAARLAQVSRAL-GVAGLSSPVARSQEP 476
Db 369 K-----LRQQQIERELNGYRAWIDKAEVYLAEN 399
QY 477 QPSGCTSRHRLSYHNLVHHHHHHHHHNGTLVPRASPELQORDANGSRRLMP 536
Db 400 KKAIGSALEVLRAI-----IKRSTAMTRDSS----- 429
QY 537 PSTPPSGPPRGASVSHFYHADCHLEPVRCQAPPRPCPEASGRTVSGKYVTVHTS 596
Db 429 ----- 429
QY 597 PPELTKALAEVAPASGPPTLTFSNIPGEPFSSMKHLLTOSTGACHSSCKTSSPCSK 656
Db 429 -----DEHCVDIS-----SVGTPLAR 444
QY 657 ADSGACGPDSCPYCARTGAGEPESADHMPDSDSEAYEFTQDAQHSDDLDPHRRQRS 716
Db 445 ASIKAKYDGVSY-----FRHKE----- 463
QY 717 LGPDAPSSVLAFWRLICDTFRKIVDSKRYGGMIALVNTLSMGTEYEDQBELTNAL 776
Db 463 -----RLLRISIRHWKSOVFYWIYLSVALNTACVALVHNNQOMQLHLL 508
QY 777 EISNIVFTSLFALMLKLVLVYGFYIKNPNYINFDGVIVYISWEIVGO-----OGGL 831
Db 509 YYAEHLFGLFLLEMSLKMVGWGRILYFHSSENFCDGVTGVSIFEVVMAIFRPGTSFGI 568

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QY 832 SVLRTFLRMVLKIVRELPAQROLVLMKTMVNAIFCMILMFIITFTSLGHLFGCK 891  
 DB 569 SVLRALRLIRLIRFKIKRYASLRNLVLSMMSKSIISLFLFIYVAFALLGQMLGGR 628  
 QY 892 FASEEDGOTLPDRKFDLSLMAIVFQILOEDMKNKLYNGM-----ASTSSAALEYFI 946  
 DB 629 F-NENDG--TPSANFDTPPALMTVFQILGEDMNEWMYNGISQGVSSGMSAIYFI 684  
 QY 947 ALMTGNVYLFNLVAIIIVEGF-QAEIGK-----REDASGOLSCIOLEPVNSGGDATKSE 1001  
 DB 685 VLLTGNTLLVFLAIVDNLANAQELTKDEQEEFAFNOKHAL-----QKAKEVSPM 738  
 QY 1002 SEPDEFPSVDGDRKRLALVALGEHAEKLSL-----LPLLIH 1043  
 DB 739 SAPNM-PSIERERRRHMS-VMEORTSOLKHHOMSSQELALNEEAPATNPLNPLPL 795  
 QY 1044 TATATP-----SLPKSSSTGVEALGSG-----SRTSSSGSAEPGAHHEKSPPS 1090  
 DB 796 SSLNPLMHPSLIXRRPRALEGIALGLALEKEFEERISRGSLKGDGDRSSALDNOQRTPL 855  
 QY 1091 AASSPHSPWSA-----ASSWTSRRSSKNSLGR-----AP 1119  
 DB 856 SLGQREPPMLARPCHGNCDPLOEAGGGEAVYTFEDRAHHRQSORSHRRVRETEGKSS 915  
 QY 1120 SLKRRSPSERSL--LSGEGQESOD-----EESSEEDRASAPAGSDHHRGSLERE 1169  
 DB 916 SASRSASOERSLDEAMPTBEGKDEHLEGNHKAKEPTIOEIRA-----QDLRTSLMVS 971  
 QY 1170 AKSSF-----DLPTLOVPGILHRTASGRSSASEHODCNKGSASGLAR----- 1213  
 DB 972 RSGGLAGLDEADTPLVLPHELE--VGKHVYLTEQEPESSEQALLGNVOLDMGRTYS 1028  
 QY 1213 -----TLRTD-----DPQDGC-----D 1224  
 DB 1029 QSEPDLSCTANTADKATTESTSVYVAIPVDPLVSTVHHISNKTDEGASPLKEAREID 1088  
 QY 1225 DNDDEGNLSKGERIQAMVRSRLPACCREDSMSAYTFPPQSRFLRLIITHKMFHDVY 1284  
 DB 1089 EEEVEKKRQKKEKRETG-KAMPYHS-----SMFISTNPIRACHIVLARFEKMI 1140  
 QY 1285 LVITFLNCTITAMERPKIDHSARLFTLSNITFVAFLAMKYVVALGMCBEQAYL 1344  
 DB 1141 LVIAASSIALAEEDVLTINSEENKV-LRYFDYVFTGVTFEMVIMKDQGLIDGSGE 1199  
 QY 1345 RSSMNVLDGLVLSYIDI-LVSMVSDSGTKILGMLRVLRLLTLPRLVISAQGLKLY 1403  
 DB 1200 RDLMTNLIDFVVVGVVALRALNALGTNGKRDITKISRLVLRPLRTIKRLKLAAY 1259  
 QY 1404 VETLMSLKPIGNIVICAFIIFGILGVOLEKGFVC--QGEDTRN-----ITNKS 1455  
 DB 1260 FDCVVSIMKAVNFILVYKLFMTIFAVIAVQLEKGFCTDSKOTKECIGNVYDHRK 1319  
 QY 1456 DCAEASTR-VWRKYNFNDIGOLMSLFVYASDGVNDIMYGLDAVGVDOQPINHNHW 1514  
 DB 1320 NKMEVYGRKKRREFFHDNITMALTFLTSTGEGPOVLOHSDVTEEDRSPSSNRE 1379  
 QY 1515 MLTYFTSLIIVAFVYLMVGVVVENFHCRQHOEEERARREKRLRLLEKKRRNLML 1574  
 DB 1380 MSFTYVYVFFFEFVNIVAILITF-----QEGDKMMEBSL-----EKNRACI 1428  
 QY 1575 DVIYASGSSASAASEACKPY--YSVYSR--FRLVHHLCTSHYLDLFTTGIVGLNVTM 1630  
 DB 1429 DPAISA-----KFLTRVMPQNRHTFQYRVWHFVSPSEFTYIMAMIALTVVL 1476  
 QY 1631 AMEHYQOPQLDLBAKICNITFVIVFESVFLVAFGFRFRFQODMNOLDALVILSLM 1690  
 DB 1477 MMKYISAPCTYELAKLNTIAFTMVSLCEVFLVAFGLNRYRDWNIFDFTVYIGSTT 1536  
 QY 1691 GITLEEEVNASLPINFTIRIMKVLRIARVLRKLKMAVAMRALDVTVQALPOVGNLQ 1750  
 DB 1537 EITLTDKLVNTSGFNMSFLKFR--APLITKLQGYIRILMTVFGSFAALPYVDL 1593  
 QY 1751 LFMILFFIIFALGVEILGDECD-ETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGI 1809

DB 1594 LRAMFTIATIGMVFQGNKIDDESH-----INRNNRSEFGSLMLLFRSATGEAMQEI 1649  
 QY 1810 MKDTL--RDCDOESTC-----YNTVISPITYSVVLAQVLAQVLAQVLAQVLAQVLAQV 1858  
 DB 1650 MLCLOEKCEPDTTAPSGQENENERCGTDLAIVYFVSFIFCPSFLMLLFAVIMDNEY 1709  
 QY 1859 SNNLEAK-----EEALEALE-----LEKTL-SPQSPPLG-----SP 1891  
 DB 1710 LTRDSSITLPPHLLDEVRVMAEYDRAAGRIHTYEMTEMLTMS-----PLGLGRCKSC 1765  
 QY 1892 FLMPGVEGVNSP-----DSPKRGAPHTTAHGAASG-----FSLHPTMV--P 1932  
 DB 1766 VAKKRLVLMNMPVAEDMTVHTFTSLMALIRLTALDIKIAKGADROOLDSELOKETLATP 1825  
 QY 1933 HPEE-----VYVPLGPDLLTYRKSGVSTHSLPNDSYMCNRGSAERSLGRGGLPKA 1966  
 DB 1826 HLSQKMLDLVPPPKASD-LTVGKIYAA--MMIDYTKOSKVKORQOL-----EE 1873  
 QY 1987 QSGSILSVSOPADTSCITQLPKDY-----HYLQPHGAPTWGAIPKLPPEGRSPLAQ 2039  
 DB 1874 QKNAFPOKMEPS-----SLPOEITANKALPYIQD--PVSGLSGRSGYPSMSPLSP 1924  
 QY 2040 RPLRQAAIRFOSLDVQGLSREDLSEVSGPCPL-----TRSSFWGSSIOYQO 2091  
 DB 1925 QDIFOLACM--DPADGQFOERQSLV--VTDPSSMRSPSTIRDKRSSNSW-----LEE 1974  
 QY 2092 RSGIOSKVSKHRLPAPCGLEPSMAKDPETRRSLELDT-ELWSWG--DLPSSQOE 2147  
 DB 1975 FMSERS-----ENTYKSRRRSTHSSIRLSAHLNDSGKSTHSSGREG 2020  
 QY 2148 P-----LSPRDLKCYSVETOSCRRRPGSWLDEORHSHIAVSCIDSGSPRLCSP 2198  
 DB 2021 RRSKERRHLSP-DVSRQNSE--RGTOADWESPERQO-----RSP 2060  
 QY 2199 SSIAGQPLGPGSRPKKSLSPSIS--IDPPSQGRPPCSG-----VCLRRRA-- 2247  
 DB 2061 SEGROTPNRQGTGSLSESSIPSVSDTSTPRRSRROLPPVPRKPRPLSYSLIRHAGSI 2120  
 QY 2247 --PASDCKDPSVSPIDSTVSPASPKDITLSGLSDPTDMDPVLPLPHLSPGADP 2304  
 DB 2121 SPPLDGEF--GSPILSQAL-----ESNNAMWLTSSNSH-----PQORQASAP-- 2163  
 QY 2305 SSASMAAFKSPTAASHEAPHLPSV 2331  
 DB 2163 -----QRTISEPYLA-LHEDSHASDCV 2183

RESULT 11  
 A54972  
 Voltage-dependent calcium channel alpha 1E-3 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 24-Sep-1999  
 C:Accession: A54972  
 R:Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.;  
 J. Biol. Chem. 269, 22347-22357, 1994  
 A:Title: Structure and functional characterization of neuronal alpha-1E calcium chan-  
 A:Reference number: A54972; M0ID:94350992  
 A:Accession: A54972  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-2270 <wild>  
 A:Cross-references: GB:129385; NID:9495869; PIDN:AAA59205.1; PID:9495870  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.3%; Score 1653; DB 2; Length 2270;  
 Best Local Similarity 23.8%; Pred. No. 2,4e-89;  
 Matches 626; Conservative 399; Mismatches 832; Indels 766; Gaps 95;

QY 41 PGSADSEA-----EGLPYPALA-----PV-----VFFY 63  
 DB 12 PGSGDGDSDGRNRQGITPVPAASGAAAYKOTKQARATMALNYPVRQNCFTVNRSLFI 71

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QY 64 LSODSRPSWCLRTVCNPMFERVSMVLTLNCLVTLMGR--PCEDIACDSORCLIAFD 121
D 72 FGEDIIVKRYAKKLDMPPFEVMIATITIANCIYALSOHLPEDDKTPMSR---LEKTE 128
QY 122 DFIFFEFVENVYKVALG-IFGKKCYIGDTWNLDFEIVIAGMLEVSLDON--VSPSA 178
D 129 PYFIFICEFEAGIKIVALGFIHKSYLRNGMVMDFIVISGLATGTFHNVHDRT 188
QY 179 VRTVAVLPLAINEVPMRILVTLTDLTLMGLVNLGCFVFFIGIVGQIMAGLLR 238
D 189 LRAVAVLPLKIVSGIPLOJVLKSIMKAMVPLLOIGLIFALIMPAITIGLEFYSGLH 248
QY 239 NRCELPENSLPLSVLDEPPYQTEHEDESPFICSOPTRENGRSCRSVYTLGEGGGGPC 298
D 249 RACFNMN-----SGLEGF-----DPPHPC-----GYOCC 273
QY 299 SLDTETVSSNTICVNMNOYTTNCISAGENPFKALFEDNIGYAMIAEQVITLEGWD 358
D 274 PAGE-----CKDW-----IGPNDGITQFDNILFAVLTFEQCITMEGWT 313
QY 359 IMEYVMDA-HSEYNYFIYILIIYGFEMINCLVIAOTSETKORESOQLMREQRYRL 417
D 314 VLYTNDLGLTWMVLYPIPIIIIGSFVNLVGLVSGEFAKERERV---ENRAFM 368
QY 418 SNASTLASFSEPGSCYEELLYVYILRKARLAOVSRAI-GVRAGLLSPVARSQEP 476
D 369 K-----LRQOQIERELNGYRAMIDAEVMALEEN 399
QY 477 QPSGCTSRHRLSVNHHVHHHHHHHHYHLNGTILVPRASPTIQORDANGSRMLPP 536
D 400 KNAGSTALEVLRRAI-----IKRSRTFAMTRDS----- 429
QY 537 PSTPTPGSGPRGAEVSHFYHADCHLEPVYCAQAPRPPCEASGRTVSGKYPTVHTS 596
D 429 ----- 429
QY 597 PPEILKDKALVENAPSPGPPTLSFNIPOGFSSMHKLESTOGACHSSCKISSPCSK 656
D 429 -----DEHCVDIS-----SVGTPRLAR 444
QY 657 ADSGACGPDSOPYCARTGAGBPESADHVPDSDSEAVYEFTOAQSDDLDPHSRRORS 716
D 445 ASIKSAVDDVSY-----FRHKE----- 463
QY 717 LGPOAEVSSVLAWEMLICDIFRKIVDSKYFGGIMAILVNTLSMGIEYHEQPEELTNAL 776
D 463 -----RLRISIRHVKSQVFWYIVLSVALNTACVALVHNNQOWMLTHLL 508
QY 777 EISNIVETSLFALEMLKLIVYGFYIKNPYINFDGVIVYISWEIYGO-----OGGL 831
D 509 YVAFELFLGFLLEMSKMKMGPRILFHSFPCFGVYVGSIFEVVMAIFRPTSFGI 568
QY 832 SVLRTFELMVLKLVRLPALOROLVYLMKTMNVATFCMLMLFTFISIIIGMHFGOK 891
D 569 SVLRALRLILFITKTKWASLRNVLWSMSKSIISLFLLEFLYVRLALMOLEGGA 628
QY 892 FASERODDTLPDRKNFDSLMAIVYFOIILTOEDMNVKVLVNGM-----ASTSSMALYFI 946
D 629 F-MFNDD---TPSANEDTFPRAIMTFEQIILGEDMNEVMYNGIRSGGVSSGMSWAIYFI 684
QY 947 ALMTFNGYVLFNLVAILVYGF-QAEIQC-----REDASQSLCIDLPPVNSOGGATKSE 1001
D 685 VLLFLGTYILLNFALAIANDNLNAOELTKDEOEDEEAEFNOKHAL-----OKAKEVSPM 738
QY 1002 SEDDFSPSYVDGGDRKKRLAL-----VALGEH-AETRKSL----- 1037
D 739 SADMN-PSIERDRRRHHMSWEPSSHLREHRRHHHMSWQRTSOQLRKHOMQSQA 796
QY 1037 -----LPLLIHTATPM-----SLPKSSSTGVCEALGSG-----SRTSS 1072
D 797 LNREAPTNPLNPLNPLSLNLNAPSLYLRPRAIEGIALGLALEKFEERISRGSL 856
QY 1073 SGSAEGCAAHHEKSPSPARSPPHSPWSA-----ASSWT 1106
D 957 KGGGDRSSALDQRTPLSLGOREPMLARPCHGNDPTQOEGAGGEAVTFEDBARHRO 916
QY 1107 SRBSRNSLGR-----APSLKRSPSGERSL---LSGGOESOD-----EESSEED 1151
D 917 SQRSRHRVRYTEGKSSSSASRSASOERSLDEAMPTEGEODHELROGNHGAKEPTIOE 976
QY 1152 RASPAQSDHRRHRSLEAKSSP-----DLPDTLOYPGHLRTASGRSSASEHODCKNG 1204
D 977 RA-----QDLRTNLSLVSRSGSIAGLGDADPRLVPHPELE---VGRHVVLTLEDEPPGS 1029
QY 1205 SASGRLAR-----TLRTP-----DPOLDG----- 1224
D 1030 SEGALLGNVOLDMGRIYSOSEPDLCTANTDKATTESTVTVAPIDVDPVDSIVVHIS 1089
QY 1224 -----DDNDEGNLSKGERIOAWVRSLPACCRERDSWSAYIFPPQR 1266
D 1090 NKTDGASPLKEAEIREDEBEYEKKOKKEKRENG-KAMVPHS-----SMEIFSTINP 1141
QY 1267 FLLCHRIITHKMFDAHVLYITFLNCITIAMERPKIDPHSAERIFLTLNLTAVFLAE 1326
D 1142 IRACHYIYNLFYFEKCLILVIAASSIALAEDPVLINSERKV-LRYFYDVYTGVTFE 1200
QY 1327 MTKVVALGMCFGEOAYLRSSWNVLDGLVILSVDI-LVSWVSSGTIKIIMRLVRL 1385
D 1201 MYIKMIDQSLIIDQSYFRLNIDFVYVVGALAFALNALGINKGRDITKISLRL 1260
QY 1386 RLRLPLRVISRAOGLKLVETLMSLKPIGNIVICAFYIIFGLGOLFCKRFVC-- 1444
D 1261 RYLRPLKTIKRLPKLKAVEDCVTSLKNVFNILYYKLFMEIFPVAIAQLRKGNFFCTD 1320
QY 1444 OGEDPRN-----TINKSDCAEASR-VWRKYNPDNIQOLMSLFVLAASOGVNDIWD 1496
D 1321 SSKDTEKECTGNVYDHEKNKKEVKGREKRRHEFDHNDIMALLTLFTVSTGEQWQVLOH 1380
QY 1497 GLDANGVDOQPIAMNHPMLLYFISFLIYAFVYVNMVGVVVENFHKRQHOEEELRR 1556
D 1381 SVDYVEEDRGPRSNNRMSKSIYVYVYVFFPVFNIVALLITF-----OEGDKM 1433
QY 1557 REEKLRLREKKRRNMLDVIYASGSSASASAESAOCKPY--YSDYSR--FRLVHNLCTS 1612
D 1434 MECGL-----EKNERACIDFAISA-----KPLTYMPONNHTPYRWHHVVS 1477
QY 1613 BYLDLFTIGVIGLVNTAMAHYQOPLDIALKICNTIFVIVFESSYKLVAFGRFR 1672
D 1478 PSFETIYAMTALNTVLMKTYSPCTYELALKYLNIAFTWFSLECVLKVIAFGFLNY 1537
QY 1673 FQDRNQDLAIVLSINGITLLEEIVNASLPIPTIIRIRVRIARVILKLMAYGMR 1732
D 1538 FQDTWNIEDFTIVAGSITIEILITDSKLVNMSGFMSLKLFR--ARILKILROGTTIR 1594
QY 1773 ALDITVOMALPOVGNLGLIFMLLFFIFRALGVELFGLECD-ETHPCEGLGRHATFRNG 1791
D 1595 ILLMTFVOSFALDYVCLILMFEIYALIGOVGNIKIDDESH-----INRHNFRSSF 1650
QY 1792 MAFLFLFRVSTGDMWNGMKDYL--RDODESTC-----YNTYISPIYVSVFLTA 1840
D 1651 GSIMLTFESAIGEAMQELMISLCEKECEPDTIAPSONENERCGLDLAVYVSPLEFC 1710
QY 1841 QFVLVNVVIAVLMKHLSESNKEA-----BEAELEAELE-----LEAKTL 1880
D 1711 SFMLNLFVAVAINFELYLFDSSILGRPHHDEVRVMAVYDRAAGRIHYTEYEMTL 1770
QY 1881 -SPQPHSPG-----SPFLMPGVGVNSP-----DSPKPGADHTTAHGAASG-- 1923
D 1771 MSP-----PLGKRCPSKVAKKRVLVLMMPVAEDMTVHTSTMALIRTAIDRIKAGGA 1826
QY 1923 -----FSLHPTVY--PHPE-----VPVPLGPDLLTYRKGVSRTSHLPDYSWCRN 1968
D 1827 DROQLDSELQKETLAIWPHLSQKMLDLVYMPKASD-LTYGKIYAA---MMLNDYKOSK 1882
QY 1969 GSTAERSLGHRGWLCPKAOGSGIISVHSGPADTSCILQPLKDV-----HYLLQPHGAP 2021
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Db 1883 VKKROOL-----EOKNAPMFORMEPS-----SLPEITIANAKALFYLOOD---P 1925  
 QY 2022 TGAIAIPKLPPEGRSPLAORPLRQOAIRTDSDVGLGSRDLSEVSPCPL----- 2076  
 Db 1926 VAGLSGRSYFPMSPSLSPDIFQIACM--DPADGQFOEROSLV--VIDPSMRRSFTSI 1981  
 QY 2076 --TRSSSEWGGSSIOVQORSGIQSVKRIPLPACPLGPEPSMAKDPETSSLELD-E 2132  
 Db 1982 RDKRSNSW-----LEEFSSMERSS-----ENTYKSRRSYSHSLSLSAHR 2021  
 QY 2133 LSWISG---DLPSQEEP-----LSPRDLKCYSVETOSCRRRRPGMLDEORHRS 2180  
 Db 2022 LNSDSGHKSDTHPSGGRERKRERKHLSP--DVSRCSNSEE---RGVQADMESEPRQS 2076  
 QY 2181 IAVSCIDSGOPRLCPSPSLGGQPLGPGSRPKRLSPSIS--IDPPESQGRHPPCSP 2238  
 Db 2077 -----RSPSEGRSQTPNRQGTSLSESSIPSVSTPRSRROLPPVP 2121  
 QY 2239 G-----VCLRRRA-----PASDKDPVSSPLDSTASPRKKDTLSLSGLSDPTDM 2286  
 Db 2122 KPRPLLSYSLIRHAGSISPPADGSEE--GSPILTSQAL---ESNNMMLTESSNSPH-- 2173  
 QY 2287 DVLPLPLPHLSPPGADPSSASMAAFILKSPTAASSHEAPHLPSV 2331  
 Db 2173 ----PQQRHASP-----QRISEPYLA-LHEDSHASDCV 2202

RESULT 12  
 A37490  
 voltage-dependent calcium channel alpha 1E - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999  
 C:Accession: A37490  
 R:Source: T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.  
 Science 260, 1133-1136, 1993  
 A:Title: Structure and functional expression of a member of the low voltage-activated ca  
 A:Reference number: A37490; MUID:93262464  
 A:Accession: A37490  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-2222 <SOO>  
 A:Cross-references: GB:LI5453; NID:9310082; PID:AAA40855.1; PID:9310083  
 A:Experimental source: brain  
 A:Note: sequence extracted from NCBI backbone (NCBIP:13101)  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.2%; Score 1649.5; DB 2; Length 2222;  
 Best Local Similarity 24.0%; Pred. No. 3.7e-89;  
 Matches 607; Conservative 393; Mismatches 835; Indels 689; Gaps 85;

QY 62 FYISODSRPSKCLRYCNWFERSMVLVILNCVTLGMR--PCDDIADGQRCRILQA 119  
 Db 21 FIFGEDNIVKRYAKKLIDWPPEFYMLATIANCIVALAEQHLPEDDKTPMSR--LEK 77  
 QY 120 FDDPTFAFFAVEMVVKWALG-IFGKKCYLGDTRNRLDEFFIVTAGMLEYSLDQN--VSF 176  
 Db 78 TEPFFITGFPEAGIKVALGFIHKGSYLKRNQNMWDFIVLSGLIATAGHFNHVL 137  
 QY 177 SAVTVLRLPRLAIVNRPMSRLIVLLDLPMLGNVLLCFVEFFIGIVGVLMACT 236  
 Db 138 RTLAIVAVLRLKLVSGISPLQIVLKIKMKAMVPLQIGLLFFAILMFAIILIEFYSCK 197  
 QY 237 LRNRCFLPEPNSLPLSVLEPIYOTENEDSPFICSPRNGRSCRSVPLTGEGGGP 296  
 Db 198 LHRACFNMN-----SGILEGF-----DPPHPC-----GVQ 222  
 QY 297 PCSLDYETYNSSNTTCVNNNOYTTNCSAGEHNPFGKAINFDNIGYAMIAIFQVITLEG 356  
 Db 223 GCPAGYE-----CKDM-----IGPNDGIQFQDNLFAVLVPCIIIMEGW 262  
 QY 357 VDIMYFVMDA-HSFYNYIFLLIIVGSFFMINCLVIAVIAFQPSRQESQLMREORVR 415

Db 263 TIVLYNTNATATWNNWLVIFLLIISGFVNLVLVGLSGFAERERV-----ENRRA 317  
 QY 416 FLTNASTLASFSEBPSQCYBELLYIILKARLAQVSRAL-CVRGGLSSPVARSGQ 474  
 Db 318 FMR-----LRQOQIERLNYRMIWIDAEVMAE 348  
 QY 475 EPQSGSCTRSHRRLSVHLLVHHHHHHHHHNGTLRVPRASPEIQDRANGSRRLML 534  
 Db 349 ENKNSGTSALVLRAT-----IKRSRTAEATPROSS----- 380  
 QY 535 PPSTPTPGCGPRGAEVSHSEYHADCHLEPVRCQAPPPRCPSEASGRTVSGKVPYVH 594  
 Db 380 ----- 380  
 QY 595 TSPPELIDKALVEVAPSPPTLTLSFNIIPPGPSMKHLETOSTGACHSSCKISSPC 654  
 Db 380 -----DEHCVDIS-----SVGTPL 393  
 QY 655 SKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVEFTQDAQSHDLRPHSRRO 714  
 Db 394 ARASIKSTKVDGASY-----FRHKE----- 414  
 QY 715 RSLGPDAPSSVLAIFKRLICDIFRKIVDSKTYRGIMAILVNTLSMGLEYHEQBELTN 774  
 Db 414 -----RLIRISIRHWYKQVFPYVILSVYALACVALVHNHNOQWMLTH 457  
 QY 775 ALFISNVFTSLFALMLKLVLVGPYGIKNPNYIFDGVIVISVWEIVGQ-----OGG 829  
 Db 458 LLYVAFELFLGLLELSLKMGMGRPLYFHSFNCDFDGVYGSIFFEVYMAIFRPGISF 517  
 QY 830 GLSLRTFRIRVYLKLVRELPALQRLVYVLMKTMNAVATFCMLMLFIFESILGHLFG 889  
 Db 518 GISVLRALRLIRFKITKYVASRLNVLVSLMSKSIISLEFLLEFIVVAFLLGQLEFG 577  
 QY 890 CKRASEMDGTLDKRNKPSDLMAIYTVQILQEDMNVLVNGM-----ASTSSAALY 944  
 Db 578 GRF-NFNDG--TPSAPFDFPAIMTVFQILGEDMNEVMYIGISQGVSSGMASALY 633  
 QY 945 FIALMTFGNVVLNVLVAIVLEGF-QAETIGK-----REDASGOLSCIQLPVNSOGDATK 999  
 Db 634 FIVLTIFGNTLLNVLPAIVDMANAOELTRKQDEEEAFNOKHAL-----QKKEYS 687  
 QY 1000 SESEPDEFSSVDGDDGRKKRAL-----VALGEH 1029  
 Db 688 PMSAPNM--PSIEDRRRRHMHMSMEPRSSHLRERRRHMSVWEORTSOLRRHMQMSQ 745  
 QY 1030 AELKKSLLPLIITATPM-----SLPKSSSTGVGALGSG-----SRTSSSG 1074  
 Db 746 EALKKEAPPNPLNPLNPLNPLNPLNAPSLYRPPRIEGLALGLGLEKCEERISRG 805  
 QY 1075 SAEPG-----AAHEHMSPPS--ARSSPHSPWSA-----ASS 1104  
 Db 806 SLKGDIGLISVLNQRSPISLGRKREPPWLPRSCHGNCDEPTQOETGGGETVTFEDRAH 865  
 QY 1105 WTSRRSSRNSLGRAPSLKRSPPSGERSLSLGGQESQDEEESSEDRASPPASDIRHG 1164  
 Db 866 RQSORRSRHRVRTEGKESASASRSR--SASOERSLDEGVSIDKEKEHEPSSRSRSE 921  
 QY 1165 SLEREAKSSPDL--PDTLOVP--GL-----HRTASGRSSASEHOCNCK 1204  
 Db 922 PTIHEEPTQLRRTNSLAMPGRSGLVGALDEAETPLVQPELEVGKDALTEQDAEBS 981  
 QY 1205 SASGRLA-----RLTRTDPOL----- 1222  
 Db 982 SEQALLNDVQDVGRIQSQSPDLSCMTTNMDKATTESTSVTAIVDPVLDVSTVNIS 1041  
 QY 1222 ---DG-----DDDNDEGLNSKGERIQAWVASRLPACCREDNSAIIFFPQSR 1266  
 Db 1042 NKTDEASPLKEAETKEEKEEVEKROKKEKRETG-KAMPBS-----SMFIFSTTN 1093  
 QY 1267 FRLLCHRTITMKMDHVLYVLIIFLNCITIAMERKIDPNSAERLFTLSVYITAVFLAE 1326

Db 1094 IRKACHYIVNRYEEMCILYIAASSIALAEDPVLNSENKV-LRFDVYENGVEFFE 1152  
 Qy 1327 MTVVVVALGMCFGEGAYLRSSMNVLGLVYISYDI-LVMSVSDSGTKILGMRLRL 1385  
 Db 1153 MWIKIDGILLQOGSFRDMLNLDVYVVGALVALANALATNGRDKIKITKSLRVL 1212  
 Qy 1386 RFLRLRIVISRAOGLKLVETILMSLRPIGNIVICAFEFILFGLIGVLFKGFECF-- 1444  
 Db 1213 RVLRLKIKRLPKLVKAVFDCVSTLKVFELIYKLFMFIVAVIOLFKGFYCTD 1272  
 Qy 1444 QGEDTRN-----ITNSDCAEASIR-WVRHKYFNDLGOALMSFVLAKDGNVIMYD 1496  
 Db 1273 SSKDTEKICIGNYVDHEKNKMEVGRKREHFYDNIIMALLFLFYSGEGMPQYLOH 1332  
 Qy 1497 GLDVGVDQOPIMNHNPMILYFISILLIVAFVLNMFVGVVYNFHKQCHQDEEARR 1556  
 Db 1333 SVDTVEDRGRSRNKRKMSFYVYVYVFPFFVNIFFALITTF-----QEGDKM 1385  
 Qy 1557 REERLRLEKRRNLMDLVIASGSSASASEAOCKPY--YSDYSR--FLLVHLCTS 1612  
 Db 1386 MECSL-----EKNRACIDFAISA-----KPLRYMQRNHTFOYRWHFVVS 1429  
 Qy 1613 HYLDLFTGVGLVNYVMAMEHYQOPOLDEALKICVITVIFVESVFKLVAFGRFF 1672  
 Db 1430 PSFEYTTMAMALNTVLMKYYSAFPTVELAKYLNIATFVFELECVLKVIAFGLNY 1489  
 Qy 1673 FODRNOOLDLAVLLSINGITILEIEVENASLPINPTIIRMLRVLRIRVILKILKMANVR 1732  
 Db 1490 FRDTWNFEFTVIGSTIELILDSKLVNSGFMSTFKLFRA---ARKLKLKOGYTTIR 1546  
 Qy 1733 ALDITVQALPQVGNLGLLEMLFFITFALGVELFGLECD-ETHPCEGLGRHATERNFG 1791  
 Db 1547 ILMTFVQSKALPYVOLLIAMLFETIYAIIGMOVFNIKIDEESH---INRNNRSEF 1602  
 Qy 1792 MAFLTFRSTGDMWNGIMDTL--RDCODESTC-----YNYISITVYVSYLTA 1840  
 Db 1603 GSLMLLRSTGEAMQETIMLSCEKCEPDTAPSGQNSESGTDLAVYVSVSIFFC 1662  
 Qy 1841 QFVLVNVVIAVLMKHLBESNKEAK-----EEALEALE-----LEKTL 1880  
 Db 1663 SFLMLNLFVAVIMDNFEYLRDSSILGPHHLDENVMAIYDRAACGRHITYEMETLIL 1722  
 Qy 1881 -SPQHPPLG-----SPFLMPGVEGVNSP-----DSPKGPATHTAHGAAG-- 1923  
 Db 1723 MSP---PGLGRKCPKVAKYKRLVLMNMPVADMTVHFTSTLMALIRLALDKIKAGGA 1778  
 Qy 1923 ---FSLHPTMV--PHPEE-----VPPLGPDILVYRKSGVSRTHSLPNDSTWCKN 1968  
 Db 1779 DRQOLDELQKETLAIWPHLSQKMLDLVMPKASD-LTGKITYAA---MTIMDYKQSK 1834  
 Qy 1969 GSTAERSLGRWGGLPKAQSGLSVHSOPAD--TSCILQLPKDHYLLOPHGAPITGAIP 2027  
 Db 1835 VKRQOOL-----EENKRNAPFQRMERSLPQELISAKALPILOD--PVSGLSG 1883  
 Qy 2028 KLPPPGSPILAQRPLRQALIRTDSDLVQSGREDLISVSGPSCPL-----TRSS 2079  
 Db 1884 KSGYPSKPLSPOLIFOLAM--DPADDOGOFQOOSLY--VYDPSMRRSFTIRDKRN 1939  
 Qy 2080 SFM-----GSSIOVOQRSQIOS-KYSKHIRLPAPCGLPEPMADDPETBSL 2129  
 Db 1940 SSWLEEFSEMSSEENTYKSRRSYHSLRLSAH-RL-----NSDSGHIS 1982  
 Qy 2130 DTLSMTSGDLLPSSQEP--LSPRDLKCYVETQSCRRRPGSWLDEQRHSHAVSCLD 2187  
 Db 1983 DTHRS--GGERGRSKERKHLSP-DVSRCONSEE--RGTQADWSPRRS----- 2029  
 Qy 2188 SGQSPRLCSPSSSLGGOPLGSGSRPKKLSPSISID-----PPESQSGSPPS 2237  
 Db 2029 ---KSPSGRQTPRRQCTGSLSSISIDSTPRRSRQRLPVPKPKPPLLS 2080  
 Qy 2238 PGVCLRRRAPASDKDPV--SPLDSTAASPKPKDTLISGLSPTMDVPLPTLPH 2296  
 Db 2081 YSLMHTGGISPPPGSEGSP---ASQALESNSALITLESSNLHQOQGHSPQHY 2136

Qy 2297 LSPP 2300  
 Db 2137 ISEP 2140  
 RESULT 13  
 A30063  
 dihydropyridine receptor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 20-Mar-1998  
 C:Accession: A30063  
 R:Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, V.; Takahashi, H.; Kangawa, K.; K  
 A:Title: Primary structure of the receptor for calcium channel blockers from skeletal  
 A:Reference number: A30063; MUID:87258269  
 A:Accession: A30063  
 A:Molecule type: mRNA  
 A:Residues: 1-1873 <TAN>  
 A:Cross-references: GB:X05921; NID:g1547; PID:g1548  
 C:Keywords: phosphoprotein; transmembrane protein  
 Query/Match 12.9% Score 1608.5; DB 2; Length 1873;  
 Best Local Similarity 23.6%; Pred. No. 7.9e-87;  
 Matches 577; Conservative 356; Mismatches 692; Indels 823; Gaps 82;  
 Qy 32 QGPGSTENDPGSADSEAGLPPALAPVFFYLSQDSRPRSMCTRTVCNPP--FERVSM 89  
 Db 7 ODEGLRKQKPKPLPEV--LPRP--PALFCILQNLPRACISIV--EKKPEFTIIL 59  
 Qy 90 VLLKCVILGMRPC-EDLADDSQCRK-LQAFDFEFAFAVEMVVKMALG-IFSKKC 146  
 Db 60 TEFAVCVALAVLAPPEP--DNNSLNLGELKLEYFELVFSIEAAMKILAYGFLPHDA 116  
 Qy 147 YLGDVWNLDFEYIAGLLEYSLDQNY-----SFAVRYRVLRPLRI 191  
 Db 117 YLRSGWNLDFEYIAGLLEYSLDQNY-----SFAVRYRVLRPLRI 176  
 Qy 192 NRVPSMRLVTLTLDTPMLGNVLLCFEYFIFGIYGVQVLMAGLIRNRFLEPNFSLPL 251  
 Db 177 SGVPSLQVAVLSIFKAMPLEPHIALVLFVWITVYAIIGLELFFKMKMKTCY----- 229  
 Qy 252 SYDLEPYQOTENDESPFCQSPRENGMRSCRVPITLRBGGGPPCSLDIETYNSSNT 311  
 Db 229 -IGTDIVATVENKPS--CART-----GSGRPC-----TINGS-- 260  
 Qy 312 TCVMNQYTYTMCASGEHNPFGKAINFDNIGYAWIAFOVITLEGVDMYFVMDA-HSFY 370  
 Db 260 -----ECRGWGPQPNNGITHFDNFGSMLTVOCTIMEGMDIVLWVNDALIGNEW 309  
 Qy 371 NFYFILLIIVGSEFPMNLCLVATATQFSETKQRESQLMREORVRLSNASTLASFSEPG 430  
 Db 310 PMYFVTLIILGSEFIIILVGLVLSGEF--TKEREKAKSR-----GTQKLEKQ 357  
 Qy 431 SCYEELIKYLVYILRKARLAQVSRALIGVRAGLSSPVARSQEPPOPSSTCRSHRRLS 490  
 Db 358 QLEEDLKRYMWTQ-----GEWADVEDLREGKLS----- 388  
 Qy 491 VHLVHHHHHHHHYHLGNGTLRVPRASPEIOPDANGSRRLMLPPSTPTPGGPRGA 550  
 Db 388 -----LEEGG----- 393  
 Qy 551 ESVHSFYHADCHLEPVQCAPPPRCSEASGRIVYSGSKYPTVHTSPPEILKDALVEY 610  
 Db 393 ----- 393  
 Qy 611 APSDPPLITSFNIPPPFSSMKHLELTOSTGACHSCKTSSPCSKNADSGACPDSCPYC 670  
 Db 393 ----- 393  
 Qy 671 ARTGAGEPESADHYMPDSDSEAYE-----FTQDAQHSDLRDPHRRRQRSISGPDAPS 724

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Db 393 -----SDTESLYEIEGLNKIIQFINH----- 414
QY 725 SVLAFWRLICDTR-----KIYDSKYFEGRMIALIVNTLSMGIEYHQBPELINALEISN 780
Db 414 -----WRQMNWVFNRKCKDLYKSRVFWLVLIALNTLSIASHHNQPLMLTHLODIAN 468
QY 781 IVFTSLFLEMLKLLVYGPFGYIKNPYNIFDGVIVVSWETVYGOOG-----GLSVLR 835
Db 469 RVLSTLFTIEMLKMYGIGLQYFMSIFNRDCEVVCOSGIELLIVESGANTPLGISVLR 528
QY 836 TFRMLRVKLVRELPALOROLVLMKTMNVATFCMLMIFIFISLIGMHLFCGCFASE 895
Db 529 CIRLRLEKTKITWTSLSNLYASLNSIRJASLALLFLFIIFALLGQMLREGRIDEF 568
QY 896 RDGDLPRKKNFDSLMAIVTVFOILTOEDMKNVLYNGMASTSS-----WALYFTALM 949
Db 589 ---DTEVRSRNDFNPQALLISVFGVLTGEDMNSVYNGIMAYGGPSYPGVLVCYIFILF 645
QY 950 TFGNVVLENLVAIIYEGF-QAEIIGKREDASGOLSCIQLPVNSOGGDATKSESEPEFIS 1008
Db 646 VCGNYILLNVFLALAVNDMLAEESL-----TSAOKAKAE----- 680
QY 1009 PSVDDGDGRKKRLALVALGEHAELKSLPLIHTATPMSLPSKSSSTGVGALSGSR 1068
Db 680 -----ERKKRKMGRGLPKTEEEKSYM----- 702
QY 1069 RTSSSGSAEPGAHHKMSPPSARSSPHSPWASASMTSRSSRNSLGRAPSLKRSPSG 1128
Db 702 -----AKLEOK-PKG 711
QY 1129 ERRSLLSGCGODEEESSEEDRASPAQSDHHRHGSLEAKSSFDLPDLQVPGIHLRT 1188
Db 712 EG---IPTTAKKAVEFESSNVEKDP-----YISADP----- 743
QY 1189 ASGRSSASEHODCNKSAAGRLARTDDPOLDDDDNDGNSLKGERRIGAWRSRLPA 1248
Db 743 -----GDDEDEPREIVSPRPPLAELOL- 767
QY 1249 CCRER-----DSMSAYIPPROSRFLCHRITTHKMPHVVLYIFLNCITIANMERPID 1303
Db 767 --KEKAVPIPEASSFEFISPIKRVKLVNATWFTNFILFTLLSSALAE-----D 820
QY 1304 PHSABRIEFTLSNYI---FTAVFLAEMTVKVALGMCGEQAYLSSNNVLDGLVLISV 1360
Db 821 PIRAESVRNOIIGYDIATSVFTVEIYIAKMTYGAFIHKSGFCNRYNIIDLLVANS- 880
QY 1361 IDLVSMVSDSGTKILGMLRLRLTRLEPRVISAQGLKIVETLSLKGICNIVVI 1420
Db 880 ---LISMGLEST--ISYVKILRLVRLVPLRAIRNAKGLKHVQCVFAIRITIGNIVLV 934
QY 1421 CCAFTIIFILIGVOLFKGFEVFCQGEDPFININKSDCAEASV-----RWV 1465
Db 935 TYLLOFMEACIGVOLFKGFESC--NDUSKMT--EEBCRGYIYVYDGDPTOMELPRQMT 991
QY 1466 RHKYNEDNLGOALMSLFLVASKDGWDVIMYDGLDAVGVDOOPINHNPMMLLYFISPLLI 1525
Db 992 HNDHFHDVLSAMSLFTVSTFEGMQQLLYRAIDSNEEDMGVYNNRYEMALFFIITYIL 1051
QY 1526 VAEFVLMFVGVYVVENFHKCRHQEERKRRBEKRLRLEKKRNLMIDVYASGSSAS 1585
Db 1052 IAFPMNIFGVFIYVTF--OEGETLEYKNC-----LDKNORQCV-----QYAL 1093
QY 1586 AASEACKPYYSYSRFRLLVHLTSHYLDLFTIGVIGLVNTVYAMEHYQPOLIDEAL 1645
Db 1094 KAPPLKC---YIRKPNYQYQWVTVYTSSTFEIYMFALIMLNTICLGMQHYHSEEMNHS 1150
QY 1646 KICNYIFTVFVESEVFKLVAEGFRFQDRMNQDLAIVLLSINGITLEEIV----- 1700
Db 1151 DILNVAFTIIFLEMLKILAFKARGYFGDDPMVDFELVISIIDVLSIEDTFLASG 1210
QY 1700 -----NASLPNPTIIRIMVRLARVILKILKNAVGKALLDVIM---QAL 1742
Db 1211 GLYCLGGCGGVNDPDESARISSAFRLFRVMRL---IKLLSRAEGVRLTLMTFIKSFQAL 1267

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QY 1743 POGVNLGILMFLIFITFALGVELFGDLE-CDETHPCEGLGRNATFBNFGAFLLFRVS 1801
Db 1268 PYV---ALLIYALFEIYAVIOMQEMGKIALVDGTO---INRNNNEFTPOAVILLRCA 1320
QY 1802 TGDNNNGIMKDTL--RDCDOES-----TCYNTVISPISFVSVLLAOFVLNVVIAV 1851
Db 1321 TGEANOELLACSYKCLDDPESDAPAGEEYTC-GINRAYYFISFYMLCAPLLINLFEVAV 1379
QY 1852 LM-----KHLEBSNKEAKEADLAE--LELEKTLSPQHSPLSGSPL 1893
Db 1380 IMDNFDYLTRODSIIGPHLDEF-KAIWAEYDPEAKGRIKHLVDVTLRLRLOPLGCKF 1438
QY 1894 WP-----GVEGVNSP-----DSPKCAPHTAIGAASGFSLEHP----- 1929
Db 1439 CRRVACKRLVGMNPLNSDGVITNATLFAVRLALKIKTEGFEQANELRALIKKIW 1498
QY 1929 --TMPHPREEVPLPLDILTVKSGVSRTHSLPNDSYMCBNGSTAESLGRMGWLPKA 1986
Db 1499 KRTSMKLDQVPIPGDDEVTKFYATFLIQEHFRKFMKRO---EYYGYR---PKK 1550
QY 1987 QS---GSTLSVHSQA-----DTSCIIQLPKDVHYHILQPHGATWCAIKLPPPG 2033
Db 1551 DTVOLQAGLRTTEEAPEIRRTISGDLTAEELELRAM-----V 1589
QY 2034 RSPLAQPLRQAAI-----RTDSL-----DVQGLSREDILSEVSGP----- 2072
Db 1590 EAMERIRTRRIGLFGQYDTFLERTNSLPYMANORLOFAEIMELLESFVLEDEPQ 1649
QY 2072 ---SCPLRSSFGSSGIQV--QQRSGIQSVKSHIRLPAPCPGLEPESMAKDPPETRSS 2126
Db 1650 DARTNPLARANTNNANAYAGNSNHNOMFSSVH-----CEREFEGETETPAAGGA 1703
QY 2127 LEIDTSLMSIGDLPLSSGEPELSPDLKKCVSVETQSCRRRPGWDEQRRHSIAVSL 2186
Db 1704 L-----SHSRALGPHS-KPC-AGLNGOLVOVPGMPLNQ----- 1736
QY 2187 DSGQPRLCPPSPSLGQPLGPGSRPKKLS-PSISIDPE--SOGSRPPSGVCL 2242
Db 1736--APPAPQOQST-----DPPEGQRRISLTSLODEAPQRSSSGSTP----- 1778
QY 2243 RRRAPASD--SKDPVSFPLDGTAAFPSPKKDTLSLGSISPTMDP 2288
Db 1778 RRPAPATALLIOEALVRGIDTLADAG---FVATISQALADACQMP 1822

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RESULT 14

S11339  
 calcium channel protein - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Mar-1998  
 C:Accession: S11339  
 R:Biel, M.; Ruth, P.; Bosse, E.; Hüllin, R.; Stuehmer, W.; Flockert, V.; Hofmann, F.  
 FEBS Lett. 269, 409-412, 1990  
 A:Title: Primary structure and functional expression of a high voltage activated calc  
 A:Reference number: S11339; MCID:90382589  
 A:Accession: S11339  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-2166 <BI>  
 A:Cross-references: GB:X55763; NID:91507; PID:91508

Query Match 12.9%; Score 1606.5; DB 2; Length 2166;  
 Best Local Similarity 23.1%; Pred. No. 1.2e-86;  
 Matches 580; Conservative 365; Mismatches 765; Indels 805; Gaps 81.

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QY 70 PRSWCLRTVCPN-----W-FERYSMVILINCYTLGMEFPC-EDIACDSQRCRI 116
Db 101 PRALLCTLKNPIRACISIVKWPFEIILITLIFANCALAIYIPFEDP---DSNATNS 157
QY 117 -LQAFDFITAFVAVENVVAVALS-IFGKKCYLGGTWRDLDFEYIACMLEYSIDL--- 172

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Db 158 NLERVEYLLIFTEAEFLKAYAGLLEFHPNAYLRNGWNLDELIVVGLSAILLEQATK 217  
 QY 172 -----QWSEFSAVRVRLVRLPRLAINRVSMAILVTLLDITPMGLNVLICCF 220  
 Db 218 ADGANALGKGAGDFVKKLRAFRVRLPLVSGVPSLOVANSIKAVYPLHLHALLVLF 277  
 QY 221 VEFIFGIYVOLMAGLBNRCPENFSLPLSVLDEPYQTENEDESPFICOSPRENGMR 280  
 Db 278 VIIIAIIGLELPMKMKHTCNOEG-----VADVAEDDPS 314  
 QY 281 SCRSPPTLRGEGGPPCSLDIETYNSSNTTCVMMNOYTCNSAGEHNPFGAIFNDNI 340  
 Db 315 PCAL-----ETGHRGROC-----ONGTVCXKGMGDPKRGHTITFNDNF 349  
 QY 341 GYAMIAIFOVITIEGVMIMYFVMDA-HSYNYFIYILLIIVGSEFMNLCLVIAIOFS 399  
 Db 350 AFAMLTVCOTTEBMTVYLWANDVGRDPMWTFYVLTITISGFYMLNLVGLVSGEFS 409  
 QY 400 ETKQRESQLMREORVRLSNASTLASEPSCYEELLYVLTIRKARLQVSRAG 459  
 Db 410 KEREKAKARGDFOKLR-----EKQLEEDLKGYLDMT----- 442  
 QY 460 VRAGLSSPVARSQOEPOSSGSTRSRRLSVHHLVHHHHHHHHLGNGTLRVPASP 519  
 Db 442 ----- 449  
 QY 520 EIODRANGSRMLPPESTPSPGPPRGAEVSHFYHADCHLEPVRCQAAPPRCSEA 579  
 Db 450 ENEDGMDER-----PRNRTGPAG-----LHAO----- 474  
 QY 580 SGRTVSGSKYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPGPFSMKHLETO 639  
 Db 474 -----KKGKAMPSSHSET- 488  
 QY 640 STGACHSSCKISSPCSKADSGAGCPDSCPYCARTGAGEPESADHY-WPDDSEAVYEFTQ 658  
 Db 488 -----HVSMTSETESVN--TE 502  
 QY 699 DAOHSDLRDPHSRRORSIGDPAPSSVLAFWR---LIC-DTFPKIYDSYFYGIMIAI 754  
 Db 503 NVAGDIEGENCGAR---LAHRISKSKFSRYWRKRNFCRCRCAVAKSVNFWLVLFLV 559  
 QY 755 LVNTLSGIEYHEDPELTNALETISNIVETSLFALEMLKLTVYGPBGYIKNPNYTFDGV 814  
 Db 560 FLNLTITASHBYNPHMLTEVODTANKALLALFAEMLKMYSLGQAYFVSLFNRDCE 619  
 QY 815 IVVSVWEIYGQOGK-----GLSVLRTFRIMRYLKLVRFLPALQOROLVLMKMDNAVTF 869  
 Db 620 IYCGIIEITLIVETKVNPSPIGIVLCVRLTRFKITRYNNSLSNLVASLNSVRSIASL 679  
 QY 870 CMLIMEFIFISILGMHLFGCKFASEBDGTLPRDN-FDSLMAIYVFOILTODMKN 928  
 Db 680 LLLLFLEIIFISILGMOLFQKGF---NPEMDQTRSTFENFQSLTYVQIILTEDMNS 735  
 QY 929 VIKNGMAS-----TSMNALYFIALMTFGNYLVFNULVALIVEGFOAEIGKREDASQ 982  
 Db 736 VMDGIMAYGSPFPGMLVCIFYIIFLFCNGYIILNVLNLAIVDNL-----ADAESI 787  
 QY 983 LSCIOIPLVNSOGDATKSESEPDFEFSPVDGDDRRKRLALVNLGHAELRKLPLLI 1042  
 Db 788 TS-----AKKEEEE-----KERRKARTASPEKKO----- 814  
 QY 1043 HTAATPMSLPKSSSTVGALGSGSRTSSGSAEPGAHHEKSPSARSSPHSPWSAA 1102  
 Db 814 -----EYVGRPALEAKEEKIELKSTADESPPTKI----- 847  
 QY 1103 SSWTSRSSNSLSGRAPSLKRBSRSGERSLLSGEOSEODESESEEDRASPAGDHRH 1162  
 Db 847 -----NMDDLOQPNESDEKSP----- 862  
 QY 1163 RGLSLEBANKSFDLPDTIAYVGLHRTASGRSSASEHODCNGKASASRLARTLRTDPOD 1222  
 Db 862 -----YNPETTT 868

QY 1223 GDDDNENGLSKGERIQAWVRSLPACRER-----DSWAXYIFPPQSRFLCHRIITH 1277  
 Db 869 GEEDDEEPEMPVQPRDRPSELHL-----KEKAVPMEASAFIFSPNNRFLQCHRIYND 924  
 QY 1278 KMDHVVVLIIFLNCITIMERPDKIDPHSAKEIFELTSYITTAFLAEMTVKVALGMC 1337  
 Db 925 TITNLTLEFILLISISLAEDEP-VQHTSFNRHILFFYPDIPTTIFITIELALKMAYGAF 983  
 QY 1338 FGEQALRSRSMVNDGLVLISVIDLVMSDSGKILGIMRVRLRLTLPBLVISRA 1397  
 Db 984 LHKSFRCNTEFNLDLIVVSVLSISGIC-----SSAINVKILRLVRLPLRAINRA 1037  
 QY 1398 QGLKAVETLMSLKPIGNIVVICAFIIFIGLVOLERKGFVCOGEDPRNTINKSDC 1457  
 Db 1038 KGLKRVQCVFAIRTIGNIVITTLLOFMFACIGVOLFERKGLTYCSDSSKQ---TEAEC 1094  
 QY 1458 AEAZY-----RWVRKRYFEDNLGQALMSFLYAKSDGWDIMYGLDAV 1501  
 Db 1095 -KGVTTYDGEVDHPIOPRSMENSKFEDFVNLAMALFTVSTFEGMBELLYRSIDSH 1153  
 QY 1502 GVDQCPINMNMMLYFISFLIYAFVYLMFVGVVENEFKCRQHOEEBARREBEKR 1561  
 Db 1154 TEDKGPYVYRVEISIFELIYIIIAEFMMNIFGVFVTF---QEOGEOEYKNCF--- 1207  
 QY 1562 LRKLEKRRNLMLDVIYASGSASASAEBOCKPY-----YSDYRFRLLVHHLCT 1612  
 Db 1207 ---LDKNOR-----OCVEYALKARPLRRTYPRKQHYKVMYVYNS 1243  
 QY 1613 HYLDLEITGVIGLVNTVAMEHYOQPOLDEALKICNIFIVYFEEVFLVAFGRRF 1672  
 Db 1544 TYFEYLMFVLLINTICLAMOYTGOSCFKIAMNLTNLKGLFVETILKLEFKPKHY 1303  
 QY 1673 FODRMNDLALVLLSINGITILEEVNASLPINPTI-----TRIMVRLIARYLK 1723  
 Db 1304 FCDANTEFALIVGSIYDIATEVHPAEHTQCSFMAENSRISTIFFFLFVYMLYK 1363  
 QY 1724 LKMAVGRALLDYV---QALPOYGNIGLLFMILFFIYFALGYELFEDLECDETHPCEG 1780  
 Db 1364 LLSRGEIGRTLTMTFKISFOALPYV---ALLIYMLFFIYAVIGMVGKIALNDY---TE 1417  
 QY 1781 LGRHATFRNMGAFLETLFRVSGDMWNGIMKDTL--RCCODESICYMY-----IS 1829  
 Db 1418 IRRNNNFOTFPOAVYLLERKCATGEHMODIMLACPKKCADESPHNSBETPGSSFA 1477  
 QY 1830 PIYVSEVLLAQVVLVNVIAVL-----KHLESNK-EAKEEAELEAE 1873  
 Db 1478 VYFISFYMLCAFLIINLFVAVIMDNFDYLRDWSIIGPHHLDKFRIMAYEYDEAKGRI 1537  
 QY 1874 E-LEMKTLSPQSHSLGSPFLMP-----GVEGVNSPDSRPGAPHTTAHIGAASGSLE 1926  
 Db 1538 KHLDVVTLIRRIQPLGKLCPRHVACKRKLVSNNMPLN--SDGTVMENATLFLVYRALR 1596  
 QY 1927 -----HPTWVPHPEEVPVPCPDLITVRK----- 1951  
 Db 1597 IKTENLEQANBELPAILIKTKWRTSKMLDQVYPPAGDEBYVYKAYAFLLIOEYFRKT 1656  
 QY 1951 -----SGVSRTHSLPNDSYMCRNGS-TAERSLGHARGMGLPRAQS 1988  
 Db 1657 KRKEOGLVGRPSORNALSLQAGLRTLHDIGPEIRRAISGLTAEEB-----LDKAMK 1709  
 QY 1989 GSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPYWGALPKLPFPGRSLPACORPRAOI 2048  
 Db 1710 EAVSASABDIFRRAGGLFGNHVSY---YOSDSRSAPF-----QFTTQORPLH----- 1755  
 QY 2049 RUSLDVYGLSREDDLSEVSGPSCPLTRSSFWGSGSIOVQORSGIOSVSHI--RLPA 2107  
 Db 1755 -----ISKAGNNO---GDIESPHEKLVDSITFPSSYSTGSNANINANNATLALGRPL 1805  
 QY 2108 PCGLFERSMAKADPETSSLELDELTSWISGDLPLSSQOEPLSPDLKCYSVETOSCR 2167  
 Db 1806 PA-----GYBSTIVSTVE-----GHGSPISP-----AVRA 1829







Db 1185 -LDKNOR-----QCVEYALKARPLRRIYIPKNOHQKVVYVNSTY 1223

QY 1615 LDLFITGVIGLVNVTWAMEHHYQOQILDEALKCINITYIVFVESVFKLVAFGEFRFQ 1674

Db 1224 FEYIMFVILILNTICLAMOYHOSCLERIMANILNMLFTGLFVEMILKLIARPKHYFC 1283

QY 1675 DRWNQDLATVLLSIMGITLIEEIEVNASLPINPTI-----IRIMRYLIARVYKLL 1725

Db 1284 DANNTEFALIVGSIYDIATEVHPAHEHTQCSMSAEENSRISTIFFRIFRMYRIVKLL 1343

QY 1726 KMAVGRALLDYV---QALPOVNGLGLFMLFFIFALGVELFGDLDECDETHPCGGLG 1782

Db 1344 SRGEGIRTLMTFIKSFQALPYV---ALLVMLFITYAVIGMVFEGKIALNDT---TEIN 1397

QY 1783 RHATFRNFGMAFLTLFRVSTGDNMNGIMKDTL--RDCDOSTCYNTV-----ISPI 1831

Db 1398 RNNNFQTFPOAVYLLFRCAIGEMODIMLACMGKCAPESEPSNSTEGETPCGSSFAYF 1457

QY 1832 YFVSEVLLAQFVLNVNVIAYLM-----KHLEESNK-EAKEEAELEAELE- 1875

Db 1458 YFISFYMLCAFLIINFVAVIMDNFDYLRDMSILGPHHLEDEKRIWAEYDEAKGRIKH 1517

QY 1875 LEMKTLSPQHSPLGSPFLMP-----GVEGVNSPDSPKPGAPHTTAHGAAGFSLE-- 1927

Db 1518 LDVYTLRLRIQPLGFGKLCPRHVACKRLVSMNMLN-SDGTYMENVATLFLAVRTALRIK 1576

QY 1927 -----HPTMVPHEEVPIGLPDLITVRK----- 1951

Db 1577 TEGNEEQANBELRAIIKKIIMKRTSMKLLDQVVPAGDDEVYGFATFLIOEYFRKFKK 1636

QY 1951 -----SGVSRTHSLPNDSYMCRNGS-TAERSIG----- 1978

Db 1637 RKEQGLVGRPSORNALSLQAGLRTLHDIGPEIRAIISGDLTAEEELDKAMKEAVSASFD 1696

QY 1978 ---HRGMGL-----PKAOSGS-----ILSVHQPADTSCILQLP---KDY 2011

Db 1697 DIFRRAGGLFGNHNVSYYQSDSNFPQTATQRPPLHINKTGNQADT---ESPSEKLY 1752

QY 2012 HYILOPHGAPITWGALPKLPPEGRSPLAQRPRLRQAAIRTDLSLDVGLSGREDLSEVSGP 2071

Db 1753 DSTFTPSYSYSTGSNNANINNANNATLGRFP--HPAGYSTVSTVEGHGP-----P 1800

QY 2072 SCPLTR-SSSFWGSSIQYQOQSGIOSKYSKHIKLPAPCGLEPSMAKDPPTRSSLELD 2130

Db 1801 LSPAYRVOEAMKLSKRSCHRESQATVSQDM-----FPDETRSSVRLS 1845

QY 2131 TEL-----SWISGDLPPSSOEPLSPRDLKCCYSVETQSCRARP-GSWLDEQ---RRHS 2180

Db 1846 EYEVYCESEPSLSTDLISYQDE---NRQL-TCLEEDKREIOPSPKRSFLNSASISGRRAS 1901

QY 2181 IAVSCL---DSG---SQPRICP-----SPSSLGQPL---GGPGSRPKKILSPPSI 2222

Db 1902 FHLECLKRKQKDGCDISQKTAFLPLVHQAALAVAGLSPLQRSHTSPFRPRPTPV- 1961

QY 2223 SIDPPESGSRPPCSGVCARRARAPASDSDSVSSPLDSTASPKKDTLSGLSSD 2282

Db 1961 ---TSGSKR--PLQPIPLRLGAESEK---LNSSPFSIHCS-SWSEETTACSGGSSM 2011

QY 2283 PTDMDPVLLTLPNHLSPG 2301

Db 2012 ARARPVSLTVPSQAGAPG 2030

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=> s calcium channel

L2 66128 CALCIUM CHANNEL

=> s calcium (adj) channel

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=> s l2 and t()type

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=> s calcium () channel

L4 66128 CALCIUM (W) CHANNEL

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L5 916 L4 AND PANCREA?

=> s l5 and nucleo?

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=> s l5 and nucle?

L7 57 L5 AND NUCLE?

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L8 44 DUP REM L7 (13 DUPLICATES REMOVED)

=> d l8 ibib tot

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DOCUMENT NUMBER: 131:114762

TITLE: Chronic hyperglycemia triggers loss of  
**pancreatic** .beta. cell differentiation in an  
animal model of diabetes

AUTHOR(S): Jonas, Jean-Christophe; Sharma, Arun; Hasenkamp,  
Wendy; Ilkova, Hasan; Patane, Giovanni; Laybutt,  
Ross;

Bonner-Weir, Susan; Weir, Gordon C.  
CORPORATE SOURCE: Section Islet Transplantation and Cell Biology,  
Joslin

Diabetes Center, Boston, MA, 02215, USA  
SOURCE: J. Biol. Chem. (1999), 274(20), 14112-14121  
CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular  
Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

L8 ANSWER 2 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1999:265498 CAPLUS

DOCUMENT NUMBER: 131:39992



TITLE: Miniglucagon (glucagon 19-29), a potent and efficient inhibitor of secretagogue-induced insulin release through a Ca<sup>2+</sup> pathway  
AUTHOR(S): Dalle, Stephane; Smith, Paul; Blache, Philippe; Le-Nguyen, Dung; Le Brigand, Laurence; Bergeron, Francois; Ashcroft, Frances M.; Bataille, Dominique  
CORPORATE SOURCE: INSERM U376, CHU Arnaud-de-Villeneuve, Montpellier, 34295, Fr.  
SOURCE: J. Biol. Chem. (1999), 274(16), 10869-10876  
CODEN: JBCHA3; ISSN: 0021-9258  
PUBLISHER: American Society for Biochemistry and Molecular Biology  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 3 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1999:214527 CAPLUS  
DOCUMENT NUMBER: 131:28271  
TITLE: Multiple neuropeptide Y receptors regulate K<sup>+</sup> and Ca<sup>2+</sup>

channels in acutely isolated neurons from the rat arcuate **nucleus**

AUTHOR(S): Sun, Lihjen; Miller, Richard J.  
CORPORATE SOURCE: Department of Pharmacological and Physiological Sciences, The University of Chicago, Chicago, IL, 60637, USA  
SOURCE: J. Neurophysiol. (1999), 81(3), 1391-1403  
CODEN: JONEA4; ISSN: 0022-3077  
PUBLISHER: American Physiological Society  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 4 OF 44 MEDLINE

ACCESSION NUMBER: 1999180001 MEDLINE  
DOCUMENT NUMBER: 99180001  
TITLE: Conformational and functional variability supported by the BPTI fold: solution structure of the Ca<sup>2+</sup> channel blocker calciclude.  
AUTHOR: Gilquin B; Lecoq A; Desne F; Guenneugues M; Zinn-Justin S; Menez A  
CORPORATE SOURCE: CEA, Departement d'Ingenierie et d'Etudes des Proteines, Gif-sur-Yvette, France.  
SOURCE: PROTEINS, (1999 Mar 1) 34 (4) 520-32.  
Journal code: PTS. ISSN: 0887-3585.  
PUB. COUNTRY: United States  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: PDB-1BF0  
ENTRY MONTH: 199907  
ENTRY WEEK: 19990705

L8 ANSWER 5 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1999:167171 CAPLUS  
DOCUMENT NUMBER: 130:334321  
TITLE: Cloning of a novel four repeat protein related to voltage-gated sodium and calcium channels  
AUTHOR(S): Lee, Jung-Ha; Cribbs, Leanne L.; Perez-Reyes, Edward  
CORPORATE SOURCE: Department of Physiology, Loyola University Medical Center, Maywood, IL, 60153, USA  
SOURCE: FEBS Lett. (1999), 445(2,3), 231-236  
CODEN: FEBLAL; ISSN: 0014-5793  
PUBLISHER: Elsevier Science B.V.  
DOCUMENT TYPE: Journal  
LANGUAGE: English





L8 ANSWER 6 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 2000:1139 BIOSIS  
DOCUMENT NUMBER: PREV200000001139  
TITLE: Role of Ca<sup>2+</sup> in apoptosis evoked by human amylin in  
**pancreatic** islet beta-cells.  
AUTHOR(S): Bai, Ji-Zhong; Saafi, Edward L.; Zhang, Shaoping; Cooper,  
Garth J. S. (1)  
CORPORATE SOURCE: (1) School of Biological Sciences, University of Auckland,  
Auckland New Zealand  
SOURCE: Biochemical Journal, (Oct. 1, 1999) Vol. 343, No. 1, pp.  
53-61.  
ISSN: 0264-6021.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
SUMMARY LANGUAGE: English

L8 ANSWER 7 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1998:461708 CAPLUS  
DOCUMENT NUMBER: 129:240124  
TITLE: GH signaling in **pancreatic** .beta.-cells  
AUTHOR(S): Sekine, Nobuo; Wollheim, Claes B.; Fujita, Toshiro  
CORPORATE SOURCE: Fourth Department of Internal Medicine, University of  
Tokyo School of Medicine, Tokyo, 112, Japan  
SOURCE: Endocr. J. (Tokyo) (1998), 45(Suppl.), S33-S40  
CODEN: ENJOEO; ISSN: 0918-8959  
PUBLISHER: Japan Endocrine Society  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 8 OF 44 MEDLINE DUPLICATE 1  
ACCESSION NUMBER: 1998288284 MEDLINE  
DOCUMENT NUMBER: 98288284  
TITLE: Rapid activation and **nuclear** translocation of  
mitogen-activated protein kinases in response to  
physiological concentration of glucose in the MIN6  
**pancreatic** beta cell line.  
AUTHOR: Benes C; Roisin M P; Van Tan H; Creuzet C; Miyazaki J;  
Fagard R  
CORPORATE SOURCE: Laboratoire Signalisation Cellulaire et Parasites, UFR  
Cochin Universite Rene Descartes, Pavillon Gustave Roussy  
(6<sup>eme</sup> etage), 27, rue du Faubourg Saint Jacques, 75674  
Paris cedex 14, France.  
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Jun 19) 273 (25)  
15507-13.  
Journal code: HIV. ISSN: 0021-9258.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Cancer Journals  
ENTRY MONTH: 199809  
ENTRY WEEK: 19980902

L8 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1998:383101 CAPLUS  
DOCUMENT NUMBER: 129:118063  
TITLE: Class A **calcium channel** variants  
in **pancreatic** islets and their role in  
insulin secretion  
AUTHOR(S): Ligon, Brooke; Boyd, Aubrey E., III; Dunlap, Kathleen  
CORPORATE SOURCE: Departments of Neuroscience and Physiology, Tufts  
University School of Medicine, Boston, MA, 02111, USA  
SOURCE: J. Biol. Chem. (1998), 273(22), 13905-13911  
CODEN: JBCHA3; ISSN: 0021-9258  
PUBLISHER: American Society for Biochemistry and Molecular  
Biology  
DOCUMENT TYPE: Journal



LANGUAGE: English

L8 ANSWER 10 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1998:297535 CAPLUS  
DOCUMENT NUMBER: 129:65836  
TITLE: A novel lipid-anchored A-kinase anchoring protein facilitates cAMP-responsive membrane events  
AUTHOR(S): Fraser, Iain D. C.; Tavalin, Steven J.; Lester, Linda B.; Langeberg, Lorene K.; Westphal, Ann M.; Dean, Rebecca A.; Marrion, Neil V.; Scott, John D.  
CORPORATE SOURCE: Howard Hughes Medical Institute, Oregon Health Sciences University, Portland, OR, 97201, USA  
SOURCE: EMBO J. (1998), 17(8), 2261-2272  
CODEN: EMJODG; ISSN: 0261-4189  
PUBLISHER: Oxford University Press  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 11 OF 44 MEDLINE DUPLICATE 2  
ACCESSION NUMBER: 1998278957 MEDLINE  
DOCUMENT NUMBER: 98278957  
TITLE: Calcium-dependent clustering of inositol 1,4,5-trisphosphate receptors.  
AUTHOR: Wilson B S; Pfeiffer J R; Smith A J; Oliver J M; Oberdorf J  
CORPORATE SOURCE: A; Wojcikiewicz R J  
Department of Pathology and Cancer Research and Treatment Center, University of New Mexico, Albuquerque, New Mexico 87131, USA.. bwilson@rapunzel.unm.edu  
CONTRACT NUMBER: GM50562 (NIGMS)  
HL56384 (NHLBI)  
GM49814 (NIGMS)  
+  
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (1998 Jun) 9 (6) 1465-78.  
Journal code: BAU. ISSN: 1059-1524.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199809  
ENTRY WEEK: 19980903

L8 ANSWER 12 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1998:483379 BIOSIS  
DOCUMENT NUMBER: PREV199800483379  
TITLE: Serum from diabetic BB/W rats enhances calcium currents in primary sensory neurons.  
AUTHOR(S): Ristic, Helen; Srinivasan, Shanthi; Hall, Karen E.; Sima, Anders A. F.; Wiley, John W. (1)  
CORPORATE SOURCE: (1) Veterans Aff. Med. Cent., 2215 Fuller Rd., Rm. B501a, Box 111D, Ann Arbor, MI 48105 USA  
SOURCE: Journal of Neurophysiology (Bethesda), (Sept., 1998) Vol. 80, No. 3, pp. 1236-1244.  
ISSN: 0022-3077.  
DOCUMENT TYPE: Article  
LANGUAGE: English

L8 ANSWER 13 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1998:126168 CAPLUS  
DOCUMENT NUMBER: 128:266280  
TITLE: Cellular regulation of islet hormone secretion by the incretin hormone glucagon-like peptide 1  
AUTHOR(S): Gromada, J.; Holst, Jens Juul; Rorsman, Patrik  
CORPORATE SOURCE: The Symbion Science Park, Novo Nordisk A/S,  
Department  
of Islet Cell Physiology, Fruebjergvej 3, Copenhagen,



SOURCE: DK-2100, Den.  
Pfluegers Arch. (1998), 435(5), 583-594  
CODEN: PFLABK; ISSN: 0031-6768  
PUBLISHER: Springer-Verlag  
DOCUMENT TYPE: Journal; General Review  
LANGUAGE: English

L8 ANSWER 14 OF 44 MEDLINE

ACCESSION NUMBER: 1998324886 MEDLINE  
DOCUMENT NUMBER: 98324886  
TITLE: Interplay between cytoplasmic Ca<sup>2+</sup> and the ATP/ADP ratio:  
a  
feedback control mechanism in mouse **pancreatic**  
islets.  
AUTHOR: Detimary P; Gilon P; Henquin J C  
CORPORATE SOURCE: Unit of Endocrinology and Metabolism, University of  
Louvain  
Faculty of Medicine, UCL 55.30, Avenue Hippocrate 55,  
B-1200 Brussels, Belgium.  
SOURCE: BIOCHEMICAL JOURNAL, (1998 Jul 15) 333 ( Pt 2) 269-74.  
Journal code: 9YO. ISSN: 0264-6021.  
PUB. COUNTRY: ENGLAND: United Kingdom  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Cancer Journals  
ENTRY MONTH: 199811  
ENTRY WEEK: 19981102

L8 ANSWER 15 OF 44 MEDLINE

ACCESSION NUMBER: 1998355757 MEDLINE  
DOCUMENT NUMBER: 98355757  
TITLE: Secretory effects of ATP on nontransformed dog  
**pancreatic** duct epithelial cells.  
AUTHOR: Nguyen T D; Moody M W; Savard C E; Lee S P  
CORPORATE SOURCE: Department of Medicine, University of Washington, and  
Veterans Affairs Puget Sound Health Care System, Seattle,  
Washington 98108, USA.  
CONTRACT NUMBER: DK-50246 (NIDDK)  
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1998 Jul) 275 (1 Pt 1)  
G104-13.  
Journal code: 3U8. ISSN: 0002-9513.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199810  
ENTRY WEEK: 19981005

L8 ANSWER 16 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:72127 CAPLUS  
DOCUMENT NUMBER: 128:213105  
TITLE: Okadaic acid-induced decrease in the magnitude and  
efficacy of the Ca<sup>2+</sup> signal in **pancreatic**  
.beta. cells and inhibition of insulin secretion  
AUTHOR(S): Sato, Yoshihiko; Mariot, Pascal; Detimary, Philippe;  
Gilon, Patrick; Henquin, Jean-Claude  
CORPORATE SOURCE: Unite d'Endocrinologie et Metabolisme, UCL 55.30,  
University of Louvain Faculty of Medicine, Brussels,  
B-1200, Belg.  
SOURCE: Br. J. Pharmacol. (1998), 123(1), 97-105  
CODEN: BJPCBM; ISSN: 0007-1188  
PUBLISHER: Stockton Press  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 17 OF 44 CAPLUS COPYRIGHT 2000 ACS



ACCESSION NUMBER: 1997:414611 CAPLUS  
DOCUMENT NUMBER: 127:119916  
TITLE: Polarized expression of Ca<sup>2+</sup> channels in  
**pancreatic** and salivary gland cells.  
Correlation with initiation and propagation of  
[Ca<sup>2+</sup>]<sub>i</sub> waves  
AUTHOR(S): Lee, Min Goo; Xu, Xin; Zeng, Weizhong; Diaz, Julie;  
Wojcikiewicz, Richard J. H.; Kuo, Tuan H.; Wuytack,  
Frank; Racymaekers, Luc; Muallem, Shmuel  
CORPORATE SOURCE: Department of Physiology, University of Texas  
Southwestern Medical Center, Dallas, TX, 75235, USA  
SOURCE: J. Biol. Chem. (1997), 272(25), 15765-15770  
CODEN: JBCHA3; ISSN: 0021-9258  
PUBLISHER: American Society for Biochemistry and Molecular  
Biology  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 18 OF 44 MEDLINE

ACCESSION NUMBER: 97375339 MEDLINE  
DOCUMENT NUMBER: 97375339  
TITLE: Atrial natriuretic peptide and cyclic **nucleotides**  
affect glucose-induced Ca<sup>2+</sup> responses in single  
**pancreatic** islet beta-cells: correlation with  
(Ca<sup>2+</sup>) + Mg<sup>2+</sup>-ATPase activity.  
AUTHOR: Lee B; Laychock S G  
CORPORATE SOURCE: Department of Pharmacology and Toxicology, School of  
Medicine and Biomedical Sciences, State University of New  
York at Buffalo, 14214, USA.  
CONTRACT NUMBER: DK-25705 (NIDDK)  
SOURCE: DIABETES, (1997 Aug) 46 (8) 1312-8.  
Journal code: E8X. ISSN: 0012-1797.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals  
ENTRY MONTH: 199710

L8 ANSWER 19 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1997:307834 CAPLUS  
DOCUMENT NUMBER: 127:105147  
TITLE: Identification of four trp1 gene variants murine  
**pancreatic** beta-cells  
AUTHOR(S): Sakura, H.; Ashcroft, F. M.  
CORPORATE SOURCE: Laboratory Physiology, University Oxford, Oxford, OX1  
3PT, UK  
SOURCE: Diabetologia (1997), 40(5), 528-532  
CODEN: DBTG AJ; ISSN: 0012-186X  
PUBLISHER: Springer  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 20 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1997:193494 CAPLUS  
DOCUMENT NUMBER: 126:272641  
TITLE: G protein-dependent inhibition of L-type Ca<sup>2+</sup>  
currents  
by acetylcholine in mouse **pancreatic** B-cells  
AUTHOR(S): Gilon, Patrick; Yakel, Jerrel; Gromada, Jesper; Zhu,  
Yu; Henquin, Jean-Claude; Rorsman, Patrik  
CORPORATE SOURCE: Islet Cell Physiology, Novo Nordisk A/S, Copenhagen,  
DK-2100, Den.  
SOURCE: J. Physiol. (Cambridge, U. K.) (1997), 499(1), 65-76  
CODEN: JPHYA7; ISSN: 0022-3751  
PUBLISHER: Cambridge University Press





DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 21 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1996:309675 CAPLUS  
DOCUMENT NUMBER: 125:6550  
TITLE: Regulation of the inositol 1,4,5-trisphosphate-  
activated Ca<sup>2+</sup> channel by activation of G proteins  
AUTHOR(S): Xu, Xin; Zeng, Weizhong; Muallem, Shmuel  
CORPORATE SOURCE: Dep. Physiol., Univ. Texas Southwest. Med. Sch.,  
Dallas, TX, 75235, USA  
SOURCE: J. Biol. Chem. (1996), 271(20), 11737-11744  
CODEN: JBCHA3; ISSN: 0021-9258  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 22 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1996:491197 CAPLUS  
DOCUMENT NUMBER: 125:186268  
TITLE: Up-regulation of L- and non-L, non-N-type Ca<sup>2+</sup>  
channels by basal and stimulated protein kinase C  
activation in insulin-secreting RINm5F cells  
AUTHOR(S): Platano, D.; Pollo, A.; Carbone, E.; Aicardi, G.  
CORPORATE SOURCE: Dipartimento di Neuroscienze, Corso Raffaello 30,  
Turin, 10125, Italy  
SOURCE: FEBS Lett. (1996), 391(1,2), 189-194  
CODEN: FEBLAL; ISSN: 0014-5793  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 23 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1996:297205 CAPLUS  
DOCUMENT NUMBER: 124:333720  
TITLE: Noradrenaline inhibition of Ca<sup>2+</sup> channels and  
secretion in single patch-clamped insulinoma cells  
AUTHOR(S): Sher, Emanuele; Codignola, Agnese; Rogers, Marc;  
Richmond, Janet  
CORPORATE SOURCE: Bekesy Laboratory of Neurobiology, Pacific Biomedical  
Research Center, University of Hawaii, 1993 East West  
Road, Honolulu, HI 96822, USA  
SOURCE: FEBS Lett. (1996), 385(3), 176-180  
CODEN: FEBLAL; ISSN: 0014-5793  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 24 OF 44 MEDLINE DUPLICATE 3  
ACCESSION NUMBER: 96030778 MEDLINE  
DOCUMENT NUMBER: 96030778  
TITLE: Subunit composition of G(o) proteins functionally coupling  
galanin receptors to voltage-gated calcium channels.  
AUTHOR: Kalkbrenner F; Degtiar V E; Schenker M; Brendel S; Zobel  
A;  
Heschler J; Wittig B; Schultz G  
CORPORATE SOURCE: Institut fur Pharmakologie der Freien Universitat Berlin,  
Germany.  
SOURCE: EMBO JOURNAL, (1995 Oct 2) 14 (19) 4728-37.  
Journal code: EMB. ISSN: 0261-4189.  
PUB. COUNTRY: ENGLAND: United Kingdom  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199602

L8 ANSWER 25 OF 44 MEDLINE DUPLICATE 4  
ACCESSION NUMBER: 95269695 MEDLINE  
DOCUMENT NUMBER: 95269695



TITLE: Evidence that Rap1 carboxylmethylation is involved in regulated insulin secretion.  
AUTHOR: Leiser M; Efrat S; Fleischer N  
CORPORATE SOURCE: Department of Medicine, Albert Einstein College of Medicine, Bronx, New York 10461, USA.  
CONTRACT NUMBER: DK-20541 (NIDDK)  
SOURCE: ENDOCRINOLOGY, (1995 Jun) 136 (6) 2521-30.  
Journal code: EGZ. ISSN: 0013-7227.  
PUB. COUNTRY: United States  
LANGUAGE: English  
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals; Cancer Journals  
ENTRY MONTH: 199508

L8 ANSWER 26 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1995:513975 CAPLUS  
DOCUMENT NUMBER: 122:282706  
TITLE: **Pancreatic** polypeptide inhibits calcium channels in rat sympathetic neurons via two signaling pathways  
AUTHOR(S): Wollmuth, Lonnie P.; Shapiro, Mark S.; Hille, Bertil  
CORPORATE SOURCE: Department of Physiology and Biophysics, University of Washington, Seattle, WA, 98195, USA  
SOURCE: J. Neurophysiol. (1995), 73(3), 1323-8  
CODEN: JONEA4; ISSN: 0022-3077  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 27 OF 44 MEDLINE

ACCESSION NUMBER: 95314638 MEDLINE  
DOCUMENT NUMBER: 95314638  
TITLE: The regulatory site of functional GTP binding protein coupled to the high affinity cholecystokinin receptor and phospholipase A2 pathway is on the G beta subunit of Gq protein in **pancreatic** acini.  
AUTHOR: Tsunoda Y; Owyang C  
CORPORATE SOURCE: Department of Internal Medicine, University of Michigan, Ann Arbor 48109, USA.  
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1995 Jun 15) 211 (2) 648-55.  
Journal code: 9Y8. ISSN: 0006-291X.  
PUB. COUNTRY: United States  
LANGUAGE: English  
FILE SEGMENT: Cancer Journals; Priority Journals  
ENTRY MONTH: 199509

L8 ANSWER 28 OF 44 MEDLINE

DUPLICATE 5

ACCESSION NUMBER: 96044438 MEDLINE  
DOCUMENT NUMBER: 96044438  
TITLE: The structures of the human **calcium channel** alpha 1 subunit (CACNL1A2) and beta subunit (CACNLB3) genes.  
AUTHOR: Yamada Y; Masuda K; Li Q; Ihara Y; Kubota A; Miura T; Nakamura K; Fujii Y; Seino S; Seino Y  
CORPORATE SOURCE: Department of Metabolism and Clinical Nutrition, Kyoto University Faculty of Medicine, Japan..  
SOURCE: GENOMICS, (1995 May 20) 27 (2) 312-9.  
Journal code: GEN. ISSN: 0888-7543.  
PUB. COUNTRY: United States  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-D43701; GENBANK-D43702; GENBANK-D43703;



GENBANK-D43704; GENBANK-D43705; GENBANK-D43706;  
GENBANK-D43707; GENBANK-D43708; GENBANK-D43709;  
GENBANK-D43710; GENBANK-D43711; GENBANK-D43712;  
GENBANK-D43713; GENBANK-D43714; GENBANK-D43715;  
GENBANK-D43716; GENBANK-D43717; GENBANK-D43718;  
GENBANK-D43719; GENBANK-D43720; GENBANK-D43721;  
GENBANK-D43722; GENBANK-D43723; GENBANK-D43724;  
GENBANK-D43725; GENBANK-D43726; GENBANK-D43727;  
GENBANK-D43728; GENBANK-D43729; GENBANK-D43730; +

ENTRY MONTH: 199601

L8 ANSWER 29 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1996:93533 CAPLUS

DOCUMENT NUMBER: 124:136099

TITLE: Voltage-dependent calcium channels in  
insulin-secreting cells

AUTHOR(S): Seino, Susumu; Fujii, Yasukazu; Ihara, Yu; Inagaki,  
Nobuya; Seino, Yutaka; Yamada, Yuichiro; Gonoi, Tohru

CORPORATE SOURCE: School Medicine, Chiba University, Chiba, 260, Japan

SOURCE: Int. Congr. Ser. (1995), 1100(Diabetes 1994), 187-92

DOCUMENT TYPE: Journal

LANGUAGE: English

L8 ANSWER 30 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 6

ACCESSION NUMBER: 1995:155906 BIOSIS

DOCUMENT NUMBER: PREV199598170206

TITLE: Molecular diversity and functional characterization of  
voltage-dependent calcium channels (CACN4) expressed in  
**pancreatic** beta-cell.

AUTHOR(S): Ihara, Yu (1); Yamada, Yuichiro; Fujii, Yasukazu; Gonoi,  
Tohru; Yano, Hideki; Yasuda, Koichiro; Inagaki, Nobuya;  
Seino, Yutaka; Seino, Susumu

CORPORATE SOURCE: (1) Dep. Metabol. Clin. Nutr., Kyoto Univ. Fac. Med., 54  
Shogoin-Kawaharacho, Sakyo-ku, Kyoto 606 Japan

SOURCE: Molecular Endocrinology, (1995) Vol. 9, No. 1, pp.  
121-130.

ISSN: 0888-8809.

DOCUMENT TYPE: Article

LANGUAGE: English

L8 ANSWER 31 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1993:647986 CAPLUS

DOCUMENT NUMBER: 119:247986

TITLE: Human monoclonal antibodies and methods for their  
production

INVENTOR(S): Whitaker, Robert Blake

PATENT ASSIGNEE(S): Immunet, USA

SOURCE: PCT Int. Appl., 52 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE     |
|--|------|----------|-----------------|----------|
| WO 9319197   | A1   | 19930930 | WO 1993-US2479  | 19930318 |
| W: AU, CA, JP  |      |          |                 |          |
| RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE |      |          |                 |          |
| AU 9339232   | A1   | 19931021 | AU 1993-39232   | 19930318 |
| EP 651819  | A1   | 19950510 | EP 1993-908394  | 19930318 |
| R: CH, DE, FR, GB, IT, LI  |      |          |                 |          |
| JP 07507923  | T2   | 19950907 | JP 1993-516719  | 19930318 |
| PRIORITY APPLN. INFO.:   |      |          | US 1992-856088  | 19920320 |
|  |      |          | WO 1993-US2479  | 19930318 |



L8 ANSWER 32 OF 44 MEDLINE

ACCESSION NUMBER: 93186832 MEDLINE

DOCUMENT NUMBER: 93186832

TITLE: Membrane depolarization and calcium influx induce glucagon gene transcription in **pancreatic** islet cells through the cyclic AMP-responsive element.

AUTHOR: Schwaninger M; Lux G; Blume R; Oetjen E; Hidaka H; Knepel W

CORPORATE SOURCE: Department of Biochemical Pharmacology, University of Goettingen, Germany.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1993 Mar 5) 268 (7) 5168-77.

Journal code: HIV. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals; Cancer Journals

ENTRY MONTH: 199306

L8 ANSWER 33 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1993:463946 CAPLUS

DOCUMENT NUMBER: 119:63946

TITLE: Neuropeptide Y and **pancreatic** polypeptide reduce calcium currents in acutely dissociated

neurons

AUTHOR(S): Foucart, S.; Bleakman, D.; Bindokas, V. P.; Miller, R.

CORPORATE SOURCE: J.  
Dep. Pharmacol. Physiol. Sci., Univ. Chicago, Chicago,

SOURCE: IL, USA  
J. Pharmacol. Exp. Ther. (1993), 265(2), 903-9

CODEN: JPETAB; ISSN: 0022-3565

DOCUMENT TYPE: Journal

LANGUAGE: English

L8 ANSWER 34 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1993:388776 BIOSIS

DOCUMENT NUMBER: PREV199396064076

TITLE: Increased activity of L-type calcium channels exposed to serum from patients with type I diabetes.

AUTHOR(S): Juntti-Berggren, Lisa; Larsson, Olof; Rorsman, Patrik; Ammala, Carina; Bokvist, Krister; Wahlander, Karin; Nicotera, Pierluigi; Dypbukt, Jeanette; Orrenius, Sten; et al.

CORPORATE SOURCE: Inq.: Per-Olof Berggren, Dep. Endocrinol., Karolinska Inst., Box 60500, Karolinska Hosp., S-104 01 Stockholm Sweden

SOURCE: Science (Washington D C), (1993) Vol. 261, No. 5117, pp. 86-90.

ISSN: 0036-8075.

DOCUMENT TYPE: Article

LANGUAGE: English

L8 ANSWER 35 OF 44 MEDLINE

DUPLICATE 7

ACCESSION NUMBER: 93140024 MEDLINE

DOCUMENT NUMBER: 93140024

TITLE: Effect of Ca++ channel blockers on energy level and stimulated insulin secretion in isolated rat islets of Langerhans.

AUTHOR: Ohta M; Nelson J; Nelson D; Meglasson M D; Erecinska M

CORPORATE SOURCE: Department of Pharmacology, University of Pennsylvania School of Medicine, Philadelphia..

CONTRACT NUMBER: DK-35808 (NIDDK)





SOURCE: DK-19525 (NIDDK)  
JOURNAL OF PHARMACOLOGY AND EXPERIMENTAL THERAPEUTICS,  
(1993 Jan) 264 (1) 35-40.  
PUB. COUNTRY: Journal code: JP3. ISSN: 0022-3565.  
United States  
LANGUAGE: Journal; Article; (JOURNAL ARTICLE)  
English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199304

L8 ANSWER 36 OF 44 MEDLINE DUPLICATE 8  
ACCESSION NUMBER: 92115705 MEDLINE  
DOCUMENT NUMBER: 92115705  
TITLE: Cloning of the alpha 1 subunit of a voltage-dependent  
**calcium channel** expressed in  
**pancreatic** beta cells.  
AUTHOR: Seino S; Chen L; Seino M; Blondel O; Takeda J; Johnson J  
H;  
CORPORATE SOURCE: Bell G I  
Howard Hughes Medical Institute, University of Chicago, IL  
60637..  
CONTRACT NUMBER: DK20595 (NIDDK)  
DK42086 (NIDDK)  
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE  
UNITED STATES OF AMERICA, (1992 Jan 15) 89 (2) 584-8.  
PUB. COUNTRY: Journal code: PV3. ISSN: 0027-8424.  
United States  
LANGUAGE: Journal; Article; (JOURNAL ARTICLE)  
English  
FILE SEGMENT: Priority Journals; Cancer Journals  
OTHER SOURCE: GENBANK-M83566  
ENTRY MONTH: 199204

L8 ANSWER 37 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1993:150382 BIOSIS  
DOCUMENT NUMBER: PREV199344069182  
TITLE: Is the neuronal voltage-sensitive **calcium**  
**channel** of human brain, human **pancreatic**  
beta cells and rat brain much larger than predicted by its  
cDNA sequence.  
AUTHOR(S): Osherov, Azriel; Goldberg, Doron; Atlas, Daphne (1)  
CORPORATE SOURCE: (1) Otto Lowe Cent. Mol. and Cell. Biol., Jerusalem 91904  
Israel  
SOURCE: Neuroscience Letters, (1992) Vol. 147, No. 2, pp.  
233-235.  
ISSN: 0304-3940.  
DOCUMENT TYPE: Article  
LANGUAGE: English

L8 ANSWER 38 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1992:76799 CAPLUS  
DOCUMENT NUMBER: 116:76799  
TITLE: Mastoparan-induced hormone release from rat  
**pancreatic** islets  
AUTHOR(S): Komatsu, Mitsuhisa; Aizawa, Toru; Yokokawa, Nakako;  
Sato, Yoshihiko; Okada, Naomi; Takasu, Nobuyuki;  
Yamada, Takashi  
CORPORATE SOURCE: Sch. Med., Shinshu Univ., Matsumoto, Japan  
SOURCE: Endocrinology (Baltimore) (1992), 130(1), 221-8  
CODEN: ENDOAO; ISSN: 0013-7227  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 39 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1992:125438 CAPLUS  
DOCUMENT NUMBER: 116:125438



TITLE: Inhibition of L-type calcium channels by internal GTP[.gamma.S] in mouse **pancreatic** .beta. cells  
AUTHOR(S): Ammala, Carina; Berggren, Per Olof; Bokvist, Krister; Rorsman, Patrik  
CORPORATE SOURCE: Dep. Med. Phys., Goeteborg Univ., Goeteborg, S-400 33,  
Swed.  
SOURCE: Pfluegers Arch. (1992), 420(1), 72-7  
CODEN: PFLABK; ISSN: 0031-6768  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 40 OF 44 MEDLINE

ACCESSION NUMBER: 93122387 MEDLINE  
DOCUMENT NUMBER: 93122387  
TITLE: Ion channels.  
AUTHOR: Catterall W; Epstein P N  
CORPORATE SOURCE: Department of Pharmacology, School of Medicine, University of Washington, Seattle.  
SOURCE: DIABETOLOGIA, (1992 Dec) 35 Suppl 2 S23-33. Ref: 49  
Journal code: E93. ISSN: 0012-186X.  
PUB. COUNTRY: GERMANY: Germany, Federal Republic of  
Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199304

L8 ANSWER 41 OF 44 MEDLINE

ACCESSION NUMBER: 91250424 MEDLINE  
DOCUMENT NUMBER: 91250424  
TITLE: Glucose induces insulin gene transcription in a murine **pancreatic** beta-cell line.  
AUTHOR: Efrat S; Surana M; Fleischer N  
CORPORATE SOURCE: Department of Molecular Pharmacology, Albert Einstein College of Medicine, Bronx, New York 10461.  
CONTRACT NUMBER: DK20541 (NIDDK)  
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Jun 15) 266 (17) 11141-3.  
Journal code: HIV. ISSN: 0021-9258.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Cancer Journals  
ENTRY MONTH: 199109

L8 ANSWER 42 OF 44 MEDLINE

ACCESSION NUMBER: 91132190 MEDLINE  
DOCUMENT NUMBER: 91132190  
TITLE: Neuropeptide Y receptor in vascular smooth muscle.  
AUTHOR: Shigeri Y; Mihara S; Fujimoto M  
CORPORATE SOURCE: Shionogi Research Laboratories, Shionogi and Co., Ltd., Osaka, Japan..  
SOURCE: JOURNAL OF NEUROCHEMISTRY, (1991 Mar) 56 (3) 852-9.  
Journal code: JAV. ISSN: 0022-3042.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199105

L8 ANSWER 43 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1991:624520 CAPLUS  
DOCUMENT NUMBER: 115:224520



TITLE: Alpha2-adrenoreceptor stimulation does not inhibit  
L-type calcium channels in mouse **pancreatic**  
.beta.-cells  
AUTHOR(S): Bokvist, Krister; Aemmaelae, Carina; Berggren, Per  
Olof; Rorsman, Patrik; Waahlander, Karin  
CORPORATE SOURCE: Dep. Med. Phys., Gothenburg Univ., Goeteborg, S-400  
33, Swed.  
SOURCE: Biosci. Rep. (1991), 11(3), 147-57  
CODEN: BRPTDT; ISSN: 0144-8463  
DOCUMENT TYPE: Journal  
LANGUAGE: English

L8 ANSWER 44 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1982:251466 BIOSIS  
DOCUMENT NUMBER: BA74:23946  
TITLE: CALCIUM MOVEMENTS AND INSULIN RELEASE IN **PANCREATIC**  
ISLET CELLS.  
AUTHOR(S): HERCHUELZ A; MALAISSE W J  
CORPORATE SOURCE: LAB. PHARMACODYNAMIE, THERAPEUTIQUE, UNIV. LIBRE  
BRUXELLES,  
BLVD. WATERLOO 115, B-1000 BRUXELLES, BELG.  
SOURCE: DIABETE METAB, (1981 (RECD 1982)) 7 (4), 283-288.  
CODEN: DIMEDU. ISSN: 0338-1684.  
FILE SEGMENT: BA; OLD  
LANGUAGE: English

=> d history

(FILE 'HOME' ENTERED AT 16:16:13 ON 19 JAN 2000)

FILE 'MEDLINE, BIOSIS, LIFESCI, CAPLUS' ENTERED AT 16:16:54 ON 19 JAN  
2000  
L1 0 S CALCIUM ADJ CHANNEL  
L2 66128 S CALCIUM CHANNEL  
L3 1453 S L2 AND T()TYPE  
L4 66128 S CALCIUM () CHANNEL  
L5 916 S L4 AND PANCREA?  
L6 41 S L5 AND NUCLEO?  
L7 57 S L5 AND NUCLE?  
L8 44 DUP REM L7 (13 DUPLICATES REMOVED)

=> s l5 and (antisens? or (anti())sens?) or ribozym? or triplex)

3 FILES SEARCHED...

L9 9 L5 AND (ANTISENS? OR (ANTI(W) SENS?) OR RIBOZYM? OR TRIPLEX)

=> dup rem l9

PROCESSING COMPLETED FOR L9

L10 6 DUP REM L9 (3 DUPLICATES REMOVED)

=> d l10

L10 ANSWER 1 OF 6 MEDLINE  
AN 1999052336 MEDLINE  
DN 99052336  
TI Contribution of Na/Ca exchange to Ca<sup>2+</sup> outflow and entry in the rat  
**pancreatic** beta-cell: studies with **antisense**  
oligonucleotides.  
AU Van Eylen F; Lebeau C; Albuquerque-Silva J; Herchuelz A  
CS Laboratory of Pharmacology, Universite Libre de Bruxelles, School of  
Medicine, Brussels, Belgium.  
SO DIABETES, (1998 Dec) 47 (12) 1873-80.



Journal code: E8X. ISSN: 0012-1797.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Abridged Index Medicus Journals; Priority Journals  
EM 199902  
EW 19990204

=> d l10 tot ibib abs

L10 ANSWER 1 OF 6 MEDLINE  
ACCESSION NUMBER: 1999052336 MEDLINE  
DOCUMENT NUMBER: 99052336  
TITLE: Contribution of Na/Ca exchange to Ca<sup>2+</sup> outflow and entry  
in the rat **pancreatic** beta-cell: studies with  
**antisense** oligonucleotides.  
AUTHOR: Van Eylen F; Lebeau C; Albuquerque-Silva J; Herchuelz A  
CORPORATE SOURCE: Laboratory of Pharmacology, Universite Libre de Bruxelles,  
School of Medicine, Brussels, Belgium.  
SOURCE: DIABETES, (1998 Dec) 47 (12) 1873-80.  
Journal code: E8X. ISSN: 0012-1797.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals  
ENTRY MONTH: 199902  
ENTRY WEEK: 19990204  
AB To characterize the role played by Na/Ca exchange in the  
**pancreatic** beta-cell, phosphorothioated **antisense**  
oligonucleotides (AS-oligos) were used to knock down the exchanger in rat  
**pancreatic** beta-cells. Na/Ca exchange activity was evaluated by  
measuring cytosolic free Ca<sup>2+</sup> concentration ([Ca<sup>2+</sup>]<sub>i</sub>) in single cells  
using fura-2. Exposure of beta-cells to 500 nmol/l of the AS-oligos for  
24 h inhibited Na/Ca exchange activity by approximately 77%. In contrast,  
control oligonucleotides (scrambled and mismatched) did not affect Na/Ca  
exchange activity. In AS-oligo-treated cells, the increase in [Ca<sup>2+</sup>]<sub>i</sub>  
induced by membrane depolarization (K<sup>+</sup> or the hypoglycemic sulfonylurea,  
tolbutamide) was reduced by 28 or 40%, respectively. Likewise, the rate  
of [Ca<sup>2+</sup>]<sub>i</sub> decrease after K<sup>+</sup> or tolbutamide removal was reduced by 72 or  
40%, respectively. AS-oligos treatment also abolished the nifedipine-resistant  
increase in [Ca<sup>2+</sup>]<sub>i</sub> induced by K<sup>+</sup> and profoundly altered the oscillatory  
or sustained increases in [Ca<sup>2+</sup>]<sub>i</sub> induced by 11.1 mmol/l glucose. The  
present study shows that AS-oligos may specifically inhibit Na/Ca  
exchange in rat **pancreatic** beta-cells. In those cells, Na/Ca exchange  
appears to mediate Ca<sup>2+</sup> entry in response to membrane depolarization and  
to be responsible for up to 70% of Ca<sup>2+</sup> removal from the cytoplasm upon  
membrane repolarization.

L10 ANSWER 2 OF 6 MEDLINE  
ACCESSION NUMBER: 1999039911 MEDLINE  
DOCUMENT NUMBER: 99039911  
TITLE: Cysteine-string proteins regulate exocytosis of insulin  
independent from transmembrane ion fluxes.  
AUTHOR: Zhang H; Kelley W L; Chamberlain L H; Burgoyne R D;  
Wollheim C B; Lang J  
CORPORATE SOURCE: Departement de Medecine Interne, Centre Medical  
Universitaire, Gen'ève, Switzerland.  
SOURCE: FEBS LETTERS, (1998 Oct 23) 437 (3) 267-72.  
Journal code: EUH. ISSN: 0014-5793.





PUB. COUNTRY: Netherlands  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Cancer Journals  
ENTRY MONTH: 199902  
ENTRY WEEK: 19990204

AB Cysteine-string proteins (Csps) are vesicle proteins involved in exocytosis of synaptic vesicles in *Drosophila* and modulation of presynaptic calcium influx. As both the contribution of **calcium channel** regulation to the role of Csp in exocytosis and a function of Csp outside the nervous system are unknown, we studied its function in endocrine exocytosis from large dense core vesicles (LDCVs) using insulin-secreting **pancreatic** beta-cells. Csps were expressed in primary and derived beta-cell lines on insulin-containing LDCVs. Suppression of Csp expression reduced not only depolarisation induced insulin release but also exocytosis in permeabilised cells directly stimulated by  $Ca^{2+}$ . Thus, Csp is a secretory granule protein and is required for endocrine exocytosis independent of the modulation of transmembrane calcium fluxes.

L10 ANSWER 3 OF 6 MEDLINE  
ACCESSION NUMBER: 96440205 MEDLINE  
DOCUMENT NUMBER: 96440205  
TITLE: AR4-2J cell line coexpresses dihydropyridine and omega-conotoxin sensitive  $Ca^{2+}$  channels.  
AUTHOR: Bertrand V; Bastie M J; Bouisson M; Vaysse N; Pradayrol L  
CORPORATE SOURCE: INSERM U 151, Institut Federatif de Recherches Louis Bugnard, CHU Rangueil, Toulouse, France.  
SOURCE: CELL CALCIUM, (1996 Jun) 19 (6) 495-500.  
Journal code: CQE. ISSN: 0143-4160.  
PUB. COUNTRY: SCOTLAND: United Kingdom  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199707  
ENTRY WEEK: 19970702

AB For the first time, we have demonstrated in AR4-2J cells, an experimental model of azaserine-induced carcinoma in the rat exocrine **pancreas**, the co-expression of alpha 1 subunit of dihydropyridine-sensitive  $Ca^{2+}$  channel and the alpha 1 sub-unit of omega-conotoxin-sensitive  $Ca^{2+}$  channel

RNA messengers which share homologous sequences with, respectively, rbc

II

and rbb I sub-types described in the rat brain. These two types of voltage-dependent  $Ca^{2+}$  channels which are functionally expressed, emphasize the acquisition during carcinogenesis of neuroendocrine features

of AR4-2J cells. Additionally, using **antisense** phosphorothioate oligodeoxynucleotide, we demonstrated clearly the involvement of dihydropyridine-sensitive  $Ca^{2+}$  channels in the control of AR4-2J cell proliferation.

L10 ANSWER 4 OF 6 MEDLINE  
ACCESSION NUMBER: 96030778 MEDLINE  
DOCUMENT NUMBER: 96030778  
TITLE: Subunit composition of G(o) proteins functionally coupling galanin receptors to voltage-gated calcium channels.  
AUTHOR: Kalkbrenner F; Degtiar V E; Schenker M; Brendel S; Zobel A;  
Heschler J; Wittig B; Schultz G  
CORPORATE SOURCE: Institut fur Pharmakologie der Freien Universitat Berlin, Germany.  
SOURCE: EMBO JOURNAL, (1995 Oct 2) 14 (19) 4728-37.  
Journal code: EMB. ISSN: 0261-4189.  
PUB. COUNTRY: ENGLAND: United Kingdom  
Journal; Article; (JOURNAL ARTICLE)



LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199602  
AB The neuropeptide galanin is widely expressed in the central nervous system

and other tissues and induces different cellular reactions, e.g. hormone release from pituitary and inhibition of insulin release from **pancreatic** B cells. By microinjection of **antisense** oligonucleotides we studied the question as to which G proteins mediate the galanin-induced inhibition of voltage-gated Ca<sup>2+</sup> channels in the rat **pancreatic** B-cell line RINm5F and in the rat pituitary cell line GH3. Injection of **antisense** oligonucleotides directed against alpha 01, beta 2, beta 3, gamma 2 and gamma 4 G protein subunits reduced the inhibition of Ca<sup>2+</sup> channel current which was induced by galanin, whereas no change was seen after injection of cells with **antisense** oligonucleotides directed against alpha i, alpha q, alpha 11, alpha 14, alpha 15, beta 1, beta 4, gamma 1, gamma 3, gamma 5, or gamma 7 G protein subunits or with sense control oligonucleotides. In view of these data

and of previous results, we conclude that the galanin receptors in GH3 and in RINm5F cells couple mainly to the G(0) protein consisting of alpha 01  
beta 2 gamma 2 to inhibit Ca<sup>2+</sup> channels and use alpha 01beta 3 gamma 4 less efficiently. The latter G protein composition was previously shown to be used by muscarinic M4 receptors to inhibit Ca<sup>2+</sup> channels.

L10 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1994:420035 BIOSIS

DOCUMENT NUMBER: PREV199497433035

TITLE: G proteins involved in the **calcium channel** signalling.

AUTHOR(S): Hescheler, J. (1); Kalkbrenner, F. (1); Degtiar, V. E. (1);

Wittig, B.; Schultz, G. (1)  
CORPORATE SOURCE: (1) Inst. Pharmakol., Freie Univ. Berlin, D-14195 Berlin Germany

SOURCE: Cell Biology International, (1994) Vol. 18, No. 5, pp. 530.

Meeting Info.: IVth European Cell Biology Congress Prague, Czech Republic June 26-July 1, 1994  
ISSN: 1065-6995.

DOCUMENT TYPE: Conference

LANGUAGE: English

L10 ANSWER 6 OF 6 MEDLINE

ACCESSION NUMBER: 93292746 MEDLINE

DOCUMENT NUMBER: 93292746

TITLE: Expression of **calcium channel** mRNAs in rat **pancreatic** islets and downregulation after glucose infusion.

AUTHOR: Iwashima Y; Pugh W; Depaoli A M; Takeda J; Seino S; Bell G I; Polonsky K S

CORPORATE SOURCE: Department of Medicine, University of Chicago, IL 60637..

CONTRACT NUMBER: DK-20595 (NIDDK)

DK-44840 (NIDDK)

SOURCE: DIABETES, (1993 Jul) 42 (7) 948-55.

Journal code: E8X. ISSN: 0012-1797.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 199309

AB Recent studies have shown that two different voltage-dependent Ca<sup>2+</sup> channels are expressed in **pancreatic** islets, the beta-cell/neuroendocrine-brain and the cardiac subtypes. The effects of chronic hyperglycemia on the levels in **pancreatic** islets of the



mRNAs encoding the alpha 1-subunits of the beta-cell and cardiac subtype Ca2+ channels were studied in rats made hyperglycemic by infusion of glucose for 48 h. A competitive reverse transcriptase-polymerase chain reaction procedure was used to obtain quantitative data on the levels of these two transcripts in islets obtained from individual rats. The quantitative polymerase chain reaction data indicate that the levels of mRNA encoding the alpha 1-subunit of the beta-cell Ca2+ channel are 2.5-fold greater than those for the cardiac subtype. The levels of beta-cell Ca2+ channel mRNA were 72.9% lower in the glucose-infused animals when compared with the saline-infused animals (P < 0.005) and those of the cardiac channel were 72.1% lower in the animals infused with glucose (P < 0.02). In contrast, glucose infusion resulted in a twofold increase in insulin mRNA levels and did not significantly alter levels of beta-actin mRNA. In situ hybridization studies revealed that the mRNAs

for

these two Ca2+ channels are expressed at higher levels in normal rat islets than in the surrounding acinar tissue, which suggests that the observed changes in mRNA levels occur within cells of the

**pancreatic** islet. To assess the possible functional consequences of this reduction in expression of mRNA for the Ca2+ channels, the

insulin

secretory responses of perfused **pancreases** to the Ca2+ channel agonist Bay K8644 were studied. (ABSTRACT TRUNCATED AT 250 WORDS)

=> d history

(FILE 'HOME' ENTERED AT 16:16:13 ON 19 JAN 2000)

FILE 'MEDLINE, BIOSIS, LIFESCI, CAPLUS' ENTERED AT 16:16:54 ON 19 JAN

2000

L1 0 S CALCIUM ADJ CHANNEL  
L2 66128 S CALCIUM CHANNEL  
L3 1453 S L2 AND T()TYPE  
L4 66128 S CALCIUM () CHANNEL  
L5 916 S L4 AND PANCREA?  
L6 41 S L5 AND NUCLEO?  
L7 57 S L5 AND NUCLE?  
L8 44 DUP REM L7 (13 DUPLICATES REMOVED)  
L9 9 S L5 AND (ANTISENS? OR (ANTI()SENS?) OR RIBOZYM? OR TRIPLEX)  
L10 6 DUP REM L9 (3 DUPLICATES REMOVED)

=> d 18 5 9 19 28 29 30 31 36 37 ibib abs

L8 ANSWER 5 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1999:167171 CAPLUS  
DOCUMENT NUMBER: 130:334321  
TITLE: Cloning of a novel four repeat protein related to voltage-gated sodium and calcium channels  
AUTHOR(S): Lee, Jung-Ha; Cribbs, Leanne L.; Perez-Reyes, Edward  
CORPORATE SOURCE: Department of Physiology, Loyola University Medical Center, Maywood, IL, 60153, USA  
SOURCE: FEBS Lett. (1999), 445(2,3), 231-236  
CODEN: FEBLAL; ISSN: 0014-5793  
PUBLISHER: Elsevier Science B.V.  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Cloning has led to the discovery of more ion channels than predicted by functional studies, yet there remain channels that have not been cloned. We report the cloning of a novel protein that contains the four domain structure found in voltage-gated Ca2+ and Na+ channels. Phylogenetic relationships suggested that the protein might have diverged from an ancestral four repeat channel before the divergence of Ca2+ and Na+ channels. Northern blot anal. showed that mRNA transcripts encoding the



protein are expressed predominantly in the brain, moderately in the heart, and weakly in the **pancreas**. Despite extensive expression attempts, currents from the putative channel were not detected. Based on its sequence, we propose that the novel protein might be a voltage-activated cation channel with unique gating properties.

L8 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:383101 CAPLUS

DOCUMENT NUMBER: 129:118063

TITLE: Class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion

AUTHOR(S): Ligon, Brooke; Boyd, Aubrey E., III; Dunlap, Kathleen  
CORPORATE SOURCE: Departments of Neuroscience and Physiology, Tufts University School of Medicine, Boston, MA, 02111, USA

SOURCE: J. Biol. Chem. (1998), 273(22), 13905-13911

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The initiation of insulin release from rat islet .beta. cells relies, in large part, on calcium influx through dihydropyridine-sensitive (.alpha.1D) voltage-gated calcium channels. Components of calcium-dependent insulin secretion and whole cell calcium current, however, are resistant to L-type channel blockade, as well as to .omega.-conotoxin GVIA, a potent inhibitor of .alpha.1B channels, suggesting the expression of addnl. exocytotic calcium channels in the islet. The authors used a reverse transcription-polymerase chain reaction-based strategy to ascertain at the mol. level whether the .alpha.1A **calcium channel** isoform was also present. Revealed two new variants of the rat brain .alpha.1A channel in the islet with divergence in a putative extracellular domain and in the C-terminus. Using antibodies and cRNA probes specific for .alpha.1A channels, the authors found that the majority of cells in rat **pancreatic** islets were labeled, indicating expression of the .alpha.1A channels in .beta. cells, the predominant islet cell type. Electrophysiol. recording from isolated islet cells demonstrated that the dihydropyridine-resistant current was sensitive to the .alpha.1A channel blocker, .omega.-agatoxin IVA. This toxin also inhibited the dihydropyridine-resistant component

of glucose-stimulated insulin secretion, suggesting functional overlap among **calcium channel** classes. These findings confirm the presence of multiple high voltage-activated calcium channels in the rat islet and implicate a physiol. role for .alpha.1A channels in excitation-secretion coupling in .beta. cells.

L8 ANSWER 19 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1997:307834 CAPLUS

DOCUMENT NUMBER: 127:105147

TITLE: Identification of four trp1 gene variants murine **pancreatic** beta-cells

AUTHOR(S): Sakura, H.; Ashcroft, F. M.

CORPORATE SOURCE: Laboratory Physiology, University Oxford, Oxford, OX1 3PT, UK

SOURCE: Diabetologia (1997), 40(5), 528-532

CODEN: DBTGAI; ISSN: 0012-186X

PUBLISHER: Springer

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Of the 6 mammalian transient receptor potential (trp) genes (trp1-6), only

trp1 was expressed at high levels in the mouse insulinoma cell line MIN6, which constitutes a pure beta-cell population. The murine homolog of human trp1 from MIN6 cells was cloned. 4 Variants





(.alpha.,.beta.,.gamma.,.delta.) generated by alternative splicing near the N-terminus of the protein were identified. Only the .alpha. and .beta. splice variants were efficiently expressed. The .beta. variant is the dominant form in MIN6 cells (and probably in mouse **pancreatic** islets), whereas the .alpha. variant is the major type in the mouse brain.  
The .beta. variant showed 99 % identity to the human homolog at the amino acid level.

L8 ANSWER 28 OF 44 MEDLINE DUPLICATE 5  
ACCESSION NUMBER: 96044438 MEDLINE  
DOCUMENT NUMBER: 96044438  
TITLE: The structures of the human **calcium**  
**channel** alpha 1 subunit (CACNL1A2) and beta subunit  
(CACNLB3) genes.  
AUTHOR: Yamada Y; Masuda K; Li Q; Ihara Y; Kubota A; Miura T;  
Nakamura K; Fujii Y; Seino S; Seino Y  
CORPORATE SOURCE: Department of Metabolism and Clinical Nutrition, Kyoto  
University Faculty of Medicine, Japan..  
SOURCE: GENOMICS, (1995 May 20) 27 (2) 312-9.  
Journal code: GEN. ISSN: 0888-7543.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE:

GENBANK-D43701; GENBANK-D43702; GENBANK-D43703;  
GENBANK-D43704; GENBANK-D43705; GENBANK-D43706;  
GENBANK-D43707; GENBANK-D43708; GENBANK-D43709;  
GENBANK-D43710; GENBANK-D43711; GENBANK-D43712;  
GENBANK-D43713; GENBANK-D43714; GENBANK-D43715;  
GENBANK-D43716; GENBANK-D43717; GENBANK-D43718;  
GENBANK-D43719; GENBANK-D43720; GENBANK-D43721;  
GENBANK-D43722; GENBANK-D43723; GENBANK-D43724;  
GENBANK-D43725; GENBANK-D43726; GENBANK-D43727;  
GENBANK-D43728; GENBANK-D43729; GENBANK-D43730; +  
ENTRY MONTH: 199601

AB Calcium influx in **pancreatic** beta-cells is regulated mainly by L-type voltage-dependent calcium channels (VDCCs) and triggers insulin secretion. The alpha 1 subunit (CACN4) and the beta subunit (beta 3) of VDCCs, both of which are expressed in **pancreatic** islets, are major components for the VDCC activity, and so they may play a critical role in the regulation of insulin secretion. We have determined the structures of the human CACN4 (CACNL1A2) and the human beta 3 (CACNLB3) genes. The CACNL1A2 gene spans more than 155 kb and has 49 exons. Most of the positions interrupted by introns are well conserved between the CACNL1A2 gene and the previously reported L-type VDCC alpha 1 subunit, CACNL1A1, gene. On the other hand, the CACNLB3 gene distributes in approximately 8 kb and comprises 13 exons, most of which are located together within approximately 5 kb. Comparisons of the genomic sequences of CACNL1A2 with the previously reported cDNA sequences indicate that there are a number of polymorphisms in the human CACNL1A2 gene. In addition, the PCR-SSCP procedure of exon 1 of CACNL1A2 revealed a change from 7 to 8 ATG trinucleotide repeats in a patient with non-insulin-dependent diabetes mellitus (NIDDM), resulting in an addition of methionine at the amino-terminus of CACN4. The determination of the structures of the human CACNL1A2 and CACNLB3 genes should facilitate study of the role of these genes in the development of NIDDM and also other genetic diseases such as long QT syndrome.

L8 ANSWER 29 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1996:93533 CAPLUS  
DOCUMENT NUMBER: 124:136099  
TITLE: Voltage-dependent calcium channels in  
insulin-secreting cells  
AUTHOR(S): Seino, Susumu; Fujii, Yasukazu; Ihara, Yu; Inagaki,



CORPORATE SOURCE: Nobuya; Seino, Yutaka; Yamada, Yuichiro; Gono, Tohru  
SOURCE: School Medicine, Chiba University, Chiba, 260, Japan  
Int. Congr. Ser. (1995), 1100 (Diabetes 1994), 187-92  
CODEN: EXMDA4; ISSN: 0531-5131  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The authors cloned 2 subtypes (rCACN4A and rCACN4B) of the .beta.-cell/neuroendocrine type VDCC .alpha.1 subunit (CACN4) from a rat insulin-secreting cell line RINm5F cDNA library. Subtype rCACN4B is a C-terminal truncated form of rCACN4A. Heterologous expression study using CHO cells has shown that the VDCC currents detected in CHO cells coexpressing the rCACN4A and .beta.1 subunit are an L-type and that the .beta. subunit is necessary for functional expression of the CACN4-directed channel activity. Insulin secretion is partly regulated by the modulation of VDCC activity by G protein signaling. Accordingly, the authors studied the mechanism of inhibition of VDCC activity mediated by the somatostatin receptor which is coupled to G protein. Somatostatin inhibits the L-type VDCC currents in RINm5F which stably express cloned human somatostatin receptor subtype 2 (hSSTR2), while somatostatin does not inhibit the currents in RINm5F which stably express cloned hSSTR1. A G protein specifically coupled to SSTR2, most probably Go, may serve as a signal for the inhibition of the VDCC activity and, thereby, might inhibit insulin secretion. Characterization of the structure, electrophysiol. properties, and regulation of VDCC, expressed in RINm5F cells should provide a better understanding of the mol. mechanisms of insulin secretion.

L8 ANSWER 30 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 6

ACCESSION NUMBER: 1995:155906 BIOSIS

DOCUMENT NUMBER: PREV199598170206

TITLE: Molecular diversity and functional characterization of voltage-dependent calcium channels (CACN4) expressed in **pancreatic** beta-cell.

AUTHOR(S): Ihara, Yu (1); Yamada, Yuichiro; Fujii, Yasukazu; Gono, Tohru; Yano, Hideki; Yasuda, Koichiro; Inagaki, Nobuya; Seino, Yutaka; Seino, Susumu

CORPORATE SOURCE: (1) Dep. Metabol. Clin. Nutr., Kyoto Univ. Fac. Med., 54 Shogoin-Kawaharacho, Sakyo-ku, Kyoto 606 Japan

SOURCE: Molecular Endocrinology, (1995) Vol. 9, No. 1, pp. 121-130.

ISSN: 0888-8809.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Dihydropyridine-sensitive voltage-dependent calcium channels (VDCC) play a crucial role in insulin secretion. We recently have cloned a human alpha-1-subunit of the VDCC expressed in **pancreatic** beta-cells, designated CACN4. In this study we have isolated complementary DNAs encoding two forms of rat CACN4 (rCACN4A and rCACN4B) from a rat insulinoma RINm5F complementary DNA library. Rat CACN4A is a protein of 2203 amino acids and is the rat homolog of human CACN4, whereas rCACN4B lacks 535 amino acids in the carboxyl-terminal region, probably due to alternative splicing. We have found two additional variations, one in the intracellular loop between repeats I and II and the other in the extracellular region between the third and fourth segments of repeat IV. Reverse transcriptase-polymerase chain reaction analysis of rat **pancreatic** islet messenger RNA reveals that these variants are present in **pancreatic** islets. In addition, whole-cell voltage-clamp recordings of Chinese hamster ovary cells stably expressing the alpha-1-subunit (rCACN4A or rCACN4B) with or without the **calcium channel** beta-2-subunit show that coexpression of rCACN4A with the beta-2-subunit or rCACN4B with the beta-2-subunit elicits



L-type VDCC currents, whereas expression of the alpha-1-subunit alone does not, indicating that CACN4 can associate functionally with the beta-2-subunit and that the beta-subunit is essential for functional expression of CACN4. These results suggest that there are various subtypes of CACN4 expressed in **pancreatic** beta-cells, and that both rCACN4A and rCACN4B can function as VDCC. Furthermore, the present study suggests that the expression of the beta-subunit as well as the alpha-subunit may participate in the regulation of insulin secretion.

L8 ANSWER 31 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1993:647986 CAPLUS  
DOCUMENT NUMBER: 119:247986  
TITLE: Human monoclonal antibodies and methods for their production  
INVENTOR(S): Whitaker, Robert Blake  
PATENT ASSIGNEE(S): Immunet, USA  
SOURCE: PCT Int. Appl., 52 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

| PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE     |
|--|------|----------|-----------------|----------|
| WO 9319197   | A1   | 19930930 | WO 1993-US2479  | 19930318 |
| W: AU, CA, JP  |      |          |                 |          |
| RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE |      |          |                 |          |
| AU 9339232   | A1   | 19931021 | AU 1993-39232   | 19930318 |
| EP 651819  | A1   | 19950510 | EP 1993-908394  | 19930318 |
| R: CH, DE, FR, GB, IT, LI  |      |          |                 |          |
| JP 07507923  | T2   | 19950907 | JP 1993-516719  | 19930318 |
| PRIORITY APPLN. INFO.:   |      |          | US 1992-856088  | 19920320 |
|  |      |          | WO 1993-US2479  | 19930318 |

AB An immortalized cell line that produces antigen-specific human monoclonal antibody of high affinity is derived from fusion of a human chromosome-contg. heterohybrid fusion partner with peripheral blood lymphocytes (PBL) of a first seropos. donor. A mixed lymphocyte response is generated by incubating the PBL in the presence of allogeneic lymphocytes. When the selected antigen is included in the incubation mixt., the PBL of the first seropos. donor form secondary lymphoblasts which are fused to the heterohybrid fusion partner. The resulting secondary immune response generates monoclonal antibodies of high affinity. The method was used to produce human monoclonal antibody to human IgE by immunization of a mixed culture of human spleen cells and PBL with IgE, followed by PEG-induced cell fusion and screening of the hybrid cells.

L8 ANSWER 36 OF 44 MEDLINE DUPLICATE 8  
ACCESSION NUMBER: 92115705 MEDLINE  
DOCUMENT NUMBER: 92115705  
TITLE: Cloning of the alpha 1 subunit of a voltage-dependent **calcium channel** expressed in **pancreatic** beta cells.  
AUTHOR: Seino S; Chen L; Seino M; Blondel O; Takeda J; Johnson J H;  
Bell G I  
CORPORATE SOURCE: Howard Hughes Medical Institute, University of Chicago, IL 60637..  
CONTRACT NUMBER: DK20595 (NIDDK)  
DK42086 (NIDDK)  
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1992 Jan 15) 89 (2) 584-8.



JOURNAL CODE: PV3. ISSN: 0027-8424.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Cancer Journals  
OTHER SOURCE: GENBANK-M83566  
ENTRY MONTH: 199204

AB The isoforms of the alpha 1 subunits of voltage-dependent Ca<sup>2+</sup> channels expressed in human **pancreatic** islets were identified by using a pair of degenerate oligonucleotide primers and the polymerase chain reaction (PCR) to amplify mRNAs encoding alpha 1 subunit-like sequences. The sequences of the PCR products indicate that islets express the heart-type alpha 1 subunit as well as a second isoform whose complete sequence has not been previously reported. The sequences of cloned cDNAs encoding the human beta-cell, or neuroendocrine-type, alpha 1 subunit indicate that it is composed of 2181 amino acids. It shares 68%, 64%, and 41% identity with the sequences of the alpha 1 subunits of rabbit heart, skeletal muscle, and brain, respectively, and is predicted to have a similar structure including four homologous domains composed of six membrane-spanning segments each. RNA blotting studies indicate that the beta-cell-type alpha 1 subunit is also expressed in brain as well as in the insulin-producing cell lines RINm5F and beta TC-3; however, it could not be detected by RNA blotting in a third cell line, HIT-T15. In situ hybridization studies revealed expression of beta-cell-type alpha 1 subunit mRNA in beta cells of rat **pancreatic** islets, implying that this protein may play a role in the regulation of insulin secretion.

L8 ANSWER 37 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1993:150382 BIOSIS

DOCUMENT NUMBER: PREV199344069182

TITLE: Is the neuronal voltage-sensitive **calcium**  
**channel** of human brain, human **pancreatic**  
beta cells and rat brain much larger than predicted by its  
cDNA sequence.

AUTHOR(S): Osherov, Azriel; Goldberg, Doron; Atlas, Daphne (1)

CORPORATE SOURCE: (1) Otto Lowei Cent. Mol. and Cell. Biol., Jerusalem 91904  
Israel

SOURCE: Neuroscience Letters, (1992) Vol. 147, No. 2, pp.  
233-235.

ISSN: 0304-3940.

DOCUMENT TYPE: Article

LANGUAGE: English

=> d 18 5 9 19 28 29 30 31 36 37 ibib kwic

L8 ANSWER 5 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1999:167171 CAPLUS

DOCUMENT NUMBER: 130:334321

TITLE: Cloning of a novel four repeat protein related to  
voltage-gated sodium and calcium channels

AUTHOR(S): Lee, Jung-Ha; Cribbs, Leanne L.; Perez-Reyes, Edward  
CORPORATE SOURCE: Department of Physiology, Loyola University Medical  
Center, Maywood, IL, 60153, USA

SOURCE: FEBS Lett. (1999), 445(2,3), 231-236

CODEN: FEBLAL; ISSN: 0014-5793

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB . . . that mRNA transcripts encoding the protein are expressed  
predominantly in the brain, moderately in the heart, and weakly in the  
**pancreas**. Despite extensive expression attempts, currents from  
the putative channel were not detected. Based on its sequence, we  
propose  
that the. . .





IT Brain  
Heart  
Molecular evolution  
**Pancreas**  
Repeat motifs (protein)  
(cloning of novel four repeat protein related to voltage-gated sodium and calcium channels)

IT **Calcium channel**  
Sodium channel  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(cloning of novel four repeat protein related to voltage-gated sodium and calcium channels)

IT 218889-95-3, GenBank AF078779  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
(**nucleotide** sequence; cloning of a novel four repeat protein related to voltage-gated sodium and calcium channels)

L8 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:383101 CAPLUS

DOCUMENT NUMBER: 129:118063

TITLE: Class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion

AUTHOR(S): Ligon, Brooke; Boyd, Aubrey E., III; Dunlap, Kathleen  
CORPORATE SOURCE: Departments of Neuroscience and Physiology, Tufts University School of Medicine, Boston, MA, 02111, USA

SOURCE: J. Biol. Chem. (1998), 273(22), 13905-13911

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

TI Class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion

AB . . . the islet. The authors used a reverse transcription-polymerase chain reaction-based strategy to ascertain at the mol. level whether the .alpha.1A **calcium channel** isoform was also present. Revealed two new variants of the rat brain .alpha.1A channel in the islet with divergence in. . . C-terminus. Using antibodies and cRNA probes specific for .alpha.1A channels, the authors found that the majority of cells in rat **pancreatic** islets were labeled, indicating expression of the .alpha.1A channels in .beta. cells, the predominant islet cell type. Electrophysiol. recording from. . . .alpha.1A channel

blocker, .omega.-agatoxin IVA. This toxin also inhibited the dihydropyridine-resistant component of glucose-stimulated insulin secretion, suggesting functional overlap among **calcium channel** classes. These findings confirm the presence of multiple high voltage-activated calcium channels in the rat islet and implicate a physiol. . . .

ST **calcium channel pancreas** islet insulin secretion

IT Genes (animal)

RL: PRP (Properties)

(BCCA1; class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT Calcium transport (biological)

Islet of Langerhans

Protein sequences

Rat

cDNA sequences

.beta.-Cell

(class A **calcium channel** variants in

**pancreatic** islets and their role in insulin secretion)

IT **Calcium channel**



RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
(class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT **Calcium channel**  
RL: PRP (Properties)  
(class A-type; class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT 210099-97-1 210099-98-2  
RL: PRP (Properties)  
(amino acid sequence; class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT 9004-10-8, Insulin, biological studies  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT 7440-70-2, Calcium, biological studies  
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)  
(class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

IT 205659-23-0, GenBank AF051526 205659-31-0, GenBank AF051527  
RL: PRP (Properties)  
(nucleotide sequence; class A **calcium channel** variants in **pancreatic** islets and their role in insulin secretion)

L8 ANSWER 19 OF 44 CAPLUS COPYRIGHT 2000 ACS  
ACCESSION NUMBER: 1997:307834 CAPLUS  
DOCUMENT NUMBER: 127:105147  
TITLE: Identification of four trp1 gene variants murine **pancreatic** beta-cells  
AUTHOR(S): Sakura, H.; Ashcroft, F. M.  
CORPORATE SOURCE: Laboratory Physiology, University Oxford, Oxford, OX1 3PT, UK  
SOURCE: Diabetologia (1997), 40(5), 528-532  
CODEN: DBTGAJ; ISSN: 0012-186X  
PUBLISHER: Springer  
DOCUMENT TYPE: Journal  
LANGUAGE: English

TI Identification of four trp1 gene variants murine **pancreatic** beta-cells

AB . . . .beta. splice variants were efficiently expressed. The .beta. variant is the dominant form in MIN6 cells (and probably in mouse **pancreatic** islets), whereas the .alpha. variant is the major type in the mouse brain. The .beta. variant showed 99 % identity. . .

ST trp1 gene variant expression beta cell; **calcium channel** insulin secretion MIN6 cell; mouse splicing alternative gene trp1 sequence

IT Insulinoma  
(MIN6 cells; .beta.-isoform expression in; identification of 4 trp1 gene variants murine **pancreatic** beta-cells)

IT Splicing (RNA)  
(alternative; identification of 4 trp1 gene variants murine **pancreatic** beta-cells)

IT **Calcium channel**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(calcium-release channel; identification of 4 trp1 gene variants murine **pancreatic** beta-cells)

IT DNA sequences  
Mouse  
Protein sequences  
cDNA sequences  
(identification of 4 trp1 gene variants murine **pancreatic**



beta-cells)  
 IT Gene expression  
 (of .alpha. and .beta. splice variants; identification of 4 trp1 gene  
 variants murine **pancreatic** beta-cells)  
 IT Genes (animal)  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (trp1; identification of 4 trp1 gene variants murine **pancreatic**  
 beta-cells)  
 IT Brain  
 (.alpha.-isoform expression in; identification of 4 trp1 gene variants  
 murine **pancreatic** beta-cells)  
 IT Islet of Langerhans  
 (.beta.-cell, .beta.-isoform dominance in; identification of 4 trp1  
 gene variants murine **pancreatic** beta-cells)  
 IT 192269-47-9 192269-49-1  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (amino acid sequence; identification of 4 trp1 gene variants murine  
**pancreatic** beta-cells)  
 IT 9004-10-8, Insulin, biological studies  
 RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
 (identification of 4 trp1 gene variants murine **pancreatic**  
 beta-cells)  
 IT 192269-19-5 192269-48-0  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (nucleotide sequence and efficient expression; identification  
 of 4 trp1 gene variants murine **pancreatic** beta-cells)

L8 ANSWER 28 OF 44 MEDLINE

DUPLICATE 5

ACCESSION NUMBER: 96044438 MEDLINE

DOCUMENT NUMBER: 96044438

TITLE: The structures of the human **calcium**  
**channel** alpha 1 subunit (CACNL1A2) and beta subunit  
 (CACNLB3) genes.

AUTHOR: Yamada Y; Masuda K; Li Q; Ihara Y; Kubota A; Miura T;  
 Nakamura K; Fujii Y; Seino S; Seino Y

CORPORATE SOURCE: Department of Metabolism and Clinical Nutrition, Kyoto  
 University Faculty of Medicine, Japan..

SOURCE: GENOMICS, (1995 May 20) 27 (2) 312-9.

Journal code: GEN. ISSN: 0888-7543.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-D43701; GENBANK-D43702; GENBANK-D43703;  
 GENBANK-D43704; GENBANK-D43705; GENBANK-D43706;  
 GENBANK-D43707; GENBANK-D43708; GENBANK-D43709;  
 GENBANK-D43710; GENBANK-D43711; GENBANK-D43712;  
 GENBANK-D43713; GENBANK-D43714; GENBANK-D43715;  
 GENBANK-D43716; GENBANK-D43717; GENBANK-D43718;  
 GENBANK-D43719; GENBANK-D43720; GENBANK-D43721;  
 GENBANK-D43722; GENBANK-D43723; GENBANK-D43724;  
 GENBANK-D43725; GENBANK-D43726; GENBANK-D43727;  
 GENBANK-D43728; GENBANK-D43729; GENBANK-D43730; +

ENTRY MONTH: 199601

TI The structures of the human **calcium channel** alpha 1  
 subunit (CACNL1A2) and beta subunit (CACNLB3) genes.

AB Calcium influx in **pancreatic** beta-cells is regulated mainly by  
 L-type voltage-dependent calcium channels (VDCCs) and triggers insulin  
 secretion. The alpha 1 subunit (CACN4) and the beta subunit (beta 3) of  
 VDCCs, both of which are expressed in **pancreatic** islets, are  
 major components for the VDCC activity, and so they may play a critical  
 role in the regulation of. . .

CT . . . Support, Non-U.S. Gov't



Base Sequence

\*Calcium Channels: GE, genetics

Diabetes Mellitus, Non-Insulin-Dependent: GE, genetics

Molecular Sequence Data

Mutation

Polymorphism (Genetics)

**Repetitive Sequences, Nucleic Acid**

L8 ANSWER 29 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1996:93533 CAPLUS

DOCUMENT NUMBER: 124:136099

TITLE: Voltage-dependent calcium channels in  
insulin-secreting cells

AUTHOR(S): Seino, Susumu; Fujii, Yasukazu; Ihara, Yu; Inagaki,  
Nobuya; Seino, Yutaka; Yamada, Yuichiro; Gono, Tohru  
CORPORATE SOURCE: School Medicine, Chiba University, Chiba, 260, Japan  
SOURCE: Int. Congr. Ser. (1995), 1100(Diabetes 1994), 187-92  
CODEN: EXMDA4; ISSN: 0531-5131

DOCUMENT TYPE: Journal

LANGUAGE: English

ST somatostatin receptor **calcium channel pancreas**

IT G proteins (guanine **nucleotide**-binding proteins)

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(somatostatin receptors and voltage-dependent calcium channels in  
insulin-secreting cells)

IT **Pancreatic** islet of Langerhans  
(.beta.-cell, somatostatin receptors and voltage-dependent calcium  
channels in insulin-secreting cells)

L8 ANSWER 30 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 6

ACCESSION NUMBER: 1995:155906 BIOSIS

DOCUMENT NUMBER: PREV199598170206

TITLE: Molecular diversity and functional characterization of  
voltage-dependent calcium channels (CACN4) expressed in  
**pancreatic** beta-cell.

AUTHOR(S): Ihara, Yu (1); Yamada, Yuichiro; Fujii, Yasukazu; Gono, Tohru;  
Yano, Hideki; Yasuda, Koichiro; Inagaki, Nobuya;  
Seino, Yutaka; Seino, Susumu

CORPORATE SOURCE: (1) Dep. Metabol. Clin. Nutr., Kyoto Univ. Fac. Med., 54  
Shogoin-Kawaharacho, Sakyo-ku, Kyoto 606 Japan

SOURCE: Molecular Endocrinology, (1995) Vol. 9, No. 1, pp.  
121-130.

ISSN: 0888-8809.

DOCUMENT TYPE: Article

LANGUAGE: English

TI Molecular diversity and functional characterization of voltage-dependent  
calcium channels (CACN4) expressed in **pancreatic** beta-cell.

AB. . . (VDCC) play a crucial role in insulin secretion. We recently have  
cloned a human alpha-1-subunit of the VDCC expressed in **pancreatic**  
beta-cells, designated CACN4. In this study we have isolated

complementary

DNAs encoding two forms of rat CACN4 (rCACN4A and rCACN4B). . . in the  
extracellular region between the third and fourth segments of repeat IV.

Reverse transcriptase-polymerase chain reaction analysis of rat

**pancreatic** islet messenger RNA reveals that these variants are

present in **pancreatic** islets. In addition, whole-cell

voltage-clamp recordings of Chinese hamster ovary cells stably expressing  
the alpha-1-subunit (rCACN4A or rCACN4B) with or without the

**calcium channel** beta-2-subunit show that coexpression of

rCACN4A with the beta-2-subunit or rCACN4B with the beta-2-subunit

elicits

L-type VDCC currents, whereas expression. . . beta-subunit is  
essential

for functional expression of CACN4. These results suggest that there are  
various subtypes of CACN4 expressed in **pancreatic** beta-cells,  
and that both rCACN4A and rCACN4B can function as VDCC. Furthermore, the





present study suggests that the expression of. . .

IT Sequence Data  
amino acid sequence; molecular sequence data; **nucleotide**  
sequence

IT Miscellaneous Descriptors  
BETA-CELL; BETA-SUBUNIT; DNA; INSULIN SECRETION REGULATION;  
INTRACELLULAR LOOP

L8 ANSWER 31 OF 44 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1993:647986 CAPLUS  
DOCUMENT NUMBER: 119:247986  
TITLE: Human monoclonal antibodies and methods for their  
production  
INVENTOR(S): Whitaker, Robert Blake  
PATENT ASSIGNEE(S): Immunet, USA  
SOURCE: PCT Int. Appl., 52 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

| PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE     |
|--|------|----------|-----------------|----------|
| WO 9319197   | A1   | 19930930 | WO 1993-US2479  | 19930318 |
| W: AU, CA, JP  |      |          |                 |          |
| RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE |      |          |                 |          |
| AU 9339232   | A1   | 19931021 | AU 1993-39232   | 19930318 |
| EP 651819  | A1   | 19950510 | EP 1993-908394  | 19930318 |
| R: CH, DE, FR, GB, IT, LI  |      |          |                 |          |
| JP 07507923  | T2   | 19950907 | JP 1993-516719  | 19930318 |
| PRIORITY APPLN. INFO.:   |      |          | US 1992-856088  | 19920320 |
|  |      |          | WO 1993-US2479  | 19930318 |

IT Neutrophil  
**Pancreatic** islet of Langerhans  
Adrenal gland, composition  
(autoantigen of cytoplasm of, monoclonal antibody to, prodn. of,  
hybridoma prep. from human memory B-cell and allogeneic lymphocyte  
for)

IT Blood corpuscle  
Blood platelet  
Cell membrane  
Cell **nucleus**  
Cytoplasm  
Erythrocyte  
Sperm  
Brain, composition  
Heart, composition  
Muscle, composition  
(autoantigen of, monoclonal antibody to, prodn. of, hybridoma prep.  
from human memory B-cell and allogeneic lymphocyte for)

IT Blood-coagulation factors  
Cardiolipins  
Deoxyribonucleic acids  
**Nucleoproteins**  
Ribonucleoproteins  
Thyroglobulins  
Collagens, biological studies  
RL: PREP (Preparation)  
(monoclonal antibody to, prodn. of, hybridoma prep. from human memory  
B-cell and allogeneic lymphocyte for)

IT Proteins, specific or class  
RL: PREP (Preparation)  
(lamins, of cell **nucleus**, monoclonal antibody to, prodn. of,  
hybridoma prep. from human memory B-cell and allogeneic lymphocyte  
for)



IT Nerve, composition  
(terminal, **calcium channel** of, monoclonal antibody  
to, prodn. of, hybridoma prepn. from human memory B-cell and  
allogeneic lymphocyte for)

L8 ANSWER 36 OF 44 MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 92115705 MEDLINE

DOCUMENT NUMBER: 92115705

TITLE: Cloning of the alpha 1 subunit of a voltage-dependent  
**calcium channel** expressed in  
**pancreatic** beta cells.

AUTHOR: Seino S; Chen L; Seino M; Blondel O; Takeda J; Johnson J  
H;

CORPORATE SOURCE: Bell G I  
Howard Hughes Medical Institute, University of Chicago, IL  
60637..

CONTRACT NUMBER: DK20595 (NIDDK)  
DK42086 (NIDDK)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE  
UNITED STATES OF AMERICA, (1992 Jan 15) 89 (2) 584-8.  
Journal code: PV3. ISSN: 0027-8424.

PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals; Cancer Journals

OTHER SOURCE: GENBANK-M83566

ENTRY MONTH: 199204

TI Cloning of the alpha 1 subunit of a voltage-dependent **calcium**  
**channel** expressed in **pancreatic** beta cells.

AB The isoforms of the alpha 1 subunits of voltage-dependent Ca<sup>2+</sup> channels  
expressed in human **pancreatic** islets were identified by using a  
pair of degenerate oligonucleotide primers and the polymerase chain  
reaction (PCR) to amplify mRNAs. . . cell line, HIT-T15. In situ  
hybridization studies revealed expression of beta-cell-type alpha 1  
subunit mRNA in beta cells of rat **pancreatic** islets, implying  
that this protein may play a role in the regulation of insulin secretion.

CT . . .  
PH, physiology

\*Calcium Channels: GE, genetics

Cloning, Molecular

Gene Expression

\*Islets of Langerhans: PH, physiology

Membrane Potentials

Molecular Sequence Data

**Nucleic Acid Hybridization**

Oligodeoxyribonucleotides: CH, chemistry

Rats

Sequence Alignment

L8 ANSWER 37 OF 44 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1993:150382 BIOSIS

DOCUMENT NUMBER: PREV199344069182

TITLE: Is the neuronal voltage-sensitive **calcium**  
**channel** of human brain, human **pancreatic**  
beta cells and rat brain much larger than predicted by its  
cDNA sequence.

AUTHOR(S): Osherov, Azriel; Goldberg, Doron; Atlas, Daphne (1)

CORPORATE SOURCE: (1) Otto Lowei Cent. Mol. and Cell. Biol., Jerusalem 91904  
Israel

SOURCE: Neuroscience Letters, (1992) Vol. 147, No. 2, pp.  
233-235.

ISSN: 0304-3940.

DOCUMENT TYPE: Article

LANGUAGE: English

TI Is the neuronal voltage-sensitive **calcium channel** of



human brain, human **pancreatic** beta cells and rat brain much  
larger than predicted by its cDNA sequence.  
IT Sequence Data  
molecular sequence data; **nucleotide** sequence  
IT Miscellaneous Descriptors  
COMPLEMENTARY DNA

=> d history

(FILE 'HOME' ENTERED AT 16:16:13 ON 19 JAN 2000)

FILE 'MEDLINE, BIOSIS, LIFESCI, CAPLUS' ENTERED AT 16:16:54 ON 19 JAN

2000

L1 0 S CALCIUM ADJ CHANNEL  
L2 66128 S CALCIUM CHANNEL  
L3 1453 S L2 AND T()TYPE  
L4 66128 S CALCIUM () CHANNEL  
L5 916 S L4 AND PANCREA?  
L6 41 S L5 AND NUCLEO?  
L7 57 S L5 AND NUCLE?  
L8 44 DUP REM L7 (13 DUPLICATES REMOVED)  
L9 9 S L5 AND (ANTISENS? OR (ANTI())SENS?) OR RIBOZYM? OR TRIPLEX)  
L10 6 DUP REM L9 (3 DUPLICATES REMOVED)

=> s l3 and pancrea?

L11 24 L3 AND PANCREA?

=> d l11 tot ibib abs

L11 ANSWER 1 OF 24 MEDLINE  
ACCESSION NUMBER: 1998231527 MEDLINE  
DOCUMENT NUMBER: 98231527  
TITLE: Voltage dependent calcium channels in adrenal glomerulosa  
cells and in insulin producing cells.  
AUTHOR: Horvath A; Szabadkai G; Varnai P; Aranyi T; Wollheim C B;  
Spat A; Enyedi P  
CORPORATE SOURCE: Department of Physiology and Laboratory of Cellular and  
Molecular Physiology, Semmelweis University of Medicine,  
Budapest, Hungary.  
SOURCE: CELL CALCIUM, (1998 Jan) 23 (1) 33-42.  
Journal code: CQE. ISSN: 0143-4160.  
PUB. COUNTRY: SCOTLAND: United Kingdom  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199808  
ENTRY WEEK: 19980803

AB We have examined the structure and function of Ca<sup>2+</sup> channels in excitable  
endocrine cell types, in rat adrenal glomerulosa cells and in two insulin  
producing cell types, the rat **pancreatic** beta cell and the INS-1  
cell line. In previous studies on glomerulosa cells, we observed low (T-  
**type**) and high threshold (L-type) voltage dependent  
Ca<sup>2+</sup> currents in addition to a K<sup>+</sup> induced inward rectifying Ca<sup>2+</sup> current  
(Igl). beta cells are known to exhibit T-, L- and N-type currents. We  
have  
now found that INS-1 cells also show low threshold (T-  
**type**) and high threshold Ca<sup>2+</sup> currents. The latter was further  
resolved by organic inhibitors into L-type and P/Q-type currents and no  
Igl was detected. The expression of the pore-forming alpha 1 subunit of  
voltage dependent Ca<sup>2+</sup> channels was studied by means of reverse  
transcription-polymerase chain reaction (RT-PCR), followed by restriction  
enzyme mapping and/or sequencing. Both in glomerulosa and



**pancreatic** beta cells, the neuroendocrine (D) class of the alpha 1 subunit, known to be responsible for L-type current, represents the majority of the PCR product. Comparable amounts of the neuroendocrine (D) and the neuronal A-type alpha 1 subunits dominate the message in INS-1 cells. Different characteristics of Ca<sup>2+</sup> currents in these cell types is discussed in view of the channel repertoire.

L11 ANSWER 2 OF 24 MEDLINE

ACCESSION NUMBER: 97081069 MEDLINE

DOCUMENT NUMBER: 97081069

TITLE: Abnormally expressed low-voltage-activated calcium channels

in beta-cells from NOD mice and a related clonal cell

line.

AUTHOR: Wang L; Bhattacharjee A; Fu J; Li M

CORPORATE SOURCE: Department of Pharmacology, University of South Alabama, College of Medicine, Mobile 36688, USA.

SOURCE: DIABETES, (1996 Dec) 45 (12) 1678-83.

Journal code: E8X. ISSN: 0012-1797.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 199703

ENTRY WEEK: 19970301

AB A macroscopic low-voltage-activated (LVA) inward current was found in **pancreatic** beta-cells isolated from NOD mice. However, this current was not present in nondiabetic prone mouse (e.g., Swiss-Webster) **pancreatic** beta-cells. We performed pharmacological analyses on this current in NOD insulinoma tumor cells (NIT-1). This cell line was developed from **pancreatic** beta-cells of a transgenic NOD mouse. The sodium-channel blocker, tetrodotoxin (TTX; 2 micromol/l) had no effect

on this LVA current. The amplitudes of currents elicited by a -20 mV test pulse retained similarity when the extracellular sodium concentration was increased from 0 to 115 mmol/l; when the extracellular calcium concentration was decreased from 10 to 2 mmol/l, there was an approximate 50% reduction of this current elicited by a -30 mV test pulse. Neither

the

L-type **calcium-channel** blocker, nifedipine (3 micromol/l), nor the N-type **calcium-channel** blocker, omega-CgTx-GVIA (1 micromol/l), at -30 mV produced an appreciable effect. The **T-type calcium-channel** blockers, nickel (3 micromol/l) and amiloride (250 micromol/l), effectively reduced the peak of this current. In 2 mmol/l calcium

external

solution, the threshold of voltage-dependent activation of this calcium current was approximately -65 mV, and the peak current occurred at -20

mV.

Half-maximum steady-state inactivation was around -43 mV. The mean time constant of slow deactivating tail currents generated by a preceding 20

mV

pulse was 2.53 ms. The intracellular free calcium concentration was two- to threefold higher in NOD mouse **pancreatic** beta-cells compared with Swiss-Webster **pancreatic** beta-cells. We concluded that there are LVA calcium channels abnormally expressed in NOD mouse beta-cells. This LVA **calcium channel** may be factorial to the high cytosolic free calcium concentration observed in these cells, and thereby may contribute to the pathogenesis of NOD mouse beta-cells.

L11 ANSWER 3 OF 24 MEDLINE

ACCESSION NUMBER: 95058263 MEDLINE

DOCUMENT NUMBER: 95058263

TITLE: Increased **calcium-channel** currents of **pancreatic** beta cells in neonatally streptozocin-induced diabetic rats.





AUTHOR: Kato S; Ishida H; Tsuura Y; Okamoto Y; Tsuji K; Horie M; Okada Y; Seino Y  
CORPORATE SOURCE: Department of Metabolism and Clinical Nutrition, Kyoto University School of Medicine, Japan.  
SOURCE: METABOLISM: CLINICAL AND EXPERIMENTAL, (1994 Nov) 43 (11) 1395-400.  
Journal code: MUM. ISSN: 0026-0495.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199502  
AB Using a whole-cell patch-clamp technique, voltage-dependent Ca(2+)-channel

activities were found to be increased in cultured single beta cells isolated from neonatally streptozocin-induced diabetic rats (NSZ rats). The current-voltage relationship and inactivation time course of Ba2+ currents via L-type Ca2+ channels were indistinguishable between NSZ and control rats. However, the current density observed in NSZ rats was significantly greater than that in control rats. Ba2+ currents via **T-type** Ca2+ channels were also found to be enhanced in NSZ beta cells. The insulin-secretory capacity of cultured **pancreatic** islets in response to a depolarizing stimulus (20 mmol/L arginine or 30 mmol/L KCl) in the presence of 11.1 mmol/L glucose was augmented in NSZ rats, whereas that in response to 11.1 and 16.7 mmol/L glucose alone was significantly reduced. It is concluded that the impaired insulinotropic action of glucose in beta cells in NSZ rats is

not

due to reduced activity of voltage-dependent Ca2+ channels. The fact that insulin secretion induced by a depolarizing stimulus was enhanced in NSZ rats may be related to the augmented activity of the voltage-dependent calcium current found in NSZ beta cells.

L11 ANSWER 4 OF 24 MEDLINE

ACCESSION NUMBER: 94265727 MEDLINE

DOCUMENT NUMBER: 94265727

TITLE: Inactivation of voltage-dependent calcium current in an insulinoma cell line.

AUTHOR: Marchetti C; Amico C; Podest'a D; Robello M

CORPORATE SOURCE: Istituto di Cibernetica e Biofisica, Consiglio Nazionale delle Ricerche, Genova, Italy.

SOURCE: EUROPEAN BIOPHYSICS JOURNAL, (1994) 23 (1) 51-8.

Journal code: EHU. ISSN: 0175-7571.

PUB. COUNTRY: GERMANY: Germany, Federal Republic of  
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199409

AB We have studied the mechanism of Ca current inactivation in the beta-cell line HIT-T15 by conventional and perforated patch recording techniques, using two pulse voltage protocols and a combination of current and tail current measurements. In 5 mM Ca, from a holding potential of -80 mV, the maximum current showed a complex time course of inactivation: a

relatively

fast, double exponential inactivation (tau h1 approximately 12 ms and tau h2 approximately 60 ms) and a very slowly inactivating component (tau > 1 s). The faster component (tau h1) was due to the voltage-dependent inactivation of a low-threshold-activated (LVA), **T-type** current, which deactivates more slowly (tau approximately 3-5 ms) than

the

other components (tau approximately 0.2-0.3 ms). The intermediate component (tau h2) was due to the Ca-dependent inactivation of a portion of the high-threshold-activated (HVA) current. A saturating dose of the dihydropyridine (DHP) nifedipine (10 microM) did not affect the LVA current, but inhibited by 68 +/- 5% the transient, Ca-sensitive portion

of



the HVA current and by 33 +/- 12% the long lasting component. We suggest that three components of the calcium current can be resolved in HIT cells and the main target of DHPs is a HVA current, which inactivates faster than the DHP-resistant HVA component and does so primarily through calcium influx.

L11 ANSWER 5 OF 24 MEDLINE  
ACCESSION NUMBER: 94065622 MEDLINE  
DOCUMENT NUMBER: 94065622  
TITLE: Ascorbic acid modulation of calcium channels in **pancreatic** beta cells.  
AUTHOR: Parsey R V; Matteson D R  
CORPORATE SOURCE: Department of Biophysics, University of Maryland School of Medicine, Baltimore 21201.  
SOURCE: JOURNAL OF GENERAL PHYSIOLOGY, (1993 Sep) 102 (3) 503-23.

JOURNAL code: I8N. ISSN: 0022-1295.  
PUB. COUNTRY: United States  
Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199403

AB We have studied the effect of ascorbic acid on voltage-dependent calcium channels in **pancreatic** beta cells. Using the whole-cell and perforated-patch variants of the patch clamp technique to record calcium tail currents, we have shown that the slowly deactivating (SD) **calcium channel**, which is similar to the **T-type** channel in other cells, is inhibited in a voltage-dependent manner by ascorbic acid (AA). The other channels that carry inward

current in beta cells, FD calcium channels and sodium channels, are unaffected by AA. Ascorbic acid causes a voltage-dependent decrease in the magnitude of the SD channel conductance which can be explained by the hypothesis that approximately 50-60% of the channels have their voltage dependence shifted by approximately 62 mV in the depolarizing direction. Thus, ascorbate appears to modify only a fraction of the SD channels. The activation kinetics of the ascorbate-modified channels are slower than control channels in a manner that is consistent with this hypothesis.

Deactivation and inactivation kinetics are unaffected by ascorbate. These effects of ascorbate require metal ions, and it appears that some of the activity of ascorbate is due to a product of its metal catalyzed oxidation, perhaps dehydroascorbate.

L11 ANSWER 6 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1999:204479 BIOSIS  
DOCUMENT NUMBER: PREV199900204479  
TITLE: Effect of cholecystokinin on cytosolic Ca<sup>2+</sup> dynamics in rat **pancreatic** B cells.  
AUTHOR(S): Kimura, Hiroyuki (1)  
CORPORATE SOURCE: (1) Department of Physiology, Faculty of Veterinary Medicine, Hokkaido University, Sapporo, 060-0818 Japan  
SOURCE: Japanese Journal of Veterinary Research, (Nov., 1998) Vol. 46, No. 2-3, pp. 129-130.  
ISSN: 0047-1917.  
DOCUMENT TYPE: Article  
LANGUAGE: English

L11 ANSWER 7 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS  
ACCESSION NUMBER: 1999:186400 BIOSIS  
DOCUMENT NUMBER: PREV199900186400  
TITLE: Cloning of the rat beta-cell **T-type calcium channel** alpha subunit and its



regulation by glucose.  
AUTHOR(S): Zhuang, H. (1); Hu, F.; Bhattacharjee, A.; Zhang, M.; Wu, S.; Berggren, P.-O.; Li, M.  
CORPORATE SOURCE: (1) Dept of Pharmacology, University of South Alabama College of Medicine, Mobile, AL USA  
SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A409.  
Meeting Info.: Forty-third Annual Meeting of the Biophysical Society Baltimore, Maryland, USA February 13-17, 1999  
ISSN: 0006-3495.  
DOCUMENT TYPE: Conference  
LANGUAGE: English

L11 ANSWER 8 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1998:441460 BIOSIS

DOCUMENT NUMBER: PREV199800441460

TITLE: omega-Phonetoxin-IIA: A **calcium channel** blocker from the spider Phoneutria nigriventer.

AUTHOR(S): Cassola, Antonio Carlos (1); Jaffe, Howard; Fales, Henry M.; Afeche, Solange Castro; Magnoli, Fabio; Cipolla-Neto, Jose

CORPORATE SOURCE: (1) Dep. Physiol. Biophysics, Inst. Biomed. Sci., Univ. Sao

Paulo, Av. Lineu Prestes 1524, Sao Paulo, SP 05508-900 Brazil

SOURCE: Pfluegers Archiv European Journal of Physiology, (Sept., 1998) Vol. 436, No. 4, pp. 545-552.  
ISSN: 0031-6768.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A peptide with neurotoxic effect on mammals, purified from the venom of the spider Phoneutria nigriventer, was studied regarding its primary structure and its effects on voltage-gated calcium channels. The peptide, named omega-phonetoxin-IIA, has 76 amino acids residues, with 14 Cys forming 7 disulphide bonds, and a molecular weight of 8362.7 Da. The neurotoxicity is a consequence of the peptide's blocking effects on high-voltage-activated (HVA) calcium channels. N-type HVA calcium channels

of rat dorsal root ganglion neurons are blocked with affinity in the sub-nanomolar concentration range. The toxin also blocks L-type channels of rat beta **pancreatic** cells, with an affinity 40 times lower. Although not studied in detail, evidence indicates that the toxin also blocks other types of HVA calcium channels, such as P and Q. No effect

was

observed on low-voltage activated, **T-type** calcium channels. The significant homologies between omega-phonetoxin-IIA and the peptides of the omega-agatoxin-III family, and the overlapping inhibitory effects on calcium channels are discussed in terms of the structure-activity relationship.

L11 ANSWER 9 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1997:308651 BIOSIS

DOCUMENT NUMBER: PREV199799616454

TITLE: Chronic **T-type** Ca-2+ channel blockade with mibefradil in hyperinsulinemic, insulin-resistant and hypertensive rats.

AUTHOR(S): Verma, Subodh; Bhanot, Sanjay; Hicke, Alan; McNeill, John H. (1)

CORPORATE SOURCE: (1) Fac. Pharmaceutical Sci., Univ. British Columbia, Vancouver, BC V6T 1Z3 Canada

SOURCE: Cardiovascular Research, (1997) Vol. 34, No. 1, pp. 121-128.

ISSN: 0008-6363.

DOCUMENT TYPE: Article

LANGUAGE: English



AB Objectives: To determine the effects of calcium antagonists on hyperinsulinemia, hypertriglyceridemia and hypertension, we examined the long-term effects of a new **calcium channel** blocker, mibefradil, on plasma insulin levels, plasma triglyceride levels and systolic blood pressure in insulin-resistant and hyperinsulinemic fructose-hypertensive (FH) rats. To this aim, both prevention and reversal protocols were employed. Methods: Prevention study: Male Sprague-Dawley rats were procured at 6 weeks of age and were divided into: control (C, n = 6), control-treated (CT, n = 5), fructose (F, n = 7) and fructose-treated (FT, n = 6). Baseline measurements of plasma glucose, insulin and systolic blood pressure were conducted in all groups. At week 7, chronic mibefradil treatment (30 mg/kg/day, orally for 6 weeks) was initiated in the CT and FT groups. At week 8, the rats in the F and FT groups were started on a 66% fructose diet to induce hyperinsulinemia and hypertension. Weekly measurements of plasma insulin, plasma triglycerides and systolic blood pressure were conducted for the following 4 weeks. Reversal protocol: In a separate study, 8-week-treated FH rats and their age-matched controls were used to examine the effects of mibefradil on reversing fructose-induced hyperinsulinemia and hypertension. Results:

The F group exhibited hyperinsulinemia ( $3.2 \pm 0.1$  vs. C  $2.3 \pm 0.07$  ng/ml, P  $< 0.05$ ), hypertension ( $148 \pm 3$  vs. C  $121 \pm 1$  mmHg, P  $< 0.002$ ) and elevated triglyceride levels ( $5.4 \pm 0.8$  vs. C  $1.6 \pm 0.3$  mM, P  $< 0.05$ ). Chronic mibefradil treatment prevented the development of hyperinsulinemia ( $1.6 \pm 0.08$  ng/ml, P  $< 0.004$  vs. F) and hypertension ( $123 \pm 1$  mmHg, P  $< 0.001$  vs. F) and attenuated the development of hypertriglyceridemia.

In the reversal study, mibefradil treatment reversed the development of hyperinsulinemia, hypertriglyceridemia and elevated BP in FH rats. Treatment did not affect the plasma glucose levels in any group (prevention or reversal). Conclusions: Long-term treatment with the calcium antagonist, mibefradil, both prevents and reverses the development of hyperinsulinemia, hypertriglyceridemia and hypertension in FH rats. These data indicate beneficial effects of mibefradil on carbohydrate and lipid metabolism in hyperinsulinemic and insulin-resistant states.

L11 ANSWER 10 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1997:21633 BIOSIS

DOCUMENT NUMBER: PREV199799320836

TITLE: Abnormally expressed low-voltage-activated calcium channels

in beta-cells from NOD mice and a related clonal cell line.

AUTHOR(S): Wang, Lin; Bhattacharjee, Arin; Fu, Jian; Li, Ming (1)

CORPORATE SOURCE: (1) Dep. Pharmacol., Univ. South Ala., Coll. Med., Mobile, AL 36688 USA

SOURCE: Diabetes, (1996) Vol. 45, No. 12, pp. 1678-1683. ISSN: 0012-1797.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A macroscopic low-voltage-activated (LVA) inward current was found in **pancreatic** beta-cells isolated from NOD mice. However, this current was not present in nondiabetic prone mouse (e.g., Swiss-Webster) **pancreatic** beta-cells. We performed pharmacological analyses on this current in NOD insulinoma tumor cells (NIT-1). This cell line was developed from **pancreatic** beta-cells of a transgenic NOD mouse. The sodium-channel blocker, tetrodotoxin (TTX;  $2 \mu\text{mol/l}$ ) had no effect on this LVA current. The amplitudes of currents elicited by a  $-20$  mV test pulse retained similarity when the extracellular sodium concentration was increased from 0 to  $115 \text{ mmol/l}$ ; when the extracellular calcium concentration was decreased from 10 to  $2 \text{ mmol/l}$ , there was an approximate 50% reduction of this current elicited by a  $-30$  mV test pulse. Neither

the





L-type **calcium-channel** blocker, nifedipine (3  $\mu\text{mol/l}$ ), nor the N-type **calcium-channel** blocker, omega-CgTx-GVIA (1  $\mu\text{mol/l}$ ), at -30 mV produced an appreciable effect. The **T-type calcium-channel** blockers, nickel (3  $\mu\text{mol/l}$ ) and amiloride (250  $\text{pmol/l}$ ), effectively reduced the peak of this current. In 2  $\text{mmol/l}$  calcium external solution, the threshold of voltage-dependent activation of this calcium current was approximately -65 mV, and the peak current occurred at -20 mV. Half-maximum steady-state inactivation was around -43 mV. The mean time constant of slow deactivating tail currents generated by a preceding 20

mV

pulse was 2.53 ms. The intracellular free calcium concentration was two- to threefold higher in NOD mouse **pancreatic** beta-cells compared with Swiss-Webster **pancreatic** beta-cells. We concluded that there are IVA calcium channels abnormally expressed in NOD mouse beta-cells. This IVA **calcium channel** may be factorial to the high cytosolic free calcium concentration observed in these cells, and thereby may contribute to the pathogenesis of NOD mouse beta-cells.

L11 ANSWER 11 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1995:36705 BIOSIS

DOCUMENT NUMBER: PREV199598051005

TITLE: Increased **calcium-channel** currents of **pancreatic** beta cells in neonatally streptozocin-induced diabetic rats.

AUTHOR(S): Kato, Seika (1); Ishida, Hitoshi; Tsuura, Yoshiyuki; Okamoto, Yoshimasa; Tsuji, Kazuo; Horie, Minoru; Okada, Yasunobu; Seino, Yutaka

CORPORATE SOURCE: (1) Dep. Metabolism, Clin. Nutr., Kyoto Univ. Sch. Med., 54

SOURCE: Shogoin Kawahara-cho, Sakyo-ku, Kyoto 606 Japan  
Metabolism Clinical and Experimental, (1994) Vol. 43, No. 11, pp. 1395-1400.  
ISSN: 0026-0495.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Using a whole-cell patch-clamp technique, voltage-dependent  $\text{Ca-2+}$ -channel activities were found to be increased in cultured single beta cells isolated from neonatally streptozocin-induced diabetic rats (NSZ rats). The current-voltage relationship and inactivation time course of  $\text{Ba-2+}$  currents via L-type  $\text{Ca-2+}$  channels were indistinguishable between NSZ and control rats. However, the current density observed in NSZ rats was significantly greater than that in control rats.  $\text{Ba-2+}$  currents via **T-type**  $\text{Ca-2+}$  channels were also found to be enhanced in NSZ beta cells. The insulin-secretory capacity of cultured **pancreatic** islets in response to a depolarizing stimulus (20  $\text{mmol/L}$  arginine or 30  $\text{mmol/L}$  KCl) in the presence of 11.1  $\text{mmol/L}$  glucose was augmented in NSZ rats, whereas that in response to 11.1 and 16.7  $\text{mmol/L}$  glucose alone was significantly reduced. It is concluded that the impaired insulinotropic action of glucose in beta cells in NSZ rats is

not

due to reduced activity of voltage-dependent  $\text{Ca-2+}$  channels. The fact

that

insulin secretion induced by a depolarizing stimulus was enhanced in NSZ rats may be related to the augmented activity of the voltage-dependent calcium current found in NSZ beta cells.

L11 ANSWER 12 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1993:521782 BIOSIS

DOCUMENT NUMBER: PREV199396135189

TITLE: Ascorbic acid modulation of calcium channels in **pancreatic** beta cells.

AUTHOR(S): Parsey, Ramin V.; Matteson, Donald R. (1)

CORPORATE SOURCE: (1) Dep. Biophys., Univ. Md. Sch. Med., 660 West Redwood St., Baltimore, MD 21201 USA

SOURCE: Journal of General Physiology, (1993) Vol. 102, No. 3, pp.



503-523.  
ISSN: 0022-1295.

DOCUMENT TYPE: Article  
LANGUAGE: English

AB We have studied the effect of ascorbic acid on voltage-dependent calcium channels in **pancreatic** beta cells. Using the whole-cell and perforated-patch variants of the patch clamp technique to record calcium tail currents, we have shown that the slowly deactivating (SD) **calcium channel**, which is similar to the **T-type** channel in other cells, is inhibited in a voltage-dependent manner by ascorbic acid (AA). The other channels that carry inward current

in beta cells, FD calcium channels and sodium channels, are unaffected by AA. Ascorbic acid causes a voltage-dependent decrease in the magnitude of the SD channel conductance which can be explained by the hypothesis that approx 50-60% of the channels have their voltage dependence shifted by approx 62 mV in the depolarizing direction. Thus, ascorbate appears to modify only a fraction of the SD channels. The activation kinetics of the ascorbate-modified channels are slower than control channels in a manner that is consistent with this hypothesis. Deactivation and inactivation kinetics are unaffected by ascorbate. These effects of ascorbate require metal ions, and it appears that some of the activity of ascorbate is due to a product of its metal catalyzed oxidation, perhaps dehydroascorbate.

L11 ANSWER 13 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1993:159625 BIOSIS

DOCUMENT NUMBER: PREV199344078425

TITLE: Two types of **calcium channel** in isolated human **pancreatic** beta-cells.

AUTHOR(S): Smith, Paul A.; Quayle, John

CORPORATE SOURCE: Univ. Lab. Physiol., Parks Rd., Oxford OX1 3PT UK

SOURCE: Journal of Physiology (Cambridge), (1993) Vol. 459, No. 0, pp. 238P.

Meeting Info.: Meeting of the Physiological Society

Oxford,

England, UK July 27-29, 1992

ISSN: 0022-3751.

DOCUMENT TYPE: Conference

LANGUAGE: English

L11 ANSWER 14 OF 24 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1990:196560 BIOSIS

DOCUMENT NUMBER: BA89:103231

TITLE: TWO TYPES OF **CALCIUM CHANNEL** IN RAT **PANCREATIC** BETA-CELLS.

AUTHOR(S): ASHCROFT F M; KELLY R P; SMITH P A

CORPORATE SOURCE: UNIV. LAB. PHYSIOL., PARKS RD., OXFORD OX1 3PT, UK.

SOURCE: PFLUEGERS ARCH EUR J PHYSIOL, (1990) 415 (4), 504-506.

CODEN: PFLABK. ISSN: 0031-6768.

FILE SEGMENT: BA; OLD

LANGUAGE: English

AB Ba currents flowing through single Ca-channels were recorded from cell-attached patches on rat **pancreatic** .beta.-cells. Two types of voltage-activated Ca-channels were found. The first (**T-type**) had a single channel conductance of 8 pS in 100 mM Ba, was activated at a low threshold (around -50mV) and inactivated by holding potentials positive to -40 mV. These properties are similar to those described for **T-type** channels in other preparations. The second type of Ca-channel (L-type) had a single channel conductance

of

20 pS in 100 mM Ba, was activated at a higher threshold (> -30m V),

showed

little inactivation during a 250 ms pulse and could be activated from a holding potential of -40m V. The dihydropyridine agonist BAYK 8644 selectively prolonged L-type Ca-channel openings. These properties are characteristic of L-type Ca-channels.



L11 ANSWER 15 OF 24 LIFESCI COPYRIGHT 2000 CSA

ACCESSION NUMBER: 94:94190 LIFESCI

TITLE: Ascorbic acid modulation of calcium channels in  
**pancreatic** beta cells

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CORPORATE SOURCE: Dep. Biophys., Univ. Maryland Sch. Med., 660 W. Redwood  
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SOURCE: J. GEN. PHYSIOL., (1993) vol. 102, no. 3, pp. 503-523.  
ISSN: 0022-1295.

DOCUMENT TYPE: Journal

FILE SEGMENT: T

LANGUAGE: English

SUMMARY LANGUAGE: English

AB We have studied the effect of ascorbic acid on voltage-dependent calcium channels in **pancreatic** beta cells. Using the whole-cell and perforated-patch variants of the patch clamp technique to record calcium tail currents, we have shown that the slowly deactivating (SD) **calcium channel**, which is similar to the **T-type** channel in other cells, is inhibited in a voltage-dependent manner by ascorbic acid (AA). The other channels that carry inward current

in beta cells, FD calcium channels and sodium channels, are unaffected by AA. Ascorbic acid causes a voltage-dependent decrease in the magnitude of the SD channel conductance which can be explained by the hypothesis that similar to 50-60% of the channels have their voltage dependence shifted by similar to 62 mV in the depolarizing direction. Thus, ascorbate appears to modify only a fraction of the SD channels. The activation kinetics of the ascorbate-modified channels are slower than control channels in a manner that is consistent with this hypothesis. Deactivation and inactivation kinetics are unaffected by ascorbate. These effects of ascorbate require metal ions, and it appears that some of the activity of ascorbate is due to a product of its metal catalyzed oxidation, perhaps dehydroascorbate.

L11 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1998:262994 CAPLUS

DOCUMENT NUMBER: 129:14620

TITLE: Voltage dependent calcium channels in adrenal glomerulosa cells and in insulin producing cells  
AUTHOR(S): Horvath, A.; Szabadkai, Gy.; Varnai, P.; Aranyi, T.;  
Wolheim, C. B.; Spat, A.; Enyedi, P.

CORPORATE SOURCE: Department of Physiology and Laboratory of Cellular and Molecular Physiology, Semmelweis University of Medicine, Budapest, H-1444, Hung.

SOURCE: Cell Calcium (1998), 23(1), 33-42  
CODEN: CECADV; ISSN: 0143-4160

PUBLISHER: Churchill Livingstone

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have examd. the structure and function of Ca<sup>2+</sup> channels in excitable endocrine cell types, in rat adrenal glomerulosa cells and in 2 insulin-producing cell types, the rat **pancreatic** .beta. cell and the INS-1 cell line. In previous studies on glomerulosa cells, we obsd. low (**T-type**) and high threshold (L-type) voltage-dependent Ca<sup>2+</sup> currents in addn. to a K<sup>+</sup>-induced inward rectifying

Ca<sup>2+</sup> current (I<sub>gl</sub>). .beta. Cells are known to exhibit T-, L-, and N-type currents. We have now found that INS-1 cells also show low threshold (**T-type**) and high threshold Ca<sup>2+</sup> currents. The latter was further resolved by org. inhibitors into L-type and P/Q-type currents and no I<sub>gl</sub> was detected. The expression of the pore-forming .alpha.1 subunit of voltage-dependent Ca<sup>2+</sup> channels was studied by means of reverse

transcription-PCR, followed by restriction enzyme mapping and/or sequencing. Both in glomerulosa and **pancreatic** .beta. cells,



the neuroendocrine (D) class of the .alpha.1 subunit, known to be responsible for L-type current, represents the majority of the PCR product. Comparable amts. of the neuroendocrine (D) and the neuronal A-type .alpha.1 subunits dominate the message in INS-1 cells. Different characteristics of Ca2+ currents in these cell types is discussed in view of the channel repertoire.

L11 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1997:552887 CAPLUS

DOCUMENT NUMBER: 127:229868

TITLE: **T-type** calcium channels facilitate insulin secretion by enhancing general excitability in

AUTHOR(S): the insulin-secreting .beta.-cell line, INS-1  
Bhattacharjee, Arin; Whitehurst, Richard M., Jr.;  
Zhang, Min; Wang, Lin; Li, Ming

CORPORATE SOURCE: Department Pharmacology, University South Alabama  
College Medicine, Mobile, AL, 36688, USA

SOURCE: Endocrinology (1997), 138(9), 3735-3740

CODEN: ENDOAO; ISSN: 0013-7227

PUBLISHER: Endocrine Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The present study addresses the function of **T-type** voltage-gated calcium channels in insulin-secreting cells. The authors used whole-cell voltage and current recordings, capacitance measurements, and RIA techniques to det. the contribution of **T-type** calcium channels in modulation of elec. activity and in stimulus-secretion coupling in a rat insulin secreting cell line, INS-1. By employing a double pulse protocol in the current-clamp mode, the authors found that activation of **T-type** calcium channels provided a low threshold depolarizing potential that decreased the latency of onset of action potentials and furthermore increased the frequency of action potentials, both of which are abolished by administration of nickel chloride (NiCl2), a selective **T-type calcium channel** blocker. Moreover application of high frequency stimulation, as compared with low frequency stimulation, caused a greater change in membrane capacitance (.DELTA.Cm), suggesting higher insulin secretion. The authors demonstrated that glucose stimulated insulin secretion in INS-1 is reduced dose dependently by NiCl2. The authors conclude that **T-type** calcium channels facilitate insulin secretion by enhancing the general excitability of these cells. In light of the pathol. effects of both hypo and hyperinsulinemia, the **T-type calcium channel** may be a therapeutic target.

L11 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1996:734585 CAPLUS

DOCUMENT NUMBER: 126:45814

TITLE: Abnormally expressed low-voltage-activated calcium channels in .beta.-cells from NOD mice and a related clonal cell line

AUTHOR(S): Wang, Lin; Bhattacharjee, Arin; Fu, Jian; Li, Ming

CORPORATE SOURCE: Dep. Pharm., Univ. South Alabama, Coll. Med., Mobile, AL, USA

SOURCE: Diabetes (1996), 45(12), 1678-1683

CODEN: DIAEAZ; ISSN: 0012-1797

PUBLISHER: American Diabetes Association, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A macroscopic low-voltage-activated (LVA) inward current was found in **pancreatic** .beta.-cells isolated from NOD mice. However, this current was not present in nondiabetic prone mouse (e.g., Swiss-Webster) **pancreatic** .beta.-cells. The authors performed pharmacol. analyses on this current in NOD insulinoma tumor cells (NIT-1). This cell





line was developed from **pancreatic .beta.-cells** of a transgenic NOD mouse. The sodium-channel blocker, tetrodotoxin (TTX; 2 .mu.mol/l) had no effect on this LVA current. The amplitudes of currents elicited by a -20 mV test pulse retained similarity when the extracellular sodium concn.; was increased from 0 to 115 mmol/l; when the extracellular calcium concn. was decreased from 10 to 2 mmol/l, there was an approx. 50% redn. of this current elicited by a -30 mV test pulse. Neither the L-type **calcium-channel** blocker, nifedipine (3 .mu.mol/l), nor the N-type **calcium-channel** blocker, .omega.-CgTx-GVIA (1 .mu.mol/l), at -30 mV produced an appreciable effect. The **T-type calcium-channel** blockers, nickel (3 .mu.mol/l) and amiloride (250 .mu.mol/l), effectively reduced the peak of this current. In 2 mmol/l calcium external soln., the threshold of voltage-dependent activation of this calcium current was approx. -65 mV, and the peak current occurred at -20 mV. Half-max. steady-state inactivation was around -43 mV. The mean time const. of slow deactivating tail currents generated by a preceding 20 mV pulse was 2.53 ms. The intracellular free calcium concn. was two- to threefold higher in NOD mouse **pancreatic .beta.-cells** compared with Swiss-Webster **pancreatic .beta.-cells**. This LVA **calcium channel** may be factorial to the high cytosolic free calcium concn. obsd. in these cells, and thereby may contribute to the pathogenesis of NOD mouse .beta.-cells.

L11 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1996:356007 CAPLUS

DOCUMENT NUMBER: 125:55238

TITLE: Alterations in basal and glucose-stimulated voltage-dependent Ca<sup>2+</sup> channel activities in **pancreatic .beta. cells** of non-insulin-dependent diabetes mellitus GK rats

AUTHOR(S): Kato, Seika; Ishida, Hitoshi; Tsuura, Yoshiyuki; Tsuji, Kazuo; Nishimura, Masayoshi; Horie, Minoru; Taminato, Tomohiko; Ikehara, Susumu; Odaka, Hiroyuki; et al.

CORPORATE SOURCE: Dep. of Metabolism and Clinical Nutrition, Kyoto Univ., Kyoto, 606-01, Japan

SOURCE: J. Clin. Invest. (1996), 97(11), 2417-2425  
CODEN: JCINAO; ISSN: 0021-9738

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In genetically occurring non-insulin-dependent diabetes mellitus (NIDDM) model rats (GK rats), the activities of L- and **T-type** Ca<sup>2+</sup> channels in **pancreatic .beta. cells** are augmented, by measuring the Ba<sup>2+</sup> currents via these channels using whole-cell patch-clamp technique, while the patterns of the current-voltage curves are indistinguishable. The hyper-responsiveness of insulin secretion to nonglucose depolarizing stimuli obsd. in NIDDM .beta. cells could be the result, therefore, of increased voltage-dependent Ca<sup>2+</sup> channel activity. Perforated patch-clamp recordings reveal that the augmentation of L-type Ca<sup>2+</sup> channel activity by glucose is markedly less pronounced in GK .beta. cells than in control .beta. cells, while glucose-induced augmentation of **T-type** Ca<sup>2+</sup> channel activity is obsd. neither in the control nor in the GK .beta. cells. This lack of glucose-induced augmentation of L-type Ca<sup>2+</sup> channel activity in GK .beta. cells might be causatively related to the selective impairment of glucose-induced insulin secretion in NIDDM .beta. cells, in conjunction with an insufficient plasma membrane depolarization due to impaired closure of the ATP-sensitive K<sup>+</sup> channels caused by the disturbed intercellular glucose metab. in NIDDM .beta. cells.

L11 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2000 ACS



ACCESSION NUMBER: 1995:293687 CAPLUS  
DOCUMENT NUMBER: 122:103057  
TITLE: Increase in Ca<sup>2+</sup> current in diabetic .beta. cells  
AUTHOR(S): Kato, Seigo; Ishida, Hitoshi; Seino, Yutaka  
CORPORATE SOURCE: Kyoto Univ., Kyoto, 606, Japan  
SOURCE: Diabetes Front. (1994), 5(5), 682  
CODEN: DIFREZ; ISSN: 0915-6593  
DOCUMENT TYPE: Journal  
LANGUAGE: Japanese

AB The no. of Ca<sup>2+</sup> channel was not increased in neonatally streptozotocin-induced diabetic (NSZ) rats, and increase in open probability and single channel conductance were suggested by measuring Ca<sup>2+</sup> channel of **pancreatic** .beta. cells using a patch clamp method. Insulin secretion induced by glucose stimulation decreased in NSZ, and depolarization-induced insulin secretion increased. Bell shape current-potential curve was obtained for L type Ca<sup>2+</sup> channel, and significant increment in current was obsd. under the depolarization conditions between -20 mV to +30 mV. **T type** Ca<sup>2+</sup> channel current also increased.

L11 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1994:698329 CAPLUS  
DOCUMENT NUMBER: 121:298329  
TITLE: Increased **calcium-channel** currents of **pancreatic** .beta. cells in neonatally streptozocin-induced diabetic rats  
AUTHOR(S): Kato, Seika; Ishida, Hitoshi; Tsuura, Yoshiyuki; Okamoto, Yoshimasa; Tsuji, Kazuo; Horie, Minoru; Okada, Yasunobu; Seino, Yutaka  
CORPORATE SOURCE: Sch. Med., Kyoto Univ., Kyoto, Japan  
SOURCE: Metab., Clin. Exp. (1994), 43(11), 1395-400  
CODEN: METAAJ; ISSN: 0026-0495  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Using a whole-cell patch-clamp technique, voltage-dependent Ca<sup>2+</sup>-channel activities were increased in cultured single .beta. cells isolated from neonatally streptozocin-induced diabetic rats (NSZ rats). The current-voltage relation and inactivation time course of Ba<sup>2+</sup> currents via L-type Ca<sup>2+</sup> channels were indistinguishable between NSZ and control rats. However, the c.d. obsd. in NSZ rats was significantly greater than that in control rats. Ba<sup>2+</sup> currents via **T-type** Ca<sup>2+</sup> channels were also enhanced in NSZ .beta. cells. The insulin-secretory capacity of cultured **pancreatic** islets in response to a depolarizing stimulus (20 mmol/L arginine or 30 mmol/L KCl) in the presence of 11.1 mmol/L glucose was augmented in NSZ rats, whereas that in response to 11.1 and 16.7 mmol/L glucose alone was significantly reduced. It is concluded that the impaired insulinotropic action of glucose in .beta. cells in NSZ rats is not due to reduced activity of voltage-dependent Ca<sup>2+</sup> channels. The fact that insulin secretion induced by a depolarizing stimulus was enhanced in NSZ rats may be related to the augmented activity of the voltage-dependent calcium current found in NSZ .beta. cells.

L11 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1994:159871 CAPLUS  
DOCUMENT NUMBER: 120:159871  
TITLE: Ascorbic acid modulation of calcium channels in **pancreatic** .beta. cells  
AUTHOR(S): Parsey, Ramin V.; Matteson, Donald R.  
CORPORATE SOURCE: Sch. Med., Univ. Maryland, Baltimore, MD, 21201, USA  
SOURCE: J. Gen. Physiol. (1993), 102(3), 503-23  
CODEN: JGPLAD; ISSN: 0022-1295  
DOCUMENT TYPE: Journal



LANGUAGE: English

AB The authors have studied the effect of ascorbic acid on voltage-dependent calcium channels in **pancreatic** .beta. cells. Using the whole-cell and perforated-patch variants of the patch clamp technique to record calcium tail currents, the authors have shown that the slowly deactivating (SD) **calcium channel**, which is similar to the **T-type** channel in other cells, is inhibited in a voltage-dependent manner by ascorbic acid (AA). The other channels that carry inward current in .beta. cells, FD calcium channels and sodium channels, are unaffected by AA. Ascorbic acid causes a voltage-dependent decrease in the magnitude of the SD channel conductance which can be explained by the hypothesis that .apprx. 50-60% of the channels have

their voltage dependence shifted by .apprx.62 mV in the depolarizing direction. Thus, ascorbate appears to modify only a fraction of the SD channels.

The activation kinetics of the ascorbate-modified channels are slower than control channels in a manner that is consistent with this hypothesis. Deactivation and inactivation kinetics are unaffected by ascorbate.

These effects of ascorbate require metal ions, and it appears that some of the activity of ascorbate is due to a product of its metal-catalyzed oxidn., perhaps dehydroascorbate.

L11 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1990:512870 CAPLUS

DOCUMENT NUMBER: 113:112870

TITLE: Single-channel recordings of two types of calcium channels in rat **pancreatic** .beta.-cells

AUTHOR(S): Sala, Salvador; Matteson, Donald R.

CORPORATE SOURCE: Sch. Med., Univ. Maryland, Baltimore, MD, 21201, USA

SOURCE: Biophys. J. (1990), 58(2), 567-71

CODEN: BIOJAU; ISSN: 0006-3495

DOCUMENT TYPE: Journal

LANGUAGE: English

AB By using the cell-attached configuration of the patch clamp technique, 2 different types of Ca channels were identified in rat **pancreatic** .beta.-cell membranes. The 2 channels differ in single channel conductance, voltage dependence, and inactivation properties. The single-channel conductance, measured with 100 mM Ba<sup>2+</sup> in the pipet, was 21.8 pS for the large channel and 6.4 pS for the small channel. The large-conductance channel is similar to the fast deactivating or L-type

Ca channel described in other preps. It is voltage dependent, has a threshold for activation around -30 mV, and can be activated from a holding potential of -40 mV. On the other hand, the small-conductance Ca channel is similar to the SD or **T type** Ca channel; it has a lower activation threshold, around -50 mV, and it can be inactivated by holding the membrane potential at -40 mV.

L11 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1990:212157 CAPLUS

DOCUMENT NUMBER: 112:212157

TITLE: Sensitivity to cadmium but resistance to nickel(2+) of

calcium(2+) inflow into rat **pancreatic** islets

AUTHOR(S): Plasman, P. O.; Hermann, M.; Herchuelz, A.; Lebrun, P.

CORPORATE SOURCE: Sch. Med., Brussels Free Univ., Brussels, B-1000, Belg.

SOURCE: Am. J. Physiol. (1990), 258(3, Pt. 1), E529-E533

CODEN: AJPHAP; ISSN: 0002-9513

DOCUMENT TYPE: Journal

LANGUAGE: English



AB The presence of different types [long lasting (L) and transient (T)] of active voltage-operated  $\text{Ca}^{2+}$  channels in islet cells was investigated by comparing the effects of  $\text{Cd}^{2+}$ ,  $\text{Ni}^{2+}$ , and 1,4-dihydropyridines on  $^{45}\text{Ca}$  uptake,  $^{45}\text{Ca}$  efflux, and insulin release in intact rat **pancreatic** islets. In several other excitable cells the L-channel has been shown to be modulated by 1,4-dihydropyridines and  $\text{Cd}^{2+}$ , whereas the T-channel was reported to be sensitive to  $\text{Ni}^{2+}$ . Nifedipine and  $\text{Cd}^{2+}$  inhibited whereas BAY K 8644 enhanced the glucose (11.1, 22.2 mM)-stimulated short-term  $^{45}\text{Ca}$  uptake,  $^{45}\text{Ca}$  efflux, and insulin release. In contrast, the stimulatory effects of glucose on  $^{45}\text{Ca}$  uptake,  $^{45}\text{Ca}$  efflux, and insulin release were unaffected by  $\text{Ni}^{2+}$ . These findings confirm that glucose provokes  $\text{Ca}^{2+}$  entry mainly by activating voltage-sensitive  $\text{Ca}^{2+}$  channels of the L-type and suggest that the B-cell plasma membrane is not equipped with active **T-type**  $\text{Ca}^{2+}$  channels.

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